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UTILITY PATENT APPLICATION TRANSMITTAL

(Only for new nonprovisional applications under 37 C.F.R. § 1.53(b))

Attorney Docket No. EPI-067191

First Inventor or Application Identifier Jonathan W. Nyce

Title LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE...

Express Mail Label No. EJ 664079305 US

APPLICATION ELEMENTS

See MPEP chapter 600 concerning utility patent application contents.

- * Fee Transmittal Form (e.g., PTO/SB/17)
(Submit an original and a duplicate for fee processing)
- Specification [Total Pages]
 - Descriptive title of the Invention
 - Cross References to Related Applications
 - Statement Regarding Fed sponsored R & D
 - Reference to Microfiche Appendix
 - Background of the Invention
 - Brief Summary of the Invention
 - Brief Description of the Drawings (if filed)
 - Detailed Description
 - Claim(s)
 - Abstract of the Disclosure
- Drawing(s) (35 U.S.C. 113) [Total Sheets]
- Oath or Declaration [Total Pages]
 - a. Newly executed (original or copy)
 - b. Copy from a prior application (37 C.F.R. § 1.63(d)) (for continuation/divisional with Box 16 completed)
 - i. DELETION OF INVENTOR(S)
Signed statement attached deleting inventor(s) named in the prior application, see 37 C.F.R. §§ 1.63(d)(2) and 1.33(b).

* NOTE FOR ITEMS 1 & 13: IN ORDER TO BE ENTITLED TO PAY SMALL ENTITY FEES, A SMALL ENTITY STATEMENT IS REQUIRED (37 C.F.R. § 1.27), EXCEPT IF ONE FILED IN A PRIOR APPLICATION IS RELIED UPON (37 C.F.R. § 1.28).

ADDRESS TO: Assistant Commissioner for Patents
Box Patent Application
Washington, DC 20231

- Microfiche Computer Program (Appendix)
- Nucleotide and/or Amino Acid Sequence Submission (if applicable, all necessary)
 - a. Computer Readable Copy
 - b. Paper Copy (identical to computer copy)
 - c. Statement verifying identity of above copies

ACCOMPANYING APPLICATION PARTS

- Assignment Papers (cover sheet & document(s))
- 37 C.F.R. § 3.73(b) Statement Power of (when there is an assignee) Attorney (2)
- English Translation Document (if applicable)
- Information Disclosure Statement (IDS)/PTO-1449 Copies of IDS Citations
- Preliminary Amendment
- Return Receipt Postcard (MPEP 503) (Should be specifically itemized)
 - * Small Entity Statement(s) Statement filed in prior application, (PTO/SB/09-12) Status still proper and desired
- Certified Copy of Priority Document(s) (if foreign priority is claimed)
- Other: checks, cover letter

16. If a CONTINUING APPLICATION, check appropriate box, and supply the requisite information below and in a preliminary amendment.

 Continuation Divisional Continuation-in-part (CIP) of prior application No: 60,127958

Prior application information: Examiner _____

Group / Art Unit: _____

For CONTINUATION or DIVISIONAL APPS only: The entire disclosure of the prior application, from which an oath or declaration is supplied under Box 4b, is considered a part of the disclosure of the accompanying continuation or divisional application and is hereby incorporated by reference. The incorporation can only be relied upon when a portion has been inadvertently omitted from the submitted application parts.

17. CORRESPONDENCE ADDRESS

<input type="checkbox"/> Customer Number or Bar Code Label	(Insert Customer No. or Attach bar code label here)				or <input checked="" type="checkbox"/> Correspondence address below
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Signature			Date APRIL 4, 2000

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SEQ. BOX

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of: : Appl. Ref.: EPI-067191
Nyce et al : Atty Ref.: 73999/01905
Appl. No: not yet assigned : Priority: US 60/127,958
Filing Date: herewith :

For: **LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE, COMPOSITIONS,
KIT & METHOD FOR TREATMENT OF AIRWAY DISORDERS
ASSOCIATED WITH BRONCHOCONTRICTION, LUNG
INFLAMMATION, ALLERGY(IES) & SURFACTANT DEPLETION**

COVER LETTER

Box: New Application

Assistant Commissioner of Patents & Trademarks
Washington, DC 20231

Sir\Madam:

Enclosed for filing are the following:

1. Utility Patent Application Transmittal Form
2. Fee Transmittal Form
3. Assignments (?) and Recordation form and \$40.00
4. U.S. Non-Provisional Patent Application
5. Sequence Listing, Declaration and diskette
6. IDS & 1449-PTO Form Listing References
7. Declarations (?)
8. Small Entity Status form
9. Postcard

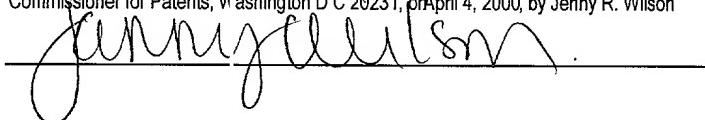
Respectfully submitted.
ARTER & HADDEN


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I hereby certify that this paper or fee is being deposited with the United States Postal Service via Express Mail service in an Express Mail Package under label No. EJ664079305US under 37 CFR 1.8 on the date indicated above and is addressed to the Assistant Commissioner for Patents, Washington D C 20231, on April 4, 2000, by Jenny R. Wilson



**VERIFIED STATEMENT (DECLARATION) CLAIMING SMALL ENTITY
STATUS (37 CFR 1.9(f) AND 1.27 (d)) - NONPROFIT ORGANIZATION**

Docket No.
P66 42161

Serial No. To Be Assigned	Filing Date Herewith	Patent No.	Issue Date

Applicant/ **Jonathan W. Nyce and W. James Metzger**

Patentee:

Invention:

Low Adenosine Anti-Sense Oligonucleotide, Compositions, Kit & Method for Treatment of Airway Disorders

Associated with Bronchoconstriction, Lung Inflammation, Allergy(ies) & Surfactant Depletion

I hereby declare that I am an official empowered to act on behalf of the nonprofit organization identified below:

NAME OF ORGANIZATION: **East Carolina University**

ADDRESS OF ORGANIZATION: **103 Spilman Building**

Greenville, North Carolina 27858

DRAFTED BY
SUSAN M. SPILMAN
SPILMAN PATENT
AND TRADEMARK
OFFICE, INC.

TYPE OF NONPROFIT ORGANIZATION:

- University or other Institute of Higher Education
- Tax Exempt under Internal Revenue Service Code (26 U.S.C. 501(a) and 501(c)(3))
- Nonprofit Scientific or Educational under Statute of State of The United States of America

Name of State:	Citation of Statute:
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- Would Qualify as Tax Exempt under Internal Revenue Service Code (26 U.S.C. 501(a) and 501(c)(3)) if Located in The United States of America
- Would Qualify as Nonprofit Scientific or Educational under Statute of State of The United States of America if Located in The United States of America

Name of State:	Citation of Statute:
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I hereby declare that the above-identified nonprofit organization qualifies as a nonprofit organization as defined in 37 C.F.R. 1.9(e) for purposes of paying reduced fees to the United States Patent and Trademark Office regarding the invention described in:

- the specification to be filed herewith.
- the application identified above.
- the patent identified above.

I hereby declare that rights under contract or law have been conveyed to and remain with the nonprofit organization with regard to the above identified invention.

If the rights held by the above-identified nonprofit organization are not exclusive, each individual, concern or organization having rights to the invention is listed on the next page and no rights to the invention are held by any person, other than the inventor, who could not qualify as an independent inventor under 37 CFR 1.9(c) or by any concern which would not qualify as a small business concern under 37 CFR 1.9(d) or a nonprofit organization under 37 CFR 1.9(e).

Each person, concern or organization to which I have assigned, granted, conveyed, or licensed or am under an obligation under contract or law to assign, grant, convey, or license any rights in the invention is listed below:

- no such person, concern or organization exists.
- each such person, concern or organization is listed below.

FULL NAME _____

ADDRESS _____

Individual Small Business Concern Nonprofit Organization

FULL NAME _____

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Individual Small Business Concern Nonprofit Organization

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Individual Small Business Concern Nonprofit Organization

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Individual Small Business Concern Nonprofit Organization

Separate verified statements are required from each named person, concern or organization having rights to the invention averring to their status as small entities. (37 CFR 1.27)

I acknowledge the duty to file, in this application or patent, notification of any change in status resulting in loss of entitlement to small entity status prior to paying, or at the time of paying, the earliest of the issue fee or any maintenance fee due after the date on which status as a small entity is no longer appropriate. (37 CFR 1.28(b))

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application, any patent issuing thereon, or any patent to which this verified statement is directed.

NAME OF PERSON SIGNING: Richard R. Eakin

TITLE IN ORGANIZATION: Chancellor

ADDRESS OF PERSON SIGNING: East Carolina University
103 Spilman Building
Greenville, North Carolina 27858

SIGNATURE: Richard R. Eakin DATE: 4/21/99

**LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE, COMPOSITIONS, KIT
& METHOD FOR TREATMENT OF AIRWAY DISORDERS ASSOCIATED
WITH BRONCHOCONSTRICION, LUNG INFLAMMATION,
ALLERGY(IES) & SURFACTANT DEPLETION**

5

BACKGROUND OF THE INVENTION

Field of the Invention

This patent relates to a composition comprising oligonucleotides (oligos) that are anti-sense to adenosine receptors, and contain low amounts of or no adenosine (A). These agents are suitable for the treatment, among others, of pulmonary diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. Examples of these diseases are allergies, asthma, impeded respiration, allergic rhinitis, pain, cystic fibrosis, and cancers such as leukemias, e.g. colon cancer, and the like. The present agent may be administered prophylactically or therapeutically in conjunction with other therapies, or may be utilized as a substitute for therapies that have significant, negative side effects.

15 **Background of the Invention**

Respiratory ailments, associated with a variety of diseases and conditions, are extremely common in the general population, and more so in certain ethnic groups, such as African Americans. In some cases they are accompanied by inflammation, which aggravates the condition of the lungs. Asthma, for example, is one of the most common diseases in industrialized countries. In the United States it accounts for about 20 1% of all health care costs. An alarming increase in both the prevalence and mortality of asthma over the past decade has been reported, and asthma is predicted to be the preeminent occupational lung disease in the next decade. While the increasing mortality of asthma in industrialized countries could be attributable to the depletion reliance upon beta agonists in the treatment of this disease, the underlying causes of asthma remain poorly understood.

25 Adenosine may constitute an important mediator in the lung for various diseases, including bronchial asthma. Its potential role was suggested by the finding that asthmatics respond favorably to aerosolized adenosine with marked bronchoconstriction whereas normal individuals do not. An asthmatic rabbit animal model, the dust mite allergic rabbit model for human asthma, responded in a similar fashion to aerosolized adenosine with marked bronchoconstriction whereas non-asthmatic rabbits showed no 30 response. More recent work with this animal model suggested that adenosine-induced bronchoconstriction and bronchial hyperresponsiveness in asthma may be mediated primarily through the stimulation of adenosine receptors. Adenosine has also been shown to cause adverse effects, including death, when administered therapeutically for other diseases and conditions in subjects with previously undiagnosed hyper reactive airways.

35 A handful of medicaments have been available for the treatment of respiratory diseases and conditions, although in general they all have limitations. Theophylline, an important drug in the treatment of asthma, is a known adenosine receptor antagonist which was reported to eliminate adenosine-mediated bronchoconstriction in asthmatic rabbits. A selective adenosine A₁ receptor antagonist, 8-cyclopentyl-1, 3-dipropylxanthine (DPCPX) was also reported to inhibit adenosine-mediated bronchoconstriction and 40 bronchial hyperresponsiveness in allergic rabbits. The therapeutic and preventative applications of currently available adenosine A₁ receptor-specific antagonists are, nevertheless, limited by their toxicity. Theophylline, for example, has been widely used in the treatment of asthma, but is associated with frequent, significant toxicity resulting from its narrow therapeutic dose range. DPCPX is far too toxic to be useful clinically. The fact that, despite decades of extensive research, no specific adenosine receptor 45 antagonist is available for clinical use attests to the general toxicity of these agents. Anti-sense oligonucleotides have received considerable theoretical consideration as potential useful pharmacological agents in human disease. Their practical application in actual models of human disease, however, has been somewhat elusive. One important impediment to their effective application has been a difficulty in finding

an appropriate route of administration to deliver them to their site of action. Many in vivo experiments were conducted by administering anti-sense oligonucleotides directly to specific regions of the brain. These applications, however, necessarily have limited clinical utility due to their invasive nature. Although anti-sense oligonucleotides have received considerable theoretical consideration for their potential use as pharmacological agents in human disease, finding practical and effective applications for these agents in actual models of human disease, however, have been few and far between, particularly because they had to be administered in large doses. Another important consideration in the pharmacologic application of these molecules is their route of administration. Many in vivo applications have involved the direct administration of anti-sense oligonucleotides to limited regions of the brain. Such applications, however, have limited clinical utility due to their invasive nature. The systemic administration of anti-sense oligonucleotides as pharmacological agents has been found to have also significant problems, not the least of which being an inherent difficulty in targeting disease-involved tissues. That is, the necessary dilution of the anti-sense oligonucleotide in the circulatory system makes extremely difficult to attain a therapeutic dose at the target tissue by intravenous or oral administration. The bioavailability of orally administered anti-sense oligonucleotides is very low, of the order of less than about 5%. Anti-sense oligonucleotides have been used in therapy by many, including the present inventor, who in his previous work successfully treated various diseases and conditions by direct administration of these agents to the lung. In many instances, other workers have had to face the difficulties associated with the delivery of DNA molecules to a desired target. Thus, the route of administration may be of extreme importance for treating generalized diseases and conditions as well as those which are localized. In contrast, up to the present time, the delivery of anti-sense agents to the lung has been relatively undeveloped. As described by the present inventor in more detail below, the lung is an excellent target for the direct administration of anti-sense oligonucleotides and provides a non-invasive and a tissue-specific route.

Clearly, there exist presently no effective therapies for treating these ailments, or at least no therapies which are effective and devoid of significant detrimental side effects. Accordingly, there is still a need for an agent for the treatment of adenosine mediated ailments afflicting the pulmonary and respiratory ailments affecting the lung airways, including respiratory problems, bronchoconstriction, inflammation, allergy(ies), depletion or hyposecretion of surfactant, etc., which is highly effective and sufficiently selective to avoid detrimental side effects produced by other therapies. In addition, there is a definite need for making available a delivery method that will require low amounts of therapeutic agents and will be effective for the rapid and targeted access of tissue genes of mRNAs and the reversal of untoward effects afflicting a subject.

SUMMARY OF THE INVENTION

The present invention generally relates to a pharmaceutical or veterinary composition, comprising an anti-sense oligonucleotide(s) (oligo(s)) which is (are) effective for alleviating bronchoconstriction and/or lung inflammation, allergy(ies), and/or surfactant depletion and/or hyposecretion, when administered to a mammal, the oligo containing about 0 to about 15% adenosine (A) and being anti-sense to a target selected from the group consisting of the initiation codon, the coding region, the 5'-end and the 3'-end genomic flanking regions, the 5' and 3' intron-exon junctions, and regions within 2 to 10 nucleotides of the junctions of a gene encoding a target polypeptide associated with lung airway dysfunction or anti-sense to the polypeptide mRNA; combinations of the oligos; and mixtures of the oligos; and a pharmaceutically or veterinarily acceptable carrier or diluent. The targets are typically molecules associated with airway disease, cancer, etc., such as transcription factors, stimulating and activating peptide factors, cytokines, cytokine receptors, chemokines, chemokine receptors, adenosine receptors, bradykinin receptors, endogenously produced specific and non-specific enzymes, immunoglobulins and antibodies, antibody receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, adhesion molecules, defensins, growth factors, vasoactive peptides and receptors, binding proteins, and malignancy associated proteins, among others. Examples are oligo(s) targeted to adenosine receptor(s) and it(they) are typically

present in the composition in an amount effective to reduce adenosine mediated effect(s), such as airway obstruction, inflammation, allergy(ies), and surfactant depletion, among others. The adenosine receptor is preferably selected from the group consisting of the adenosine A₁, A_{2b}, and A₃ receptors, and in some instances even adenosine A_{2a} receptors. The oligo of the invention may be applied to the preparation of a medicament for (a) reducing adenosine-mediated bronchoconstriction, impeded respiration, inflammation, allergy(ies), depletion production of surfactant, and other detrimental pulmonary effects in a subject in need of treatment, and/or for (b) treating specific diseases and conditions such as asthma, cystic fibrosis, allergic rhinitis, COPD, etc. For the first time this invention provides the targeted administration of one or more oligonucleotides directly into the respiratory system. The oligos may be directed to any target and are intended for fast delivery through the mucosal tissue of the lungs for hybridization to a desired target polynucleotide, e. g. mRNA, to prevent gene transcription and translation, such that protein expression will be reduced, hampered, or completely stopped. Thus, this invention also provides a more general method for administering oligonucleotides that are anti-sense to targeted genes and mRNAs associated with any type of diseases, by direct administration into the respiratory system, e. g. by inhalation, by introduction of a solution or aerosol into the respiratory airways, and/or directly into the lung.

The present oligos, moreover, are suitable for reducing effects mediated by a variety of target proteins and genes, for example adenosine-mediated effects, including pulmonary, respiratory, and other associated effects, e. g. bronchoconstriction, inflammation, immune mediated reactions, allergy(ies) and other airway problems, which may be caused by different conditions, including cancer. Examples of diseases and conditions, which may be treated preventatively, prophylactically and therapeutically with the agent of this invention, are pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary disease (COPD), bronchitis, and cancers such as leukemias, lymphomas, carcinomas, and the like, e.g. colon cancer, breast cancer, lung cancer, pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, etc., as well as all types of cancers which may metastasize or have metastasized to the lung(s), including breast and prostate cancer. The present agents are also suitable for administration before, during and after other treatments, including radiation, chemotherapy, antibody therapy, phototherapy and cancer, and other types of surgery. The present agent is effectively administered prophylactically and therapeutically in conjunction with other therapies, or by itself for conditions without known therapies or as a substitute for therapies that have significant negative side effects. The oligo(s) may be administered by any means known to a subject, e. g. to the lungs of the subject, more generally through any and all systemic and topical routes. This oligonucleotide(s) (oligo(s)) employed are anti-sense to a target DNA or RNA, e. g. an adenosine receptor DNA or RNA, and preferably consist essentially of up to about 15% adenosine (A), and more preferably contain no adenosine. The oligos are provided in the form of specific compositions and formulations, with a carrier or diluent, and optionally with other therapeutic agents and additives which are used for administration by specific routes, e.g. into the respiratory system, topically, transdermally, parenterally, by implantation, and the like. The oligo is also provided as a capsule or cartridge, and in the form of a kit. The oligos of the invention may be produced by selection of specific targeted segments of the gene or mRNA encoding the adenosine receptor as described below. In one preferred embodiment, the selection is made to obtain oligos that consist essentially of less than about 15% adenosine (A). This may be done by selecting the target as done above, which includes genes, genomic flanking regions, RNAs and polypeptide associated with an ailment afflicting the lung airways, obtaining the sequence of a mRNA(s) corresponding to the target gene(s) and/or their genomic flanking region(s) and/or the juxtap-membrane regions thereof, and mRNA(s) encoding the target polypeptide(s), selecting at least one segment of the mRNA(s), and synthesizing one or more anti-sense oligonucleotide(s) to the selected mRNA segment(s), and substituting, if necessary, an alternative, e. g. a universal base(s) or other base(s) for one or more A to reduce the proportion of A present in the oligonucleotide to less than about 15%, and down to no adenosine. Similarly, alternative and/or universal bases may be substituted for adenosine, e. g. specific

adenosine A1, A2b and A3 receptor antagonists or A2a receptor agonists, theophylline, enprophylline, and many other adenosine receptor antagonists known in the art as well as agonists with significantly reduced agonist activity with respect to adenosine, e. g. less than 0.5%, less than 0.3%, and the like.

The invention will now be described in general in conceptual and experimental terms, with reference to specific examples. Other objects, advantages and features of the present invention will become apparent to those skilled in the art from the description that follows.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

This invention arose from a desire by the inventor to improve on prior art treatments for pulmonary and other diseases, which technology is generally fraught with detrimental side effects and by the need of administering high doses of therapeutical agents. The present invention arises from the inventor's own discovery that adenosine receptor targeted anti-sense oligonucleotides (oligos) may be utilized therapeutically in the treatment of diseases or conditions which impair respiration, cause inflammation and/or allergy(ies), constrict bronchial tissue, obstruct the lung airways, depletion surfactant secretion, or otherwise impede normal breathing. In general, many diseases and conditions are associated with or cause inflammation, constrict bronchial tissue or the lung airways, depletion secretion of surfactant, augment allergy(ies), or otherwise impede normal breathing. This treatment is selective for specific targets associated with or mediating these symptoms, and the agents are administered in up to 1000-fold lower doses than those seen in the art. The inventor, in addition, wanted to provide a treatment which would improve the outcome and life style of patients undergoing other procedures or being administered other therapies, including antibody therapy, chemotherapy, radiation, phototherapy, and surgery e.g. cancer surgery, and that could be effectively administered preventatively, prophylactically or therapeutically. He reasoned that he could further improve on this discovery by selecting oligos of reduced adenosine content, or reducing the adenosine content of otherwise targeted anti-sense oligos corresponding to endogenous polynucleotide sequences. The present invention is premised on the discovery by the inventor that oligonucleotides are metabolized in vivo to their mononucleotides. Adenosine (A)-containing oligonucleotides break down and release adenosine which, in turn, activates adenosine receptors, thereby causing bronchoconstriction, inflammation, surfactant depletion, allergy(ies), and the like. He, thus, conceived of employing low adenosine-free adenosine oligos to avoid these side effects upon their administration. He succeeded in this endeavor and is providing in this patent novel and improved compositions, formulations and methods which afford greatly improved results when compared with previously known treatments for preventing and alleviating bronchoconstriction, allergy(ies), inflammation, breathing difficulties, surfactant depletion and blockage of airways, as well as for other conditions which affect the lung directly or indirectly. In different embodiments, one or more nucleic acids of the invention may be formulated alone, and/or with one or more surfactant components and/or with a carrier, and/or with other therapeutic agents and/or formulation agents known in the art. The compositions of this invention, thus, may be incorporated into a variety of formulations for systemic and topical administration. Moreover, the inventor also provides a broad method for delivery of anti-sense oligonucleotides (oligos) through the respiratory system, as a fast means of starting treatment to address acute attacks of asthma and other diseases and conditions that have a rapid onset. In addition, the present agents have long half-lives and may be administered at very low doses. This makes them ideal for once a week type therapies. In the past, anti-sense oligonucleotides received considerable theoretical consideration as being potentially useful as pharmacologic agents for the treatment of human disease. Wagner, R., Nature 372: 333-335 (1994). However, it has been difficult to actually apply these molecules to alleviating and curing human diseases. One important consideration in the pharmacologic application of these molecules has been the failure of various routes of administration to deliver the compounds to its target while avoiding invading the circulation and, therefore, other untargeted tissues which, thus, produces a plethora of side effects. Most in vivo experiments utilizing anti-sense oligonucleotides involved a direct application of the oligo to limited regions of the brain. See, Wahlestedt, C., Trends in Pharmacol. Sci. 15: 42-46 (1994); Lai, .. et al., Neuroreport 5: 1049-1052 (1994); Standifer, K., et al., Neuron 12: 805-810

(1994); Akabayashi, A., et al., Brain Res. 21: 55-61 (1994). Others applied them into the spinal fluid. See, e.g. Tseng, L., et al., European J. Pharmacol. 258: R1-3 (1994); Raffa, R., et al., European J. Pharmacol. 258: R5-7 (1994); Gillardon, F., et al., European J. Neurosci. 6: 880-884 (1994). Such applications, clearly, have no practical clinical utility due to their invasive nature. Thus, the systemic administration of 5 anti-sense oligonucleotides poses significant problems with respect to their pharmacologic application, not the least of which is the difficulty in selectively targeting disease-involved tissues. The systemic administration of anti-sense oligonucleotides also poses significant problems with respect to their pharmacologic application, not the least of which is the difficulty in selectively targeting disease-involved tissues.

10 The respiratory system, and in particular the lung, as the ultimate port of entry into the organism, however, is an excellent route of administration for anti-sense oligonucleotides. This is so not only for the treatment of lung disease, but also when utilizing the lung as a means for delivery, particularly because of its non-invasive and tissue-specific nature. Thus, local delivery of antisense oligonucleotides directly to the target tissue enables the therapeutic use of these compounds. Fomivirsen (ISIS 2302) is an example of 15 a local drug delivery into the eye to treat cytomegalovirus (CMV) retinitis, for which a new drug application has been filed by ISIS. The administration of a drug through the lung offers the further advantage that inhalation is non-invasive whereas direct injection into the vitreous of the eye is invasive. The composition and formulations of this invention are highly efficacious for preventing and treating diseases and conditions associated with bronchoconstriction, difficult breathing, impeded and obstructed 20 lung airways, allergy(ies), inflammation and surfactant depletion, among others. Examples of diseases and conditions which are suitably treated by the present method are diseases and conditions, including Acute Respiratory Distress Syndrome (ARDS), asthma, adenosine administration e.g. in the treatment of SupraVentricular Tachycardia (SVT) and other arrhythmias, and in stress tests to hyper-sensitized individuals, ischemia, renal damage or failure induced by certain drugs, infantile respiratory distress 25 syndrome, pain, cystic fibrosis, pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary disease (COPD), lung transplantation rejection, pulmonary infections, and cancers such as leukemias, lymphomas, carcinomas, and the like, including colon cancer, breast cancer, lung cancer, pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, etc., as well as all types of cancers which may metastasize or have metastasized to the lung(s), including breast and 30 prostate cancer. The invention will be described with respect to the adenosine receptors as targets, but is similarly applicable to any other target with respect to the pulmonary administration of anti-sense oligos. The examples provided below show a complete inhibition of such adenosine receptor associated symptoms in a rabbit model for human bronchoconstriction, allergy(ies) and inflammation as well as the elimination of the ability of the adenosine receptor agonist par excellence, adenosine, to cause bronchoconstriction in 35 hyper-responsive monkeys, which are animal models for human hyper-responsiveness to adenosine receptor agonists. The pharmaceutical composition and formulations of the invention, therefore, are suitable for preventing and alleviating the symptoms associated with stimulation of adenosine receptors, such as the adenosine A₁ receptors. The compositions and formulations of this invention, thus, are also suitable for prevent the untoward side effects of adenosine-mediated hyperresponsiveness in certain 40 individuals, which are generally seen in diseases affecting respiratory activity.

The method of the present invention may be used to treat airway diseases and conditions in a subject of any kind and for any reason, with the intention that the adenosine content of anti-sense compounds be minimized, reduced or eliminated so as to prevent its liberation upon anti-sense degradation. Examples of diseases and conditions, which may be treated preventatively, prophylactically and therapeutically with the compositions and formulations of this invention, are pulmonary vasoconstriction, 45 inflammation, allergies, asthma, allergic rhinitis, impeded respiration, Acute Respiratory Distress Syndrome (ARDS), renal damage and failure associated with ischemia as well as the administration of certain drugs, side effects associated with adenosine administration e.g. in SupraVentricular Tachycardia (SVT) and in adenosine stress tests, infantile Respiratory Distress Syndrome (infantile RDS), ARDS, pain,

cystic fibrosis, pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary disease (COPD), lung transplantation rejection, pulmonary infections, and cancers such as leukemias, lymphomas, carcinomas, and the like, e.g. colon cancer, breast cancer, lung cancer, pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma, metastatic cancer such as hepatic metastases, 5 lung, breast and prostate metastases, among others. The present compositions and formulations are suitable for administration before, during and after other treatments, including radiation, chemotherapy, antibody therapy, phototherapy and cancer, and other types of surgery. The present compositions and formulations may also be administered effectively as a substitute for therapies that have significant negative side effects. The terms "anti-sense" oligonucleotides generally refers to small, synthetic oligonucleotides, 10 resembling single-stranded DNA, which in this patent are applied to the inhibition of gene expression by inhibition of a target messenger RNA (mRNA). See, Milligan, J. F. et al., J. Med. Chem. 36(14), 1923-1937 (1993), the relevant portion of which is hereby incorporated in its entirety by reference. For consistency's sake, all RNAs and oligonucleotides are represented in this patent by a single strand in the 5' to 3' direction, when read from left to right, although their complementary sequence(s) is (are) also 15 encompassed within the four corners of the invention. In addition, all nucleotide bases and amino acids are represented utilizing the recommendations of the IUPAC-IUB Biochemical Nomenclature Commission, or by the known 3-letter code (for amino acids). Nucleotide sequences are presented herein by single strand only, in the 5' to 3' direction, from left to right. In addition, nucleotide and amino acids are represented herein in the manner recommended by the IUPAC-IUB Biochemical Nomenclature Commission, or (for 20 amino acids) by three letter code, in accordance with 37 CFR 1.822 and established usage. See, e.g., PatentIn User Manual, 99-102 (Nov. 1990) (U.S. Patent and Trademark Office, Office of the Assistant Commissioner for Patents, Washington, D.C. 20231); U.S. Patent No. 4,871,670 to Hudson et al. at col. 3, lines 20-43. The present method utilizes anti-sense agents to inhibit or down-regulate gene expression of target genes, including those listed in Tables 1 and 2 below. This is generally attained by hybridization of 25 the anti-sense oligonucleotides to coding (sense) sequences of a targeted messenger RNA (mRNA), as is known in the art. The exogenously administered agents of the invention decrease the levels of mRNA and protein encoded by the target gene and/or cause changes in the growth characteristics or shapes of the thus treated cells. See, Milligan et al. (1993); Helene, C. and Toulme, J. Biochim. Biophys. Acta 1049, 99-125 (1990); Cohen, J. S. D., Ed., Oligodeoxynucleotides as Anti-sense Inhibitors of Gene Expression; CRC 30 Press: Boca Raton, FL (1987), the relevant portion of which is hereby incorporated in its entirety by reference. As used herein, "anti-sense oligonucleotide or anti-sense oligo" is generally a short sequence of 35 synthetic nucleotide that (1) hybridizes to any segment of a mRNA encoding a targeted protein under appropriate hybridization conditions, and which (2) upon hybridization causes a decrease in gene expression of the targeted protein. The terms "desAdenosine" (desA) and "des-thymidine" (desT) refer to oligonucleotides substantially lacking either adenosine (desA) or thymidine (desT). In some instances, the des A or des T sequences are naturally occurring, and in others they may result from substitution of an undesirable nucleotide (A) by another lacking its undesirable activity, such as acting as an agonist or having a triggering effect at the adenosine A receptor(s). In the present context, the substitution is generally accomplished by substitution of A with a "universal or alternative base", presently known in the art or to be 40 ascertained at a later time. As used herein, the terms "prevent", "preventing", "treat" or "treating" refer to a preventative, prophylactic, maintenance, or therapeutic treatment which decreases the likelihood that the subject administered such treatment will manifest symptoms associated with adenosine receptor stimulation. The term "down-regulate" refers to inducing a decrease in production, secretion or availability and, thus, a decrease in concentration, of intracellular target product, be it a receptor e.g. adenosine A₁, 45 A_{2a}, A_{2b}, A₃, bradykinin 2B, GATA-3, or other receptors, or an increase in concentration of the adenosine A_{2a} receptor. The present technology relies on the design of anti-sense oligos targeted to mRNAs associated with ailments involving lung airway pathology(ies), and on their modification to reduce the occurrence of undesirable side effects caused by their release of adenosine upon breakdown, while preserving their activity and efficacy for their intended purpose. In this manner, the inventor targets a specific gene to

design one or more anti-sense oligonucleotide(s) (oligos) that selectively bind(s) to the corresponding mRNA, and then reduces, if necessary, their content of adenosine via substitution with an alternative or a universal base, or an adenosine analog incapable of significantly, or having substantially reduced ability for, activating or antagonizing adenosine A₁, A_{2a} or A₃ receptors or which may act as an agonist at the adenosine A_{2a} receptor. Any number of adenosines present may be substituted by an alternative and/or universal base, such as heteroaromatic bases, which binds to a thymidine base but has less than about 0.3 of the adenosine base agonist or antagonist activity at the adenosine A₁, A_{2a}, A_{2b} and A₃ receptors. Based on his prior experience in the field, the inventor reasoned that in addition to "downregulating" specific genes, he could increase the effect of the agent(s) administered by either selecting segments of RNA that are devoid, or have a low content, of thymidine (T) or, alternatively, substitute one or more adenosine(s) present in the designed oligonucleotide(s) with other nucleotide bases, so called universal bases, which bind to thymidine but lack the ability to activate adenosine receptors and otherwise exercise the constricting effect of adenosine in the lungs, etc. Given that adenosine (A) is a nucleotide base complementary to thymidine (T), when a T appears in the RNA, the anti-sense oligo will have an A at the same position.

In one aspect of this invention, the anti-sense oligonucleotide has a sequence which specifically binds to a portion or segment of a mRNA molecule which encodes a protein associated with impeded breathing, allergy(ies), lung inflammation, depletion of lung surfactant or lowering of lung surfactant, airway obstruction, bronchitis, and the like. One effect of this binding is to reduce or even prevent the translation of the corresponding mRNA and, thereby, reduce the available amount of target protein in the subject= lung. In one preferred embodiment of this invention, the phosphodiester residues of the anti-sense oligonucleotide are modified or substituted. Chemical analogs of oligonucleotides with modified or substituted phosphodiester residues, e.g., to the methylphosphonate, the phosphotriester, the phosphorothioate, the phosphorodithioate, or the phosphoramidate, α = methoxy ethyl and similar modifications, which increase the in vivo stability of the oligonucleotide are particularly preferred. The naturally occurring phosphodiester linkages of oligonucleotides are susceptible to some degree of degradation by cellular nucleases. Many of the residues proposed herein, on the contrary, are highly resistant to nuclease degradation. See, Milligan et al.; Cohen, J. S. D., supra. In another preferred embodiment of the invention, the oligonucleotides may be protected from degradation by adding a "3'-end cap" by which nuclease-resistant linkages are substituted for phosphodiester linkages at the 3' end of the oligonucleotide. See Tidd, D. M. and Warenius, H.M., Be. J. Cancer 60: 343-350 (1989); Shaw, J.P. et al., Nucleic Acids Res. 19: 747-750 (1991), the relevant section of which are incorporated in their entireties herein by reference. Phosphoramidates, phosphorothioates, and methylphosphonate linkages all function adequately in this manner for the purposes of this invention, as do α' modifications, such as α' methoxy ethyl, and the like. The more extensive the modification of the phosphodiester backbone the more stable the resulting agent, and in many instances the higher their RNA affinity and cellular permeation. See, Milligan, et al., supra. In addition, a plurality of substitutions to the carbohydrate ring are also known to improve stability of nucleic acids. Thus, the number of residues which may be modified or substituted will vary depending on the need, target, and route of administration, and may be from 1 to all the residues, to any number in between. Many different methods for replacing the entire phosphodiester backbone with novel linkages are known. See, Millikan et al, supra. Preferred backbone analogue residues include phosphoramidate, phosphorothioate, methylphosphonate, phosphotriester, phosphotriester, thioformacetal, phosphorodithioate, phosphoramidate, formacetal, triformacetal, thioether, carbamate, boranophosphate, 3'-thioformacetal, 5'-thioether, carbonate, C₅-substituted nucleotides, 5'-N-carbamate, sulfate, sulfonate, sulfamate, sulfonamide, sulfone, sulfite, 2'-O methyl, sulfoxide, sulfide, hydroxylamine, methylene(methylimino) (MMI), methoxymethyl (MOM), and methoxyethyl(MOE), and methyleneoxy(methylimino) (MOMI) residues, and combinations thereof. Phosphorothioate and methylphosphonate-modified oligonucleotides are particularly preferred due to their availability through automated oligonucleotide synthesis. See, Millikan et al, supra. Where appropriate, the agent of this

invention may be administered in the form of their pharmaceutically acceptable salts, or as a mixture of the anti-sense oligonucleotide and its salt. In another embodiment of this invention, a mixture of different anti-sense oligonucleotides or their pharmaceutically acceptable salts is administered. A single agent of this invention has the capacity to attenuate the expression of a target mRNA and/or various agents to enhance or attenuate the activity of a pathway. By means of example, the present method may be practiced by identifying all possible deoxyribonucleotide segments which are low in thymidine (T) or deoxynucleotide segments low in adenosine (A) of about 7 or more mononucleotides, preferably up to about 60 mononucleotides, more preferably about 10 to about 36 mononucleotides, and still more preferably about 12 to about 21 mononucleotides, in a target mRNA or a gene, respectively. This may be attained by searching for mono nucleotide segments within a target sequence which are low in, or lack thymidine (RNA), a nucleotide which is complementary to adenosine, or that are low in adenosine (gene), that are 7 or more nucleotides long. In most cases, this search typically results in about 10 to 30 such sequences, i.e. naturally lacking or having less than about 40% adenosine, anti-sense oligonucleotides of varying lengths for a typical target mRNA of average length, i.e., about 1800 nucleotides long. Those with high content of T or A, respectively, may be fixed by substitution of a universal base for one or more As. The agent(s) of this invention may be of any suitable length, including but not limited to, about 7 to about 60 nucleotides long, preferably about 12 to about 45, more preferably up to about 30 nucleotides long, and still more preferably up to about 21, although they may be of other lengths as well, depending on the particular target and the mode of delivery. The agent(s) of the invention may be directed to any and all segments of a target RNA. One preferred group of agent(s) includes those directed to an mRNA region containing a junction between an intron and an exon. Where the agent is directed to an intron/exon junction, it may either entirely overlie the junction or it may be sufficiently close to the junction to inhibit the splicing-out of the intervening exon during processing of precursor mRNA to mature mRNA, e.g. with the 3' or 5' terminus of the anti-sense oligonucleotide being positioned within about, for example, within about 2 to 10, preferably about 3 to 5, nucleotide of the intron/exon junction. Also preferred are anti-sense oligonucleotides which overlap the initiation codon, and those near the 5' and 3' termini of the coding region. The flanking regions of the exons may also be targeted as well as the spliced segments in the precursor mRNAs. The mRNA sequences of the adenosine receptors and of many other targets are derived from the DNA base sequence of the gene expressing either receptors, e. g. the adenosine receptors, the enzymes, factors, or other targets associated with airway disease. For example, the sequence of the genomic human A₁ adenosine receptor is known and is disclosed in U.S. Patent No. 5,320,963 to Stiles, G., et al. The A₃ adenosine receptor has been cloned, sequenced and expressed in rat (see, Zhou, F., et al., P.N.A.S. (USA) 89: 7432 (1992)) and human (see, Jacobson, M. A., et al., U.K. Patent Application No. 9304582.1 (1993)). The sequence of the adenosine A_{2b} receptor gene is also known. See, Salvatore, C. A., Luneau, C. J., Johnson, R. G. and Jacobson, M., Genomics (1995), the relevant portion of which is hereby incorporated in its entirety by reference. The sequences of many of the remaining exemplary target genes are also known. See, GenBank, NIH. The sequences of those genes whose sequences are not yet available may be obtained by isolating the target segments applying technology known in the art. Once the sequence of the gene, its RNA and/or the protein are known, an anti-sense oligonucleotides may be produced according to this invention as described above to reduce the production of the targeted protein in accordance with standard techniques. The sequences for the adenosine A_{2a} bradykinin, and other genes as well as methods for preparation of oligonucleotides are also known as those of many other target genes and mRNAs for which this invention is suitable. Thus, anti-sense oligonucleotides that downregulate the production of target sequences associated with airway disease, including the adenosine A₁, A_{2a}, A_{2b}, A₃, bradykinin, GATA-3, COX-2, and many other receptors, may be produced in accordance with standard techniques. Examples of diseases and conditions which are suitably treated by the present method are diseases and conditions, including Acute Respiratory Distress Syndrome (ARDS), asthma, adenosine administration e.g. in the treatment of SupraVentricular Tachycardia (SVT) and other arrhythmias, and in stress tests to hyper-sensitized individuals, ischemia, renal damage or failure induced by certain drugs, infantile respiratory distress

syndrome, pain, cystic fibrosis, pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, and cancers such as leukemias, lymphomas, carcinomas, and the like, including colon cancer, breast cancer, lung cancer, pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, etc., as well as all types of cancers which may metastasize or have metastasized to the lung(s), including breast and prostate cancer.

The adenosine receptors discussed above are mere examples of the high power of the inventors technology. In fact, a large number of genes may be targeted in a similar manner by the present agent(s), to reduce or down-regulate protein expression. By means of example, if the target disease or condition is one associated with impeded or reduced breathing, bronchoconstriction, chronic bronchitis, pulmonary bronchoconstriction and/or hypertension, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, allergy, asthma, cystic fibrosis, respiratory distress syndrome, cancers, which either directly or by metastasis afflict the lung, the present method may be applied to a list of potential target mRNAs, which includes the targets listed in Table 1 and Table 2 below, among others. The anti-sense agent(s) of the invention have a low A content to prevent its liberation upon in vivo degradation of the agent(s). For example, if the system is the pulmonary or respiratory system, a large number of genes is involved in different functions, including those listed in Table 1 below.

Table 1: Pulmonary Disease or Condition Pulmonary and Inflammation Targets

Nf6B Transcription Factor	Interleukin-8 Receptor (IL-8 R)
20 Interleukin-5 Receptor (IL-5R)	Interleukin-4 Receptor (IL-4R)
Interleukin-3 Receptor (IL-3R)	Interleukin-1 β (IL-1 β)
Interleukin-1 β Receptor (IL-1 β R)	Eotaxin
Tryptase	Major Basic Protein
β 2-adrenergic Receptor Kinase	Endothelin Receptor A
25 Endothelin Receptor B	Preproendothelin
Bradykinin B2 Receptor (B2BR)	IgE (High Affinity Receptor)
Interleukin-1 (IL-1)	Interleukin 1 Receptor (IL-1 R)
Interleukin-9 (IL-9)	Interleukin-9 Receptor (IL-9 R)
Interleukin-11 (IL-11)	Interleukin-11 Receptor (IL-11 R)
30 Inducible Nitric Oxide Synthase	Cyclooxygenase (COX)
Intracellular Adhesive Molecule 1 (ICAM-1)	Vascular Cellular Adhesion Molecule (VCAM)
Substance P	Endothelial Leukocyte Adhesion Molecule Endothelin ETA (ELAM-1)
Rantes	GM-CSF, Endothelin-1
Receptor	Neutrophil Chemotactic Factor
35 Cyclooxygenase-2 (COX-2)	Defensin 1,2,3
Monocyte Activating Factor	Platelet Activating Factor
Neutrophil Elastase	5-lipoxygenase
Muscarinic Acetylcholine Receptors	Substance P
Tumor Necrosis Factor α	Histamine Receptor
40 Phosphodiesterase IV	CCR-1 CC Chemokine Receptor
Substance P Receptor	Interleukin-4 (IL-4)
Chymase	Interleukin-5 (IL-5)
Interleukin-2 (IL-2)	Interleukin-7 (IL-7)
Interleukin-12 (IL-12)	Interleukin-12 Receptor (IL-12R)
45 Interleukin-6 (IL-6)	Interleukin-1 (IL-1)
Interleukin-8 (IL-8)	Interleukin-14
Interleukin-7 Receptor (IL-7R)	CCR-3 CC Chemokine Receptor
Interleukin-14 Receptor (IL-14R)	CCR-5 CC Chemokine Receptor
50 CCR-2 CC Chemokine Receptor	GATA-3 Transcription Factor
CCR-4 CC Chemokine Receptor	MAP Kinase
Prostanoid Receptors	Interleukin-15 Receptor (IL-15R)
Neutrophil Adherence Receptor	
Interleukin-15 (IL-15)	

	Interleukin-11 (IL-11)	Interleukin-11 Receptor (IL-11R)
	NFAT Transcription Factors	STAT 4
	MIP-1 α	MCP-2
	MCP-3	MCP-4
5	Cyclophilin (A, B, etc.)	Phospholipase A2
	Basic Fibroblast Growth Factor	Metalloproteinase
	CSBP/p38 MAP Kinase	Tryptase Receptor
	PDG2	Interleukin-3 (IL-3)
	Interleukin-10 (IL-10)	Cyclosporin A - Binding Protein
10	FK506-Binding Protein	$\alpha 4\beta 1$ Selectin
	Fibronectin	$\alpha 4\beta 7$ Selectin

Table 1: Pulmonary Disease or Condition Pulmonary and Inflammation Targets

	cMad CAM-1	LFA-1 (CD11a/CD18)
	PECAM-1	LFA-1 Selectin
15	C3bi	PSGL-1
	E-Selectin	P-Selectin
	CD-34	L-Selectin
	p150,95	Mac-1 (CD11b/CD18)
	Fucosyl transferase	VLA-4
20	STAT-1	STAT-2
	CD-18/CD11a	CD11b/CD18
	ICAM2 and ICAM3	C5a
	CCR3 (Eotaxin Receptor)	CCR1, CCR2, CCR4, CCR5
	LTB-4	AP-1 Transcription Factor
25	Protein kinase C	Cysteinyl Leukotriene Receptor
	Tachykinin Receptors (tach R)	I6B Kinase 1 & 2
	Interleukin-2 Receptor (IL-2R)	(e.g., Substance P, NK-1 & NK-3 Receptors)
	STAT 6	c-mas
	NF-Interleukin-6 (NF-IL-6)	Interleukin-10 Receptor (IL-10R)
30	Interleukin-3 (IL-3)	Interleukin-2 Receptor (IL-2R)
	Interleukin-13 (IL-13)	Interleukin-12 Receptor (IL-12R)
	Interleukin-14 (IL-14)	Interleukin-6 Receptor (IL-6R)
	Interleukin-16 (IL-16)	Interleukin-13 Receptor (IL-13R)
	Medullasin	Interleukin-16 Receptor (IL-16R)
35	Adenosine A ₁ Receptor (A ₁ R)	Tryptase-I
	Adenosine A _{2b} Receptor (A _{2b} R)	Adenosine A ₃ Receptor (A ₃ R)
	β Tryptase	STAT-3
	Adenosine A _{2a} Receptor (A _{2a} R)	IgE Receptor β Subunit (IgE R β)
	Fc-epsilon receptor CD23 antigen	IgE Receptor α Subunit (IgE R α)
40	IgE Receptor Fc Epsilon Receptor (IgERFc ξ R)	Substance P Receptor
	Histidine decarboxylase	Tryptase-1
	Prostaglandin D Synthase	Eosinophil Cationic Protein
	Eosinophil Derived Neurotoxin	Eosinophil Peroxidase
	Endothelial Nitric Oxide Synthase	Endothelial Monocyte Activating Factor
45	Neutrophil Oxidase Factor	Cathepsin G
	Macrophage Inflammatory Protein-1-	Interleukin-8 Receptor α Subunit (IL-8 R α)
	Alpha/Rantes Receptor	Endothelin Receptor ET-B

These genes, and others, are involved in the normal functioning of respiration as well as in diseases associated with respiratory pathologies, including cystic fibrosis, asthma, pulmonary hypertension and vasoconstriction, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, chronic bronchitis, respiratory distress syndrome (ARDS), allergic rhinitis, lung cancer and lung metastatic cancers and other airway diseases, including those with inflammatory response.

Anti-sense oligos to the target receptors, e. g. the adenosine A₁, A_{2a}, A_{2b}, and A₃ receptors, CCR3 (chemokine receptors), bradykinin 2B, CAM (vascular cell adhesion molecule), and eosinophil receptors,

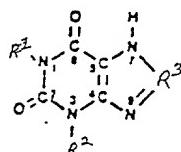
among others, have been shown to be effective in down-regulating the expression of their genes. Some of these act to alleviate the symptoms or reduce respiratory ailments and/or inflammation, for example, by "down regulation" of the adenosine A₁, A_{2a}, A_{2b}, and/or A₃ receptors and CCR3, bradykinin 2B, VCAM (vascular cell adhesion molecule) and eosinophil receptors. These agents may be utilized by the present method alone or in conjunction with anti-sense oligos targeted to other genes to validate pathway and/or networks in which they are involved. For better results, the oligos are preferably administered directly into the respiratory system, e.g., by inhalation or other means, of the experimental animal, so that they may reach the lungs without widespread systemic dissemination. This permits the use of low agent doses as compared with those administered systemically or by other generalized routes and, consequently, reduces the number and degree of undesirable side effects resulting from the agent=s widespread distribution in the body. The agent(s) of this invention has (have) been shown to reduce the amount of receptor protein expressed by the tissue. These agents, thus, rather than merely interacting with their targets, e.g. a receptor, lower the number of target proteins that other drugs may interact with. In this manner, the present agent(s) afford(s) extremely high efficacy with low toxicity. Anti-sense oligonucleotides to the A₁ , A_{2b}, A₃, bradykinin B2, GATA-3, CAM (vascular cell adhesion molecule), eosinophil receptors, and COX-2 receptors, among others, have been shown to be effective in the down-regulation of the respective receptor proteins in the cell. One novel feature of this treatment, as compared to traditional treatments for adenosine-mediated bronchoconstriction, is that administration is direct to the lungs, or in situ to other tissues, organs or systems of the body. Additionally, a receptor protein itself is reduced in amount, rather than merely interacting with a drug, and toxicity is reduced. Other proteins that may be targeted with anti-sense agents for the treatment of lung conditions include, but are not limited to: CCR3 (chemokine) receptors, human A₂, adenosine receptor, human A_{2b} adenosine receptor, human IgE receptor β, human Fc-epsilon receptor CD23 antigen, human histidine decarboxylase, human beta tryptase, human tryptase-I, human prostaglandin D synthase, human cyclooxygenase-2, human eosinophil cationic protein, human eosinophil derived neurotoxin, human eosinophil peroxidase, human intercellular adhesion molecule-1 (ICAM-1), human vascular cell adhesion molecule-1 (VCAM-1), human endothelial leukocyte adhesion molecule-1 (ELAM 1), human P selectin, human endothelial monocyte activating factor, human IL-3, human IL-4, human IL-5, human IL-6, human IL-8, human monocyte-derived neutrophil chemotactic factor, human neutrophil elastase, human neutrophil oxidase factor, human cathepsin G, human defensin 1, human defensin 3, human macrophage inflammatory protein-1-alpha, human muscarinic acetylcholine receptor HM3, human fibronectin, human GM-CSF, human tumor necrosis factor α, human leukotriene C4 synthase, human major basic protein, and human endothelin 1. Although not intended to be exclusive, a more extensive list of genes is provided below. Some of these act to alleviate the symptoms or reduce respiratory ailments and/or inflammation, for example, by "down regulation" of the adenosine A₁, A_{2a}, A_{2b}, and/or A₃ receptors and CCR3, bradykinin 2B, VCAM (vascular cell adhesion molecule) and eosinophil receptors. These agents are preferably administered directly into the respiratory system, e.g., by inhalation or other means, so that they may reach the lungs without widespread systemic dissemination. This permits the use of substantially lower doses of the agent of the invention as compared with those administered by the prior art, systemically or by other generalized routes and, consequently, reduce undesirable side effects resulting from the agent=s widespread distribution in the body. The agent(s) of this invention has (have) been shown to reduce the amount of receptor protein expressed by the tissue. These agents, thus, rather than merely interacting with their targets, e.g. a receptor, lower the number of target proteins that other drugs may interact with. In this manner, the present agent(s) afford(s) extremely high efficacy with low toxicity. In these latter targets, and in target genes in general, it is particularly imperative to eliminate or reduce the adenosine content of the corresponding anti-sense oligonucleotide to prevent their breakdown products from liberating adenosine.

As used herein, the term "treat" or "treating" asthma refers to a treatment which decreases the likelihood that the subject administered such treatment will manifest symptoms of the lung disease. The term "downregulate" refers to inducing a decrease in production, secretion or availability (and thus a

decrease in concentration) of the targeted intracellular protein. The present invention is concerned primarily with the treatment of human subjects. However, the agents and methods disclosed here may also be employed for veterinary purposes, such as is the case in the treatment of other mammals, such as cattle, horses, wild animals, zoo animals, and domestic animals, e. g. dogs and cats. Targeted proteins are preferably mammalian and more preferably of the same species as the subject being treated. In general, "anti-sense" refers to the use of small, synthetic oligonucleotides, resembling single-stranded DNA, to inhibit gene expression by inhibiting the function of the target messenger RNA (mRNA). Milligan, J. F. et al., J. Med. Chem. 36(14), 1923-1937 (1993). In the present invention, inhibition of gene expression of the A₁ or A₃ adenosine receptor is desired. Gene expression is inhibited through hybridization to coding (sense) sequences in a specific messenger RNA (mRNA) target by hydrogen bonding according to Watson-Crick base pairing rules. The mechanism of anti-sense inhibition is that the exogenously applied oligonucleotides decrease the mRNA and protein levels of the target gene or cause changes in the growth characteristics or shapes of the cells. Id. See, also Helene, C. and Toulme, J., Biochim. Biophys. Acta 1049, 99-125 (1990); Cohen, J. S. D., Ed., Oligodeoxynucleotides as Anti-sense Inhibitors of Gene Expression; CRC Press: Boca Raton, FL (1987). As used herein, "anti-sense oligonucleotide" is defined as a short sequence of synthetic nucleotide that (1) hybridizes to any coding sequence in an mRNA which codes for the targeted protein, according to hybridization conditions described below, and (2) upon hybridization causes a decrease in gene expression of the A₁ or A₃ adenosine receptor. The receptors discussed above are mere examples of the high power of the present technology. In fact, a large number of genes may be targeted in a similar manner by practicing the present methods, to significantly down-regulate or obliterate protein expression and observe any changes wrought to one or more functions within a system, e.g. the respiratory system and other lung disease associated targets. By means of example, in the respiratory system, the targets may be associated with difficulties of breathing, bronchoconstriction, inflammation, allergic rhinitis, chronic bronchitis, surfactant depletion, and others associated with diseases and conditions such as chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, inhalation burns, Acute Respiratory Distress Syndrome (ARDS), cystic fibrosis, pulmonary fibrosis, radiation pulmonitis, tonsilitis, emphysema, dental pain, oral inflammation, joint pain, esophagitis, cancers afflicting the respiratory system either directly such as lung cancer, esophageal cancer, and the like, or indirectly by means of metastases, among others. These functions are of great interest because of their association with respiratory dysfunction, as is the case in asthma, allergies, allergic rhinitis, pulmonary bronchoconstriction and hypertension, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, allergy, asthma, cystic fibrosis (CF), Acute Respiratory Distress Syndrome (ARDS) as well as infantile and pregnancy-related RDS, cancer, etc., which either directly or by metastasis afflict the lung, the present anti-sense oligonucleotides may be directed to a list of target mRNAs, which includes the targets listed in Table 1 above, among others.

The oligos of this invention may be obtained by first selecting fragments of a target nucleic acid having at least 4 contiguous nucleic acids selected from the group consisting of G and C and/or having a specific type and/or extent of activity, and then obtaining a first oligonucleotide 4 to 60 nucleotides long which comprises the selected fragment and has a thymidine (T) nucleic acid content of up to and including about 15%, preferably, about 12%, about 10%, about 7%, about 5%, about 3%, about 1%, and more preferably no thymidine. The latter step may be conducted by obtaining a second oligonucleotide 4 to 60 nucleotides long comprising a sequence which is anti-sense to the selected fragment, the second oligonucleotide having an adenosine base content of up to and including about 15%, preferably about 12%, about 10%, about 7%, about 5%, about 3%, about 1%, and more preferably no adenosine. When the selected fragment comprises at least one thymidine base, an adenosine base may be substituted in the corresponding anti-sense nucleotide fragment with a universal base selected from the group consisting of heteroaromatic bases which bind to a thymidine base but have less than about 10%, preferably less than about 1%, and more preferably less than about 0.3% of the adenosine base agonist activity at the adenosine A₁, A_{2a}, A_{2b} and A₃ receptors, and heteroaromatic bases which have no activity at the adenosine

A_{2a} receptor, when validating in the respiratory system. Other adenosine activities in other systems may be determined in other systems, as appropriate. The analogue heteroaromatic bases may be selected from all pyrimidines and purines, which may be substituted by O, halo, NH₂, SH, SO, SO₂, SO₃, COOH and branched and fused primary and secondary amino, alkyl, alkenyl, alkynyl, cycloalkyl, heterocycloalkyl, 5 aryl, heteroaryl, alkoxy, alkenoxy, acyl, cycloacyl, arylacyl, alkynoxy, cycloalkoxy, aroyl, arylthio, arylsulfoxy, halocycloalkyl, alkylcycloalkyl, alkenylcycloalkyl, alkynylcycloalkyl, haloaryl, alkylaryl, alkenylaryl, alkynyl aryl, arylalkyl, arylalkenyl, arylalkynyl, arylcycloalkyl, which may be further substituted by O, halo, NH₂, primary, secondary and tertiary amine, SH, SO, SO₂, SO₃, cycloalkyl, 10 heterocycloalkyl and heteroaryl. The pyrimidines and purines may be substituted at all positions as is known in the art, but preferred are those which are substituted at positions 1, 2, 3, 4, 7 and/or 8. More preferred are pyrimidines and purines such as theophylline, caffeine, dyphylline, etophylline, acephylline piperazine, bamifylline, enprofylline and xantine having the chemical formula



wherein R¹ and R² are independently H, alkyl, alkenyl or alkynyl and R³ is H, aryl, dicycloalkyl, 15 dicycloalkenyl, dicycloalkynyl, cycloalkyl, cycloalkenyl, cycloalkynyl, O-cycloalkyl, O-cycloalkenyl, O-cycloalkynyl, NH₂-alkylamino-ketoxyalkyloxy-aryl, mono and dialkylaminoalkyl-N-alkylamino-SO₂aryl, among others. Similar modifications in the sugar are also embodiments of this invention. Reduced adenine content of the anti-sense oligos corresponding to the thymidines (T) present in the target RNA serves to prevent the breakdown of the oligos into products that free adenine into the system, e.g. the lung, brain, heart, kidney, etc., tissue environment and, thereby, to prevent any unwanted effects due to it. 20 By means of example, the Nf6B transcription factor may be selected as a target, and its mRNA or DNA searched for low thymidine (T) or deoxymidine (desT) fragments. Only desT segments of the mRNA or DNA are selected which, in turn, will produce desA anti-sense as their complementary strand. When a number of RNA desT segments are found, the sequence of the anti-sense segments may be deduced. Typically, about 10 to 30 and even larger numbers of desA anti-sense sequences may be obtained. These 25 anti-sense sequences may include some or all desA anti-sense oligonucleotide sequences corresponding to desT segments of the mRNA of the target, such as anyone of those shown in Table 1 above, in Table 2 below, and others associated with functions of the brain, cardiovascular and renal systems, and many others. When this occurs, the anti-sense oligonucleotides found are said to be 100% A-free. For each of the original desA anti-sense oligonucleotide sequences corresponding to the target gene, e.g. the NF6B 30 transcription factor, typically about 10 to 30 sequences may be found within the target gene or RNA which have a low content of thymidine (RNA). In accordance with this invention, the selected fragment sequences may also contain a small number of thymidine (RNA) nucleotides within the secondary or tertiary or quaternary sequences. In some cases, a large adenine content may suffice to render the anti-sense oligonucleotide less active or even inactive against the target. In accordance with this invention, 35 these so called "non-fully desA" sequences may preferably have a content of adenine of less than about 15%, about 12%, about 10%, about 7%, about 5%, and about 2% adenine. Most preferred is no adenine content (0%). In some instances, however, a higher content of adenine is acceptable and the oligonucleotides still fail to show detrimental "adenine activity". A particular important embodiment is that where the adenine nucleotide is "fixed" or replaced by a "Universal or alternative" base that may 40 base-pair with similar or equal affinity to two or more of the four nucleotide present in natural DNA: A, G, C, and T.

A universal or alternative base is defined in this patent as any compound, more commonly an

adenosine analogue, which has substantial capacity to hybridize to thymidine, while at the same time having reduced, or substantially lacking, ability to bind adenosine receptors or other molecules through which adenosine may exert an undesirable side effect in the experimental animal or in a cell system. Alternatively, adenosine analogs which completely fail to activate, or have significantly reduce ability for activating, adenosine receptors, such as the adenosine A₁, A_{2b} and/or A₃ receptors, most preferably A₁ receptors, and those that may even act as agonists of the adenosine A_{2a}, receptor, may be used. One example of a universal base is α -deoxyribofuranosyl-(5-nitroindole), and an artisan will know how to select others. This "fixing" step generates further novel sequences, different from those anti-sense to the ones found in nature, that permits the anti-sense oligonucleotide to bind, preferably equally well, with the target RNA. Other examples of universal or alternative bases are 2-deoxyribosyl-(5-nitroindole). Other examples of universal bases are 3 - nitropyrrole - 2' - deoxynucleoside, 5 - nitro-indole, 2 - deoxyribosyl - (5 - nitroindole), 2'-deoxyribofuranosyl - (5-nitroindole), 2' - deoxyinosine, 2' -deoxynebularine, 6H, 8H-3,4-dihydropyrimido [4, 5 - c] oxazine - 7 - one and 2 - amino - 6 -methoxy aminopurine. In addition to the above, Universal bases which may be substituted for any other base although with somewhat reduced hybridization potential, include 3 - nitropyrrole 2' - deoxynucleoside 2 - deoxyribofuranosyl - (5 - nitroindole), 2' - deoxyinosine and 2' - deoxynebularine (Glen Research, Sterling, VA). More specific mismatch repairs may be made using "P" nucleotide, 6H, 8H - 3, 4 - dihydropyrimido [4,5 - c] [1, 2] oxazin - 7 - one, which base pairs with either guanine (G) or adenine (A) and "K" nucleotide, 2 - amino - 6 - methoxyaminopurine, which base pairs with either cytidine (C) or thymidine (T), among others. Others which are known in the art or will become available are also suitable. See, for example, Loakes, D. and Brown, D. M., Nucl. Acids Res. 22:4039-4043 (1994); Ohtsuka, E. et al., J. Biol. Chem. 260(5):2605-2608 (1985); Lin, P.K.T. and Brown, D. M., Nucleic Acids Res. 20(19):5149-5152 (1992; Nichols, R. et al., Nature 369(6480): 492-493 (1994); Rahmon , M. S. and Humayun, N. Z., Mutation Research 377 (2): 263-8 (1997); Amosova, O., et al., Nucleic Acids Res. 25 (!0): 1930-1934 (1997); Loakes D. & Brown, D. M., Nucleic Acids Res. 22 (20): 4039-4043 (1994), the entire sections relating to universal bases and their preparation and use in nucleic acid binding being incorporated herein by reference. When non-fully desT sequences are found in the naturally occurring target, they typically are selected so that about 1 to 3 universal base substitutions will suffice to obtain a 100% "desA" anti-sense oligonucleotide. Thus, the present method provides either anti-sense oligonucleotides to different targets which are low in, or devoid of, A content, as well as anti-sense oligonucleotides where one or more adenosine nucleotides, e. g. about 1 to 3, or more, may be "fixed" by replacement with a "Universal" or "replacement" base. Universal bases are known in the art and need not be listed herein. An artisan will know which bases may act as universal bases, and replace them for A. Table 2 below provides a selected number of targets to which the agents of the invention are effectively applied. Others, however, may also be targeted.

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Table 2:

<u>Transforming Oncogenes</u>	<u>Cancer Targets</u>
ras	thymidylate synthetase
src	thymidylate synthetase
myc	dihydrofolate reductase
bcl 2	thymidine kinase
	deoxycytidine kinase
	ribonucleotide reductase
Angiogenesis factors	Adhesion Molecules
Oncogenes	Folate Pathway Enzymes
DNA repair genes	(One Carbon Pool)
	Telomerase
	HMG CoA Reductase
	Farnesyl Transferase
	Glucose-6-Phosphate Transferase

A group of preferred targets for the treatment of cancer are genes associated with any of different types of cancers, or those generally known to be associated with malignancies, whether they are regulatory or involved in the production of RNA and/or proteins. Examples are transforming oncogenes, including, but not limited to, ras, src, myc, and BCL-2, among others. Other targets are those to which present cancer chemotherapeutic agents are directed to, such as various enzymes, primarily, although not exclusively, thymidylate synthetase, dihydrofolate reductase, thymidine kinase, deoxycytidine kinase, ribonucleotide reductase, and the like. The present technology is particularly useful in the treatment of cancer ailments given that traditional cancer therapies are fraught with the unresolved problem of selectively killing cancer cells while preserving normal living cells from the devastating effects of treatments such as chemotherapy, 5 radiotherapy, and the like. The present technology provides the ability of selectively attenuating or enhancing a desired pathway or target. This approach provides a significant advantage over standard treatments of cancer because it permits the selection of a pathway, including primary, secondary and possibly tertiary targets, which are not generally expressed simultaneously in normal cells. Thus, the present agent may be administered to a subject to cause a selective increase in toxicity within tumor cells 10 that, for instance, express all three targets while normal cells that may express only one or two of the targets will be significantly less affected or even spared. A group of preferred targets for the treatment of cancers are genes associated with different types of cancers, or those generally known to be associated with malignancies, whether they are regulatory or involved in the production of RNA and/or proteins. Examples are transforming oncogenes, including, but not limited to, ras, src, myc, and BCL-2, among others. Other 15 targets are those to which present cancer chemotherapeutic agents are directed to, such as various enzymes, primarily, although not exclusively, thymidylate synthetase, dihydrofolate reductase, thymidine kinase, deoxycytidine kinase, ribonucleotide reductase, and the like.

In one embodiment, at least one of the mRNAs to which the oligo of the invention is targeted encodes a protein such as transcription factors, stimulating and activating factors, intracellular and 20 extracellular receptors and peptide transmitters in general, interleukins, interleukin receptors, chemokines, chemokine receptors, endogenously produced specific and non-specific enzymes, immunoglobulins, antibody receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, adhesion molecules, defensines, growth factors, vasoactive peptides and receptors, and binding proteins, among others; or the mRNA is corresponding to an oncogene and other genes associated with various diseases or conditions. Examples of target proteins are eotaxin, major basic protein, preproendothelin, eosinophil cationic protein, P-selectin, STAT 4, MIP-1 α , MCP-2, MCP-3, MCP-4, STAT 6, c-mas, NF-IL-6, cyclophilins, PDG2, cyclosporin A-binding protein, FK5-binding protein, fibronectin, LFA-1 (CD11a/CD18), PECAM-1, C3bi, PSGL-1, CD-34, substance P, p150,95, Mac-1 (CD11b/CD18), VLA-4, CD-18/CD11a, CD11b/CD18, C5a, 25 CCR1, CCR2, CCR4, CCR5, and LTB-4, among others. Others are, however, suitable, as well. In another embodiment, at least one of the mRNAs to which the oligo is targeted encodes intracellular and extracellular receptors and peptide transmitters such as sympathomimetic receptors, parasympathetic receptors, GABA receptors, adenosine receptors, bradykinin receptors, insulin receptors, glucagon receptors, prostaglandin receptors, thyroid receptors, androgen receptors, anabolic receptors, estrogen receptors, progesterone receptors, receptors associated with the coagulation cascade, adrenohypophyseal 30 receptors, adrenohypophyseal peptide transmitters, and histamine receptors (HisR), among others. However others are also contemplated. The encoded sympathomimetic receptors and parasympathomimetic receptors include acetylcholinesterase receptors (AcChaseR) acetylcholine receptors (AcChR), atropine receptors, muscarinic receptors, epinephrine receptors (EpiR), dopamine receptors (DOPAR), and norepinephrine receptors (NEpiR), among others. Further examples of encoded receptors are adenosine A₁ receptor, adenosine A_{2B} receptor, adenosine A₃ receptor, endothelin receptor A, endothelin receptor B, IgE high affinity receptor; muscarinic acetylcholine receptors, substance P receptor, histamine receptor, CCR-1 CC chemokine receptor, CCR-2 CC chemokine receptor, CCR-3 CC chemokine receptor (Eotaxin Receptor), interleukin-1 β receptor (IL-1 β R), interleukin-1 receptor (IL-1R), interleukin-1 β receptor (IL-40 45

1 β R), interleukin-3 receptor (IL-3R), CCR-4 CC chemokine receptor, cysteinyl leukotriene receptors, prostanoid receptors, GATA-3 transcription factor receptor, interleukin-1 receptor (IL-1R), interleukin-4 receptor (IL-4R), interleukin-5 receptor (IL-5R), interleukin-8 receptor (IL-8R), interleukin-9 receptor (IL-9R), interleukin-11 receptor (IL-11R), bradykinin B2 receptor, sympathomimetic receptors, parasympathomimetic receptors, GABA receptors, adenosine receptors, bradykinin receptors, insulin receptors, glucagon receptors, prostaglandin receptors, thyroid receptors, androgen receptors, anabolic receptors, estrogen receptors, progesterone receptors, receptors associated with the coagulation cascade, adrenohypophyseal receptors, and histamine receptors (HisR). Others are also contemplated even though not listed herein. The encoded enzymes for development of the oligos of the invention include synthetases, kinases, oxidases, phosphatases, reductases, polysaccharide, triglyceride, and protein hydrolases, esterases, elastases, and , polysaccharide, triglyceride, lipid, and protein synthases, among others. Examples of target enzymes are tryptase, inducible nitric oxide synthase, cyclooxygenase (Cox), MAP kinase, eosinophil peroxidase, β 2-adrenergic receptor kinase, leukotriene c-4 synthase, 5-lipoxygenase, phosphodiesterase IV, metalloproteinase, tryptase, CSBP/p38 MAP kinase, neutrophil elastase, phospholipase A₂, cyclooxygenase 2 (Cox-2), fucosyl transferase, chymase, protein kinase C, thymidylate synthetase, dihydrofolate reductase, thymidine kinase, deoxycytidine kinase, and ribonucleotide reductase, among others. Any enzyme associated with a disease or condition, however, is suitable as a target for this invention. Suitable encoded factors for application of this invention are, among others, Nf6B transcription factor, granulocyte macrophage colony stimulating factor (GM-CSF), AP-1 transcription factor, GATA-3 transcription factor, monocyte activating factor, neutrophil chemotactic factor, granulocyte/macrophage colony-stimulating-factor (G-CSF), NFAT transcription factors, platelet activating factor, tumor necrosis factor α (TNF α), and basic fibroblast growth factor (BFGF). Additional factors are also within the invention even though not specifically mentioned. Suitable adhesion molecules for use with this invention include intracellular adhesion molecules 1 (ICAM-1), 2 (ICAM-2) and 3 (ICAM-3), vascular cellular adhesion molecule (VCAM), endothelial leukocyte adhesion molecule-1 (ELAM-1), neutrophil adherence receptor, mad CAM-1, and the like. Other known and unknown factors (at this time) may also be targeted herein. Among the cytokines, lymphokines and chemokines preferred are interleukin-1 (IL-1), interleukin-1 β (IL-1 β), interleukin-3 (IL-3), interleukin-4 (IL-4), interleukin-5 (IL-5), interleukin-8 (IL-8), interleukin-9 (IL-9), interleukin-11 (IL-11), CCR-5 CC chemokine, and Rantes. Others, however, may also be targeted, as they are known to be involved in specific diseases or conditions to be treated, or for their generic activities, such as inflammation. Examples of defensins for the practice of this invention are defensin 1, defensin 2, and defensin 3, and of selectins are α 4 β 1 selectin, α 4 β 7 selectin, LFA-1 selectin, E-selectin, P-selectin, and L-selectin. Examples of oncogenes, although not an all inclusive list, are ras, src, myc, and bcBCL. Others, however, are also suitable for use with this invention.

The agents administered in accordance with this invention are preferably designed to be anti-sense to target genes and/or mRNAs related in origin to the species to which it is to be administered. When treating humans, the agents are preferably designed to be anti-sense to a human gene or RNA. The agents of the invention encompass oligonucleotides which are anti-sense to naturally occurring DNA and/or RNA sequences, fragments thereof of up to a length of one (1) base less than the targeted sequence, preferably at least about 7 nucleotides long, oligos having only over about 0.02%, more preferably over about 0.1%, still more preferably over about 1%, and even more preferably over about 4% adenosine nucleotides, and up to about 30%, more preferably up to about 15%, still more preferably up to about 10% and even more preferably up to about 5%, adenosine nucleotide, or lacking adenosine altogether, and oligos in which one or more of the adenosine nucleotides have been replaced with so-called universal bases, which may pair up with thymidine nucleotides but fail to substantially trigger adenosine receptor activity. Examples of human sequences and fragments, which are not limiting, of anti-sense oligonucleotide of the invention are the following fragments as well as shorter segments of the fragments and of the full gene or mRNA coding sequences, exons and intron-exon junctions encompassing preferably 7, 10, 15, 18 to 21, 24, 27, 30, n-1 nucleotides for each sequence, where n is the sequence=s total number of nucleotides. These fragments

may be selected from any portion of the longer oligo, for example, from the middle, 5'- end, 3'- end or starting at any other site of the original sequence. Of particular importance are fragments of low adenosine nucleotide content, that is, those fragments containing less than or about 30%, preferably less than or about 15%, more preferably less than or about 10%, and even more preferably less than or about 5%, and most preferably those devoid of adenosine nucleotide, either by choice or by replacement with a universal base in accordance with this invention. The agent of the invention includes as a most preferred group sequences and their fragments where one or more adenosines present in the sequence have been replaced by a universal base (B), as exemplified here. Similarly, also encompassed are all shorter fragments of the B-containing fragments designed by substitution of B(s) for adenosine(s) (A(s)) contained in the sequences, 10 fragments thereof or segments thereof, as described above. A limited list of sequences and fragments is provided below.

Some of the examples of anti-sense oligonucleotide sequence fragments target the initiation codon of the respective gene, and in some cases adenosine is substituted with a universal or alternative base adenosine analogue denoted as "B", which lacks ability to bind to the adenosine A₁ and/or A₃ receptors. In fact, such replacement nucleotide acts as a "spacer". Many of the examples shown below provide one such sequence and many fragments overlapping the initiation codon, preferably wherein the number of nucleotides n is about 7, about 10, about 12, about 15, about 18, about 21 and up to about 28, about 35, about 40, about 50, about 60.

Human Receptor-related Antisense Polynucleotide

20 5'-GGCGGCCCTGG AAAGCTGAGA TGGAGGGCGG CATGGCGGGC ACAGGGCTGGG C TGCTTTCT TTTCTGGGCC
TCTGTGGTCT GTT TTTCCT GGCCTGCTG GGGCGCTCTC CGCCGCCCGC CTGGCTCCCG GBGCCCCBTGB
TGGGCBTGCC GTC GTTCTTG CCCTCCTTTG GCTGCCGTGC CCGCTCCCCG GCCTCTGGC GGGTGGCCGT
TGGGCCCGTG TTC CCCTGGG GCCTGGGGCT CCCTTCTCTC GCCCTTCTTG CTGGGCCTCT GCTGCTGCTG
GTGCTGTGGC CCC CGTACA CCGAGGAGCC CATGATGGGC ATGCCACAGA CGACAGGCGT BCBCCGBGGB
25 GCCCBTGBTG GGCFTGCCBC BGBCGBCBGG C GGC GCC GTG CCG CGT CTT GGT GGC GGC GG GTT CGC GCC
CGC GCG GGG CCC CTC CGG TCC GTT CGC GCC CGC GCG GGG CCC CTC CGG TCC CGG GTC GGG GCC CCC
CGC GGC C GCC TCG GGG CTG GGG CGC TGG TGG CCG GG CCG CGC CTC CGC CTG CCG CTT CTG GCT GGG
CCC CGG GCG CCC CCT CCC CTC TTG CTC GGG TCC CCG TG ACA GCG CGT CCT GTG TCT CCA GCA GCA TGG
CCG GGC CAG CTG GGC CCC BCB GCG CGT CCT GTG TCT CCB GCB GCB TGG CCG GGC CBG CTG GGC CCC ACA
30 GAG CAG TGC TGT TGT TGG GCA TCT TGC CTT CCC AGG G BCB GBG CB TGC TGT TGT TGG GCB TCT TGC CTT
CCC BGG GCC CTT TTC TGG TGG GGT GGT GCT GTT GGG CTT TCT TCT GTT CCC BCB GBG CBG TGC TGT
TGT TGG GCB TCT TGC CTT CCC BGG GCC CTT TTC TGG TGG GGT GCT GTT GGT GGG C TTT CTT CTG TTC
CC TTT CCC CTG GGT CTT CC CTC CTG CTC TTT TTT C ATT TGC TCT CCT ATT ACT TTC TGT GTC CAT TTT
TTC ATT AAC CGA GCT GT BTT TGC TCT CCT BTT BCT TTC TGT GTC CBT TTT TTC BTT BBC CGB GCT GT GCC
35 TGT GTC TGT CCT CCT GCT TCG TTC CTC TCG TTC CTG CTT GGT GCC CTT GGC G GTC CTG CTC CTC CCG GCT
GTG G GTC GTG GCC CTG GCT CCG GCT GGT GGG CTC CCC TGG CCT TCG CTG GCT GGC GGC GTG C GGG
TCT TGC TCT GGG CCT GGC TGT GGC CGT GGT TGG GGG TCT TC GCT GCC TCC GTT TGG GTG GC TCT CTG
AAT ATT GAC CTT CCT CCA TGG CGG TCC TGC TTG GAT TCT CCC GA TCT CTG BBT BTT GBC CTT CCT CCB
TGG CGG TCC TGC TTG GBT TCT CCC GB GCC TTT CCT GGT TCT CTT GTT GGT TTT GGG GTT TGG CTT ACA
40 GTA GAG TAG GGG ATT CCA TGG CAG GAG CCA TCT TCT TCA TGG ACT CC TTC AAG GAG ACC TTA GGT TTC
TGA GGG ACT GCT AAC ACG CCA TCT GGA GC BCB GTB GBG TBG GGG BTT CCB TGG CBG GBG CCB TCT TCT
TCB TGG BCT CC TTC BBG GBG BCC TTG GGT TTC TGB GGG BCT GCT BBC BCG CCB TCT GGB GC GTT GTT
TTT GGG GTT TGG CTT GCC TTT CCT GGT TCT CTT BCB GTB GBG TBG GGG BTT CCB TGG CBG GBG CCB TCT
TCT TCB TGG BCT CC TTC BBG GBG BCC TTG GGT TTC TGB GGG BCT GCT BBC BCG CCB TCT GGB GC GCC TGT
45 GTC TGT CCT CCT GCT TCG TTC CTC TCG CTT GGT GCC CTT GGC G GTC CTG CTC CTC CCG GCT GTG
G GTC CTC GCC CTG GCT CCG GCT GGT GGG CTC CCC TGG CCT TCG CTG GCT GGC GGC GTG C CCC BGB BCG
BGB CCC GGB CCG BCB GGC CGT GGT TGG GGG TCT TC GCT GCC TCC GTT TGG GTG GC GAT CTC TGA ATA
TTGA CCT TCC ATG GCG GTC CTG CTT GGA GBT CTC TGB BTB TTGB CCT TCC BTG GCG GTC CTG CTT GGB
TCT GGG GTG TCC TGG CCT TCG TGG TTC CTC TTC CTT CGT TTG CCG TCC GCG GGG GCC CCC GGG CCT GGC
50 TGC GCT CCT GCC CCG CCT CTT TCC CGG GCT CTT GCG CTG GGG GGT GCT CC CGT GTG TTT GCG CCC TC

CTC CTG GTC GCG CTT GTC GTT TTG GGG CCG GCT TTG CCC GCC TCC CGG CGC CTG GCC CGG CC TTC CTG
 5 GGC TGC GTG CGC CTT CTG TTC TTC CTG GCT CTG GGG TGT CCT GGC CTT CGT GGT TCC TCT TCC TTC
 GTT TGC CGT CCG CGG GGG CCC CCG GGC CT GGC TGC GCT CCT GCC CGG CCT CTT TCC CGG GCT CTT GCG
 CTG GGG GGT GCT CCC GTG TGT TTG CGC CCT CCT GGT CGC GCT TGT CGT TTT GG GGC CGG CTT TGC
 CCG CCT CCC GGC GCC TGG CCC GGC CTT CCT GGG CTG CGT GCG CGT TCT GTT CTT CCT GGC GCA GGA
 10 GAC AGG GCA GGG CGA TCA GGA GCA GCG TGA GCC AAA GGA GGA CCA TCG GGA ACG CAG CTC CGG AAC
 GCA GGA CAG AGG TGC C GC BGG BGB CBG GGC BGG GCG BTC BGG BGC BGC GTG BGC CBB BGG BGG BCC
 BTC GGG BBC GCB GCT CCG GBB CGC BGG BCB GBG GTG CC TCT GCC CTG TCC GCC GGC TCT TCG GTG GCT
 CGG CCC CGC TCC TTG TCT TGC CGC GGG TTG GTT CCT GGG CCT GGT TCT TGC GGG CGT TTC GGT CTG CTG
 GCT GGT CTG GGC CCG CGG TGC GGC GGG TGG CTT GCT GTT CTG CCT GGG CTC TCC CCT CTC CTC CTT TTC
 15 TCC CTT CCT CTG TCT TGC CTC CCT CCT CTG GGT CCT CTT GGC CTG GGC GCT CTT CCC CTC CGG CGG CTG
 CGG GCG CTC GTG CTG CCT GGT CCG CTC CCT GGG GGT GCT CCT TCC CTT TCC CGG CTC GTG GGG TTT GCG
 GGG CTG GGC TGC CCT GGG GGG TCT GGG CCT TTT GGG GTC GGC TGG CTG CTG CCT CGG GCC TGG GCT
 TCC CTG TGC CCC T T CCT CTG CTG GGT CCC CCT CCC GTT CCA AGC TGC ACC GCA CAG ACC GGC GCT ACA
 GGA CAG AGC CAG GCA AGC ACC CAT GGG GAT CCA GGC CCA GCT GTT CCB BGC TGC BCC GCB CBG BCC
 GGC GCT BCB GGB CBG BGC CBG BGC BCC CBT GGG GBT CCB GGC CCB GCT G CTCAGTGGCC
 CCCAAAGGA TGA GTAATAC ATGCGCCACG ATGATCATAT CCTTTTACT ATGAGGCCGT GTCTGTCGT
 TCTTCCCTT GCTCTGGTG TGTCTTGTCT GTGCCCTGCC TCTCTGCC CGTGTCTGTC GTGTCTTCC TTTGCTCTTG
 20 GTGTGTCTT GCTGTGCCCT GCCTCTCTGC GGGGGTGGCT TCCCTGCCCG TCTCTGGGCC GTCCCCTGCC
 TCGGCCCCGC GCCCGCTCG GCTCCTCTCC CTCTGGCCCG GCTCGGGCG GGGCGGGCG GTGGGCGGGC
 GGCCTGCCCG TGCCCGCGGC GCTGGCCCGT GCTGGCCGTC GGCTGCCGCG TGCTGGCTGC CCTGCTGGCC
 GCGCCGGGGC CTG TCCGCCT CTGCGGGCGC TGTCTCTGG CTTGTCTTCC GGCTCTCTG CTGGGGTGGG
 GCTGGCGGC CGGCCCGGGTG CTGGGGCTCC TCAGGGGGGGGG GGGCTCTTCC GGCTGTCTC CCTCCGGGGC
 25 GGGGGTTTCT GGGCGTGGGG GTCTTGCTG GCCTCCGGGC TCCCTGTTGT CTTGCCTTCC TTCTCTGGTC
 GGTTGTGGCT CGGGGCTCCG TGGGTCCCTG GCGCCGTT GTGTTTGTCT TTTCCCTG GCGTCCCTGT
 GCCCCTCTCC TCTCCTTCT CTGCTTCTCG CTCTCTTTC TGGGGCCCTC CCTGCTGCTC TTGGTTTGG
 GCTTTTTTC TCTTCTCTCT TTTCCTGCG TGGGCCTCC GCACGCCCT TGCCACCTCC TGCGCAGGGC
 AGCGCTTGG GGCCAGCGCC GCTCCCGCGC CGGCCAGCAG GGCAAGCCAG AGCGCGCAGC CGACGGCCAG
 30 CATGCTTCCCT CCTCGGCTAC CACTCCATGG TCCCGCAGAG GCGGACAGGC GCBGCGCTC TTGCCBCCTC
 CTGCGCBGGG CBGCGCCTTG GGGCCBGCAGC CGCTCCCGGC GCGGCCBGB GGGCBGCCBG CBGCGCGBG
 CCGBCGGCCB GCBTGCTTCC TCCCTGGCTB CCBCTCCBTG GTCCCGCBGB GGCGGBCBGG C GCTGCCGGC
 GGGGTGTGCG CTTCGCGCTC CGTGCTCGG TTCTCTGTCT CCCGGTCCCC CTTGCCTGGC GTCTCGGGCC
 TTCGCTCTCT TCCCTCTCTT CCTTCCGCTC CGTGGGGGCT GCTTGGTGGG GGCTGTGCCT CGGGGTCCCG
 35 GGGCTTCTGG CCCTGCCGT TCATGGTGGC TAGGTGGGC GTTCBTGGTG GCTBGGTGGG GC GGG GTG GGT
 BGG CCG TGT CTG GGGGTT GGC CBT GTT GGT TGC CTCT TGG TGG TGC GCC GGG CGCG TCT TGG CTT TCT
 TCT CCT TCG GGC CCT CGG GCC GGT GCT TGT GGGCT CCT CCC GGG CGG CCT CCC CGG GCG GGG GCT TCT
 TGGCG CTG GCG GGG GGG CCT CCTGCT CTG TGG CTG GGC GTT CCT TGG TGT TCT GGG TGGTGG CGG GCG
 TGG TGG CCT CTG TGTGGG CCC GCG GCT GCB GGG GTTG CCT GTC TGC TTC GTCCCT TGC GCT CCC GGG CCG
 40 CCGGG GTG GGT AGG CCG TGT CTG GGGGTT GGC CAT GTT GGT TGC CGGG CCC GCG GCT GCA GGG G
 ACAGGGGCTG TAACTTCATC TGCAAGTGGC ATGCCAGTGA AATTAGATC ATCAAATCC CACATCTGTG
 GATCTGTAAT ATTGACATG TCCCTTCAG TTTCAGCAAT GGTTGATCT AACTGAAGCA CGGCCAGGB
 CBGGGGCTGT BBTCCTCBTC TGCBGGTGGC BTGCCBGTGB BBTTTBGBTG BTCCBBTCC CBCBTCTGTG
 GBTCTGTBTT BTTTGBCBTG TCCCTTCAG TTTCBGCB TGGTTTGBTG TBBCTGBBGC BCCGGCCBGG
 45 TGGCTCGGTG CCTCTGCCCT TGTTGTTGCG GCGCTCGGTT GGTGTGGCCC CTGTGGTGCT TCGTTTCCCC
 CTCTTCTCT TTGTCTGGGG GTTCTTGTGG CGGGCTGCTT GTCTCGTTC GCCCTGTCGG CGGGGAAGGC
 TCTCTCTCT CCCAGATC CGCGACAGGC CGCAGGCAAG AACCAAGCGA ACCAGGGCGC GTCCGCACAG
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40	CCC ATTGTCT	ATG'CTTACCG	GAACCGAGAC	TTCCGCTACA	CTTTTCACAA	AATTATCTCC	AGGTATCTTC
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	ATCTAGGCTC	TCG'CTCTTC	CAGGAGAAGA	TACAAATCCA	CAAGAAACAA	AGAGGACACG	GCTGGTTTC
	ATTGTGAAAG	ATAGCTACAC	CTCACAAGGA	AATGGACTGC	CTCTCTTGAG	CACTCCCTG	GAGCTACAC
	GTATCTAGCT	AATA' TGTATG	TGTCAGTAGT	AGGCTCCAAG	GATTGACAA	TATATTATG	ATCTATT
45	CTGCTTTAC	TGTGTGGATT	ATGCCAACAG	CTTGAATGGA	TTCTAACAGA	CTCTTTGTT	TTTAAAAGTC
	TGCCTTGTTT	ATGGTGGAAA	ATTACTGAA	CTATTTACT	GTGAAACAGT	GTGAACTATT	ATAATGCAA
	TACTTTAA	CITACAGGCA	ATGGAAAAT	AAAAGTTGAC	TGTACTAAA	ATG	GAATTCCAG
	GTGGCTGGC	TGG'GACCT	AA GTGTGTCT	CCTGCCTTA	TTCTCTCTAG	TGGGTTATT	TTTCATGTGG
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50	GA CTGATTCC	AAA.GAAC	ACCTATGTAC	TGGGGTAGGG	GAGGGAGGGT	TTTTGCA	ATTTAACTAA
	GGTTCAAAGA	GTG'CTATATA	GTGAGAAAGG	CTTCTTTTTT	TTTTTTTTT	TTTTTGGCA	GAGTGCTGCC
	TCCTAGAAAT	TTCTCTGGT	AACTCCCTC	TCTGAAGCAC	AGATAAAGAA	AACAATTACA	GTAGAAACAT

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	GCTCAGGGAG	AAATGACAAG	TCTGGCGGGG	ACAAGTATGG	GATTGGTAA	GACTTGGATC	AACTTGGGAT
5	ACAGGGTGGG	GGTGGGGAGT	GGAATCAATG	AATGATGCCA	GAGCAGATCA	ACTAACAAAGA	GGACCCTGAT
	GAGCCCCAGG	CACAGGCAGTC	TCCCTTATGC	CCCACTCTGA	AGTGGTTGTT	AGTAAACACC	AGAACGCAT
	TGTTGTTACT	GCTGAATTTC	ATTTTGGGCT	GTACATATTT	AGATGCTAA	GGTAAAATG	ATAAAGCCCT
	CAAGCCACTG	TGTGGGTTTG	GGTCCAAGTG	TTCCTTCTTG	CTGCCTCTCT	AACACGCCTG	GTTAAAATAA
10	TCCCTTGGG	TGG'GCTGAG	AAGCACCTGA	ACCAAGTGGG	TCCCCAAATA	ACAATGGCGT	GCAAGTGTCT
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	TCCTGCGGGG	ATG3GGGCTGA	GGCTTGGGG	ATGTGGGCAG	GAGGATATGC	CATTGATTTC	TGTTGCACAC
	GTTCTTTCC	CTTCTTCTG	TATGTCCTG	CATTCTGCTA	TTCTGTCCTT	CCTCACATAG	GTTGGACATT
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	GACCAAGGAT	CTT'GCTGCA	AAGGCTGGG	ATCGGCTGTG	CTCAGCAAAG	CGTCAACTCG	TGCAAGAACT
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	CGTTTGCCTC	CTTATCATGA	GATCTTTTG	CTAACGCTGGC	AGAAAGATTG	CATAGTCAGT	GCTTCCAGCT
	CTGCTCCCAC	CTGATCCTGC	ACTGTCCTCT	GGTCCCTGAA	TGAATGAACT	CTGATACCCA	ATCTTGTCTC
	GAGCCTCTC	TATGCCACTC	ATGGCTCCTC	TTCTGCTCTT	TCCATCTTT	TGCTGAGAGT	TCTGAGCTCT
25	GTACTTCCTC	TTGCCCCATC	TCACITCTG	AAACACCCCT	GAAGAGGGTT	GCTTATCTTG	ATGGAACCTCA
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	AGATTCAAGTC	CATATAGAGC	TGTCCTACAG	CATTCTGGAA	ACTTGAGGAT	GTGCGGTGCA	TAAAGGGGCT
	GGAAGTGAAC	CACCTGTGAT	GAGCCCTTTC	TAAGGAGAG	GGTTTCCAAG	AGATCACCCC	ACCAGAAAAG
30	GGTAGGAATG	AGCAAGTTGG	GAATTTAGA	CTGCACTGC	ACATGGACCT	CTGGGAAGAC	GTCTGGCGAG
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	ACCACCTTCT	ATTTCATTGT	CTCTCTAGCC	CTGGCTGACA	TTGCTGTTGG	GGTGCCTGGTC	ATGCCCTTGG
	CCATTGTGT	CAGCCTGGGC	ATCACAATCC	ACTTCTACAG	CTGCCTTTT	ATGACTTGCC	TACTGTTAT
40	CTTTACCCAC	GCCTCCATCA	TGCTCTTGCT	GGCCATCGCT	GTGGACCGAT	ACTTGCGGGT	CAAGCTTACC
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	AAGTTGGTGA	CTACIGTAAGC	GACTCAGGG	GAGGGGCTGA	TTCCCAGACA	GTCGCCTGTT	CCTGCTGGGA
50	TGGGGCTGAG	GCT'GGGGAA	TGTGGGCAGG	AGGATATGCC	ATTGATTCT	GTTGCACACG	TTCTTTCCC
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	CTGATCCTGC	ACTCTCCCT	GGTCCCTGAA	TGAATGAACT	CTGATACCCA	ATCTTGTCTC	GAGCCTTCTC
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45	CTTGGCCCAT	CTCACTTCC	AAAACACCC	TGAAGAGGGT	TGCTTATCTT	GATGGAACTC	AAAAGCCAA
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5	GACTCTGCGC	CATAGTGGGC	AACGTGCTGG	TCATCTGCGT	GGTCAAGCTG	AACCCCAGCC	TGCAGACCAC
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15	CTGAACCTAT	CTAACTCCAA	AGAGACAGGT	GCATTTATG	GACGGGAGTT	CAAGACGGCT	AAGTCCTIGT
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	GGGGACAACG	TATTATTGAT	ATTATTGTCT	GTTCCTCTTC	TTCCAATAG	AAGAATAAGT	CATGGAGCCT
	GAAGGGTGCC	TAGITGACTT	ACTGACAAAAA	GGCTCTAGTT	GGGCTGAACA	TGTGTGTGGT	GGTGACTCAT
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30	GAAATAAAACT	GAGTTAACAGG	GGGACTTAAA	CTGCTGAATT	C AAATGATAGA	CCGTCATAA	TTTGTAAAT
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	GACAGAGAGA	GACCTCCGTCT	CAAAAAAAA	AAAAAAA	AAAAAAATTAC	GCTTCAAACA	CATGATCTCT
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50	ACACACACAC	ACAACCCGC	ACTCACACAC	TTGGACATGC	ATAGACCACA	GCTTCCACA	CCCTTCCTAG
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	CCTGGTTGTT	ATATGTTTCT	ATCTATCCA	GATGAACCTG	GAAGTGAAGG	GAAGAGAGTT	AAACATTA
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25	AAGATGTTAT	GACCTAGCCT	CAGAAATCAC	ACACCATCCC	TGCCACCAT	AGTAAGAAGT	CCAGCCCACG
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	TGCTGGGAGG	ACA ACTGTC	CCAGCACAGA	GGGAGGGAGG	GAGGGCAGGGC	AGCGGGGAGA	AGTTCCCTG
	TGGTCGTGGG	GAGT GAGCTCTCA	ATATTTAGT	GAAAGCTATA	GATGAGGCTC	CATAGGGGAT	AAAGCACAGA
30	CACACCTTT	CAGAGGCTT	GTGGACTCTG	GGCAGCCTGT	CCATAGACCT	CTGCCCCAA	CTGGCAAGTC
	AGGAAAATCC	AGA TAAGGA	GCCCCAATGT	GGTGAACAG	CCAGGTGCAC	AGATGAGTC	ACCACACAGC
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	ACCCATAAAC	TGA TCTGAGA	CTCTGTTCC	CTGTCTCCAT	GATGATGGGA	TCAGGCTTGA	TTGCTGGTT
	GTAGGCTTGT	TATC AATCAA	GTCACAGGG	AGAGGAGCTG	ATGGGCTGGG	GGGACGTCCT	CTGGCCCTCC
35	TGTCTCTTCC	CCAC ATCCAC	TGGGCCACT	CTTATCTGT	CTCTTCTGAA	GGAAAGGTTT	TAAGGCTTCA
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	CCTACGCAA	CATC GAAATC	TTCCAAGAGC	CTCCCTGGCC	CCCAGGGCTC	AGAGGGTGGC	AGAGCGGAGA
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	CAGGCTGCC	CGCA GTACCA	GGGAGCGACT	GAAGTGCCA	TGCCGCTTC	TCCGGAGAAG	GTGGGTGCCG
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	TAAGCACATA TTGAGCACTT	GCTGTATATG	CAGTATTGAG	CACTGTAGGC	AAGACCCAAG	AAAGAGAAGG
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	ATAGAAGCTC	AGAG`AGATCA	AGCAATTGTC	CCAAGACCAC	ACAGCTAGGA	GTGGAACCTA	TGGCTGTCCA
	AGCCCCATGC	CTCTGCTGAA	GGTAGAGATG	AATTACAGCA	ACAAGTCTAG	AAAGGTGCCT	GCCCTATGGT
	CTGTGAGTCT	TGCC`AAAGAA	TGAAAGAGGA	GCCAGTGGGT	TAAAGATGAG	GTCACCAACA	ACGGTGGTGT
10	TGGAGTTAC	CACTGATAAT	AAGGGTGCAA	AATGTAAATT	ACTAATGTTT	ATTGAGCCTA	GTGCAGTGC
	TGGGGCATT	TGCA`CATTGT	CTCTGATCCC	TATGACAACC	CTGAGAGGTA	GTGGTTTAA	CTGCCATGTT
	ACAGGGTAGG	TCATTGTGGT	TCAAGGACGT	TAAGTAACCT	CCCCAGCGTG	ACACGGCTTA	TAAGTAAGGC
	AGCCAGGATG	TGA`ACCCAGT	AGGACTATCT	GGCTGCAAAG	TCCCCACCCC	CCTCGCCATC	TGTATCCTCC
	AATCACTTCA	GTGCTTGTG	GCATAGAAGG	TAACGGAAAT	CACGATGCCA	CAGACTGTCC	AGGAAGACAG
	AAACTAGGCA	GATGGGCTGG	CCATGGCTC	CAAGCCAGAC	TGGAATCTCC	AGGTCTGGAA	TGATATCATT
15	TTTCTCTTT	AATA`ATTAA	CTCACCCACC	ACACGGCTTT	GAGAGGCTCA	AAGTTGACCA	ACTCCCTGG
	GAGGGCCCCG	GTTCATAAGG	AAGGAACGTG	AATCCTCCCA	TCACGGAAGC	TTCAAGGAGG	TCAAGGGTCC
	AAACATTGAG	ATTGTTAGTG	CTGTTGGTGG	ATACTGGCCA	AGGAAATATC	CCAGTGGAGC	CTCGAGATGA
	AGAACATGAG	GCCC`CCGTTT	AGAACCAAGG	ATCAGAGGGG	GCTCTGTAAG	ACCCAGGGGA	GTCAGGTGCA
	CTGGAGCGCG	GGC`ATGCAGA	AAACAGCCTG	AGCTCCACCT	CGGCTTCTCC	TTGTCCTGGC	TGGTTGTCT
20	TAACCCCTGT	CTCC`TTCTGG	ACCAGTTTT	GTCCTTCCCT	TGTGACCCT	GAGGGGTAAC	AGCCTCTTTC
	CACTTTCTT	CAGC`GCCGAC	ATGCTCAATG	TCACCTTGCA	AGGGCCACT	CTTAACGGGA	CCTTTGCCA
	GAGCAAATGC	CCCC`AAGTGG	AGTGGCTGGG	CTGGCTCAAC	ACCATCCAGC	CCCCCTTCCT	CTGGGTGCTG
	TTCGTGTCTGG	CCACCCCTAGA	GAACATCTTT	GTCCTCAGCG	TCTTCTGCT	GCACAAGAGC	AGCTGCACGG
	TGGCAGAGAT	CTAC`CTGGGG	AACCTGGCCG	CAGCAGACCT	GATCCTGGCC	TGCGGGCTGC	CCTTCTGGC
	CATCACCATC	TCCA`ACAAC	TCGACTGGCT	CTTGGGGAG	ACGCTCTGCC	GCGTGGTGAA	TGCCATTATC
25	TCCATGAACC	TGTACAGCAG	CATCTGTTTC	CTGATGCTGG	TGAGCATCGA	CCGCTACCTG	GCCCTGGTGA
	AAACCATGTC	CATGGGCCGG	ATGCGCGCG	TGCGCTGGC	CAAGCTCTAC	AGCTGGTGA	TCTGGGGGTG
	TACGCTGCTC	CTGA`GCTCAC	CCATGCTGGT	GTCCTGGGACC	ATGAAGGAGT	ACAGCGATGA	GGGCCACAAC
	GTCACCCGCTT	GTGT`CATCAG	CTACCCATCC	CTCATCTGGG	AAGTGTTCAC	CAACATGCTC	CTGAATGTG
	TGGGCTCTT	GCTG`CCCCTG	AGTGTATCA	CCTCTGAC	GATGCAGATC	ATGCAGGTGC	TGCGGAACAA
30	CGAGATGCAG	AAG`TCAAGG	AGATCCAGAC	GGAGAGGAGG	GCCACGGTGC	TAGTCCTGGT	TGTGCTGCTG
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35	GGACCTCAT	CTCC`GTGGAA	CGCCAGATT	ACAAACTGCA	GGACTGGCA	GGGAGCAGAC	AGTGAGCAA
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	CCTGCCCTGC	CCAA`TTTG	AGGGAGCATG	GCTGTGAGGA	TGGGGTGAAC	TCACGCACAG	CCAAGGACTC
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40	GAGGAGGCCT	GGGG`GCAGGG	AGAGGAGTGA	CTGAGCTCC	CTCCCGTGT	TTCTCCGTCC	CTGCCCAAGC
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	GTCTGTGCCA	AAGA`AGAATC	CAATAAGCAC	ATATTGAGCA	CTTGTGTAT	ATGCAGTATT	GAGCACTGTA
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 50 CCTCAGGGCA TCCCTTGGC TGGCACTGGT TGGATGTGA ATCAGTGATA ATCCTGAGAG ATACAGCACAA
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	TACTTCAGCT	TTCAAATACA	TTAACACTGT	GATATCTTGT	ACTATTTCA	TCGTGGAAAT	GGTGGGAAAT
	GCAACTCTGC	TCAGGATCAT	TTACCAGAAC	AAATGTATGA	GGAATGGCCC	CAACCGCCTG	ATAGCCAGTC
5	TTGCCCTTGG	AGAC'CTTATC	TATGTGGTCA	TTGATCTCCC	TATCAATGTA	TTAAGCTGC	TGGCTGGCG
	CTGGCCTTTT	GATCACAAATG	ACTTTGGCGT	ATTCTTTGC	AAGCTGTTCC	CCTTTTGCA	GAAGTCCTCG
10	GTGGGGATCA	CCGT'CCTCAA	CCTCTGCGCT	CTTAGTGTG	ACAGGTACAG	AGCAGTTGCC	TCCTGGAGTC
	GTGTTCAAGG	AAT'TGGGATT	CCITTGGTAA	CTGCCATTGA	AATTGCCTCC	ATCTGGATCC	TGTCCTTAT
	CCTGGCCATT	CCTGAAGCGA	TTGGCTTCGT	CATGGTACCC	TTTGAATATA	GGGGTGGACA	GCATAAAAACC
	TGTATGCTCA	ATGCCACATC	AAAATTCATG	GAGTTCTACC	AAGATGTAAA	GGACTGGTGG	CTCTTCGGGT
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20	TAACTTGGCA	ACCA TGAATT	CATGTATAAA	CCCCATAGCT	CTGTATTTG	TGAGCAAGAA	ATTTAAAAAT
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25	GAACAAAGCAT	CCAGTGGAAAG	AACCACGATC	AAAACAACCA	CAACACAGAC	CGGAGCAGCC	ATAAGGACAG
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50	GTATAAACCC	CATA GCTCTG	TATTTTGTGA	GCAAGAAATT	AAAAATTGT	TTCCAGTCAT	GCCTCTGCTG
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	CACGATCAA	ACAACCAAA	CACAGACCGG	AGCAGCCATA	AGGACAGCAT	GAAC	CCCTAGAAAG
	CACTCCTCGG	TACT CCAA	ATCCTCTCGG	AGAAAAAAAT	CACAAGGCAA	CTGTGAGTCC	GGGAATCTCT
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40 Human Enzyme-related Antisense Polynucleotide

5'-CTT GCT CCT GGG GGC CTC CTG GTC CCT CTG GCT G TT CCC GGC CCT GGB CTG GGG CBG GGG CCG CGT
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 45 CCB CBG CGT GTG BTG BGT BGC CBT TCT CCT GCB GCC GBG GGG CGC GGG CGB GCB TCG C TTT GGG CTT
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	AATAACCAA	GGGGGAAGAA	GAAAGAGAAA	AAGGAAATCT	CTTAAAATAC	ACAGGTATAC	ATATGACAAA
	GCAAAGAAGG	AAA TGTGAGC	AGATAGTGCA	GTCCTCGTTT	CTGAAATTGG	TCCCCTGACT	GGGGCTATAC

	CTATTCCATT	TCCTCACCCCT	CAGCCAGGCA	GGTGGAGCAA	AAACCTTAAGT	CTTGGTGGAT	CTGAATCTTG
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5	CCAGCTCCGG	ATTCTCTTCT	GTTCTGTTAA	TGGTGAATG	CCCGAGAGAA	GAGTGCCTA	CTTGGCAA
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	TCTGAATATT	CTCTGGCAAC	CCCCGAGAGA	GTGAAGAAG	TGGTACAAGG	ACACTTAAGA	AGACCAGATT
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	TGAACCTAAAT	GCCITATAAA	TCTCCAAGAG	AAATGACAGT	CCACCATGTG	GACTGCTTC	TGTAAGTCCA
	GGGAAAATAA	AAGCTATGTG	CTTGAACACC	ACTTCTGATA	TTATAAGGTG	TGTGATCTT	GTCATGTTAA
	TGGGTCTGAG	TATCAATTCT	ACAATTGTA	AGTGACAGTA	ATGGTGTGTC	CCCAGGTTGT	TGTGAAAGC
15	TTGATTCTTA	ATGCAACAGT	AGGAAACCCC	AGCCTCTCTG	GAGCAAACAC	CCTCTACAT	CTTACTTCC
	CCTGCACATT	GGCAGGACTC	TATTCCCTCA	TTTCTCTCA	GTGCTAGAGC	AGAAAGGGAC	CTTGATTGAA
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	AATATATGAT	ACGCCTGAC	TCTCAGAAAA	TGCTAATTCC	AATCCAATT	GCTCTTGCA	TAAAGTTCTG
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	GTAACCTCCA	ACGGTCCCTC	AAAATTGTTG	GGTGGTTTCC	TTATAAGACG	GAACCTTGTG	CTGACGGCTG
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	TTTCCAAGAC	ACACITTCACC	ATAAGGCCA	AGGGATTTA	ACTTGCAGGT	CCAAATCTTG	CCTGGGGTCC
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	GCCACCAAGC	AGGCCTGGCG	CAATGCCCA	CGCTGCATTG	GGAGGATCCA	GTGGTCCAAC	CTGCAGGTCT
	TCGATGCCCG	CAGCTGTTC	ACTGCCGGG	AAATGTTGA	ACACATCTGC	AGACACGTGC	GTTACTCCAC
	CAACAATGGC	AACATCAGGT	CGGCCATCAC	CGTGTCCCC	CAGCGGAGTG	ATGGAAGCA	CGACTTCCGG
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Human Factor Related Anti-sense Oligonucleotide

5'-CCT CCT TCC TGG TCT GTC TGC CBG BCB BBT TTG GGB BGT GBB CBG TTT TGG BBC CBT GTT TCC CBG TCT
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	GGGTGAACTC	TGACGGGACA	CATGTAGTCA	CAATCCCATC	CTCCCATTC	CCTTCAGA	GGAAGGAAGT
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	AAGTCCACTT	GTGCAAGGCT	GCTCTTGTCT	ATAGAAGACC	TGGGACAGAG	GACTGCTGTC	TGCCCTCTCT
	GGTCACCCCTG	CCTAGCTAGA	GGATCTGTAA	GTACTACAA	ACTTAAACCT	TACACTGAGT	TTTCATCAT
	GAAGCTATGC	CTCCAACTCG	ACCTCTGACT	GTGGGGCCGC	CCCAGAGGGGA	CCCAGCGGGT	GAATCCCTGC
	TAGGAACGTC	TGTC CGGACC	TCTGGTACT	GCTGGGGACG	ATGGCTTCCA	GCTAACTTAA	TAGAGAAACT
55	CAAGCAGTTT	CCTTCTAAAT	ACACATGTCA	CATGTCCTGG	TTGACATGTC	CAGTAAGAAG	ACTATCACAG
	GTCTTGGAA	CATICTTTG	AGAGAAACCT	ATTAGGTCC	TTGGTCTGTT	TTCAATCAG	GTTGTTGAT
	TTTGCTATT	GAGITGTG	AATTCTTAT	GTATTCACT	ATTGCCCCCT	TCTGCCATGT	AGGTTTTGCA
	AATATTTCT	CTCATTTCT	GGGTTATCTT	TTCACTCGGT	TGATTGTTTC	CTTGCTGTG	CAGATGCTT
	AGCGTTAAAT	GAAGCCACAC	TTGTCTATT	TCCCTTTAT	TGCCGTGCCCC	TTTGGTGTCA	TAGCCAAGAA
60	ATCATTACCT	ACATCAATGT	CAAAAGCTT	ATCCTCTAT	ACACTCTAG	TAGTTTATGG	TTTCAGTTG
	TACATTCTAGG	TTTCAATT	ATTCTGAGTT	GATGTTCTTA	CATGGTGTGA	GATAAAGATT	TAAATACATA
	CATATATAAA	ATCATGAGGT	AGTGTACACT	ATAAATATAC	AATTGTAAT	TGTTACTCAA	GTCTAAGTAG
	AGGTGGAAAT	AATAAACCTT	CTTTTTTTA	CTTAAACCAC	TCTGTGTCA	TGAGCTGATT	TCACCTTGT
	CCTGATAAAA	TCATGTCTT	CTCCACCCCTG	ATTCCCTACAG	GAGACTACTC	ACCCCTAAC	CTCAAAACCC
	TCTTCATGAG	GATCGTAAGT	CACCTGAATC	CTGAAGTGA	TTACTCGCTA	TTCCATTGGA	ACTCATATAG
	GACACCAGAA	TCTAGACCTC	CAGAGAACAG	CAGGACCCAT	CTTCAGAAAA	TAAGAAGCAT	TTGTCCTCTG
	AGCCTGTTGA	ATCAAGTGC	AATTCTATT	CTTTTTGGAA	TGTTAAAAAG	TGAATCATAA	TATTAAGCA

	GGTGAACCCA	CGAGTAACAT	AGCAGGGTCT	TTCTTGTCA	TATTAGCTCC	AACCTAGCAC	AGACATTAAC
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	CTCTTATAAA	ATG CACACCT	CCTCTCACTG	AGATTGAGGA	AGGTTCTTG	TCTCCGAGCC	TTCTCCCAGT
5	AGAGCTATAA	ATCCAGGCTG	GCTCCTCCCT	CCCCACACAG	CTGCTCTGC	TCTCCCTCCCT	CCAGGTGACC
	CCAGCCATGA	GGACCCCTCGC	CATCCTGCT	GCCATTCTCC	TGGTGGCCCT	GCAGGCCAG	GCTGAGCCAC
	TCCAGGCAAG	AGCTGATGAG	GTTGCTGAG	CCCCGGAGCA	GATTGAGCG	GACATCCCAG	AAGTGGTGTG
	TTCCCTTGCA	TGGGACGAAA	GCTGGCTCC	AAAGCATCCA	GGTGAGAGAG	GCAGGCATGC	AGAGCTGCTA
10	AGTCTAGAGG	GAAGGACGGG	AGAGAGGTT	CAGAGTTGGG	TCTCAGCAGT	CTATGTCACT	GAGGTGGCTT
	CACTTAGAAT	CTC'GGGCAT	TGATTTCTC	ATCTAGAAAT	TGAACAGAGA	GCCAATAAA	CCTGAGAAC
	TTTATTTCTC	CAA/GACTTG	ATTCCAAGAA	ACATCTGTGA	AATTCACTAA	GTTTAAGATA	TGAAGAGACA
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15	AGCTTTAAA	AAC'GCAGCC	AAGCCTGAGG	GTAAGTTCA	GTGTGTGTTG	GATGGGGCAG	GAATGCAAA
	ATGAGAGCAA	AGC AGAATGA	GTCTCAAATT	CTGTGTGACA	AGCACTGCTC	TGCGTGTGTTA	TTCCATCGA
	CTGAGGGTGT	TCG'GCTACC	GGCTGCAATG	CAGCCAGCAT	CACCTGTCA	CTAGCATGTG	ACTCCCCGA
20	GATTCTTTT	CTTA.CCCACT	GCTAACTCA	TACTCAATTG	CTCATGCTC	CCCTGTCCCA	GGCTCAAGGA
	AAAACATGGA	CTGCTATTGC	AGAATACCA	CGTGCATTG	AGGAGAACGT	CGCTATGGAA	CCTGCATCTA
	CCAGGGAAGA	CTCTGGGCAT	TCTGCTGCTG	AGCTTGCAGA	AAAAGAAAAA	TGAGCTAAA	ATTGCTTTG
	AGAGCTACAG	GG A ATTGCTA	TTACTCCTGT	ACCTCTGCT	CAATTCTCTT	TCCTCATCTC	AAATAATGC
25	CTTGTACAA	GAT'ITCTGTG	TTTCCACCTC	TTTAATGTGT	GATATGTGTC	TGTGTCAGA	CACTTGGGAT
	ACACGTACCA	AAA CGCAAAA	TCAAATTTTT	GAACAATATA	CCTACCTTGC	TATAGAAGAC	CTGGGACAGA
	GGACTGCTGT	CTG'GCCCTCTC	TGGTCACCTC	GCCTAGCTAG	AGGATCTGTG	ACCCAGCCA	TGAGGACCT
	CGCCATCCTT	GCTGCCATT	TCCTGGTGGC	CCTGCAGGCC	CAGGCTGAGC	CACTCAGGC	AAGAGCTGAT
30	GAGGTTGCTG	CAG CCCCGGA	GCAGATTGCA	GCGGACATCC	CAGAA GTG	TGTTTCCCTT	GCATGGGACG
	AAAGCTTGGC	TCCAAGCAT	CCAGGCTCAA	GGAAAAACAT	GGACTGCTAT	TGCAAGAAC	CAGCGTGCAT
	TGCAAGGAGAA	CGT'CGCTATG	GAACCTGCAT	CTACCAGGG	AGACTCTGGG	CATTCTGCTG	CTGAGCTTGC
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	TAAATAAGGA	ATCCTCTGGG	GAGTGGTAA	GATCTGGATG	CTGGCTACAG	GATGTGTTGG	TTGTAAAAAT
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	TGTCACTGTA	GAG'AGCTCA	GTTAGCCCCA	GCAAGCCTCT	GGCTTAATCT	TGTTTACCT	TAAGCCATCA
45	GTCATTACA	AGT AGGAAA	TTCACAGGG	AAAGTAGAGT	ATAAAATCCA	GAATGAAGGT	TTACTGGGTA
	AGAGTCTCTC	CAT'TTCCAA	AGCCCCTTA	TTCTTGATT	CCAGTTCTA	AGAAGTCTCA	GCATTGTC
	TTTTTCATGT	ATCITACAA	AAGACAGCAT	GTGCTCTAA	CACCTGATAC	ATTGTATCTA	CCAGCACTG
	GTAAACAGAA	AAA ACCACA	TTTTCTGTG	AGGAGAAATT	TGGTGCCTAT	TTCTTACCA	GCACCAATAA
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	TGAGCCCTA	GAG ACTTTTC	TGTCTGTTAC	TGTTCTTCA	TCCTCATCT	GCAGAGCCAG	CCCTGAGAAG
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	TGAACACTGA	CAACCATCTG	ATCTTGACA	AAATCCACAA	AAACAAGCA	TGGAGAAAGG	ACTCCCTATT
	CCATAATGGT	GCTGGGATAA	CTGTCTAGCT	ATATACAGAA	GATTGAACCT	GGGGCCCTTC	CTTACATCAT
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	CAACAAAAAC	CAA ATTGACT	AATGAAACTA	ATGAAACTCT	TTAGTTGTAC	AACAGATAGT	TTATCTGTAC
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	CAAAGGTCTA	ATA'CCAGAA	TCTATAAGGA	ATTAAACAA	ATTTACAAGC	AAAAAAATGA	CCTCATTAAA
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	TGCAGCCATA	AAA ATGAACA	AGATCATCAT	GTCCTTGC	GCAACATGGA	TGTAGITGGA	GGCCATTATC
	CTAAGCAAAT	TAAT'GCAGGA	ACAGAAAGCC	AAATACCACA	TGTTCTCATT	TATAAGTGC	AGCTAAATAT
	TGAGTACACA	TGGA.CACAAA	GAAGGGAACA	ATAGACATGG	GACCTACTG	AGAATAGAGG	GTGGGAGGAG
	GGTGAGGATC	AAA AGTACC	CATAGGACAC	TGTGCTTATT	ACCTGGGTA	TGAAATAATT	TGCACACCAA
	ACCCCTGTGA	CAC CAATT	ACCTATATAG	AAAACCTGTG	CATGTACCC	TGAACCTAAA	AGTTAATGGT
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	ACAGTATGGA	TCT'CTGAAG	CCAAATAACT	CTTATTCAAT	GCTTAGTTGA	GAAATTAT	GGAGTAGTC
	TCAATTGTTA	TGTA-GTTCCA	CTGCAAAGGT	AAGTCTTATG	GAAAGATTCA	CTGTAATT	TTTCCTCAT
	TTGGACATCA	GCT'TTTCTT	TTCCCTCAGAC	CCGCTGAAAG	ATAATTTTA	AAATAAAAC	CTTGT
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	AGATAATAGT	GCT'AAAGAT	TTGATATATA	GACACACAC	CATATATACA	TATATATCAT	CCTAAACTTC
	TTTGATAAAA	TGTA-TATAAA	GTTTTAATA	AAAACTAGGA	GATTAATGCC	CTTGAATGA	AAATAAATAC
	AATGTGTATG	CTT'AACATC	TTGCCCTTAC	TTTATAACAT	TTATCACAGC	AGTCATGAGA	TAATGATT
	CATGGTCATT	GTTA-GTAAGC	TAATAGCTAA	GTGCGATGAC	TCTGGAGCTA	GCCTCCCTGG	ATTTTAATCC
15	CAGATCTGTC	ACTGACCAGC	TGAGCAATAC	TAGGTAATT	GCTCTGTT	CTTAGTTCT	TCATCTGAA
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	CCTACCACTA	AGCCGCGATGC	ATGCAAGGAC	CATGTTGGTT	TTGTCACACA	TTGCATCCCC	AACCTGGTAT
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20	AGAAATACCC	ATT'ACTGCA	AGTGTGCTA	ATATTGATGG	CATAATGGGG	GAAACTCAA	CTCTGGAGTC
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25	TGTCCCTGGA	GCAGTGCAGT	ATAGGAACCC	TGAGGGGACC	TACAGTATAC	TTTATAGTT	ATAGATTACA
	AATTATCCCT	TTATCAGAGT	CTCTCAAGGT	TGGATGT	TGAGGTCCAT	AAGAGCAATT	TAGGATTAAAC
	AGTAGCTGCA	GAA ACCATCT	GCAGTGTAT	TCTCATTTA	AATCCGCGGG	AAAGAAGACA	GCTATAAACT
	TGGGACCTGG	GTTC'AAGCAT	TTAAATGCC	AAAGTCACCA	TTTCTAA	CACAAACAAAT	ACCCAGTGA
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	CCTGCTCTGA	GGAA GTGGCA	CAGCCTAGAA	CAGCACCACA	GGTGAGAGAA	ATGCAAACCC	TAACCAGAGA
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	AAGTATTGGC	AGA AGAAAT	AATCTGGGT	TAACATATAAC	TAGAATATTG	ACTCTTC	TGTGGAAGAA
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	GTGAAACCCC	GTCIGTACTA	AAAATACAA	AAAAAA	AGCCAGGGCT	GGTGGTGGGC	GCCTGTAGTC
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25	CCACAATGTT	GCT'AAATTG	CTCTCAAAT	TCAAAGGGAT	GGGAAGGACA	CCTAAAGTCAT	AGAGCTTTA
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	GTTCTCAAAA	TTCT'CAGAGA	GCTTAATT	CATGCTCACC	ATAGCACC	TTTCTTCTA	AATATTG
	TTCTACCAAA	ATA'TTTGTC	CCAATT	TTTTATGGC	TATTTCTCA	TATCCACTT	CCCAAAC
	AGAAGCAGCC	CCT'CACCTT	AAACTCCTC	TTCAAAGCAA	CCTAAATACA	GGTCTGGGTT	TGTATTCTA
	GTGGGATGTT	ACAGAGGTTA	GTGTGATGCA	GAGGAGGAGT	CATGCTGTT	AAATCCATAC	TAGTCCCCAG
60	AGGCCAGGCT	GCT'CTGCCA	CCCCTACCC	TCCCGCCACA	GAGCTCTCA	GCTCTCACA	TTTCTAGTTC
	TTCTCTCTC	ACTT'CATTA	CCTTCTCT	TTTTTTTTT	CTTCTCATGT	GTCACGGGA	GCAGAGAAA
	TTAACTCCTC	TAAC TTTCT	TAACACAGAG	TGCCTTAATT	ACATATTACT	ATTGTTGAG	TTCCCTGCCAA
	CACTACCGTCT	GTAC GGTCA	ACCTGCTATA	TTAGAGGCTT	ATCAAAAAAA	GATAGCTTTC	TCCTAAAGAAG

	GGATTTGGAT	GCC'ACTAAG	ATAACTGGAT	GCCAAGATAA	GTTAACCTA	ACAAACTTA	TTATTATTAT
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5	ACTGCAGCCT	CAAAGTCCTG	AGTCATGCA	ATCCTCTGC	TTCACTCCC	TGAGTAGCTA	GGACTACAGG
	CATATGCTAC	TCTGCCAGC	TACTTTAAA	AAAATAATT	GGGATGGGGT	CTTGTGTTAT	TGCCAGGCT
	CGTCTCAAAC	TTCTGGTTC	AAGCAATCCT	CCTGCCTTT	ACCTCCCTAA	TTGTTGGAGT	TACAGGCATG
	AGCCACAGCA	CTCAACCAAG	ATTTAAAAAC	TTTAAAAGA	AATCACATA	CTTACTGTTA	TCATCATTAT
	GGTTACTACC	AGTCITAAAAA	CAATTGGTAT	TGAAAACACC	ACTACCAGAT	CAAGCTCAA	ACCAAGATGT
10	CAAGTAAATA	TTATGTGAG	ACCTCTGAGC	CCAAGCCTGC	AGGTATACAC	CCAGATGGCC	TGAAGCAAGT
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	GAGTACCTTG	TGACCCCCAC	CCCTGCCAC	AAGTAAAAAA	CCCCCTTGA	CTGTAATT	CCACTACCCA
	CCAAATCCT	ATAAACAGC	CTCACCCCTA	TCTCCCTCG	CTGACTCTCT	TTTCAGACTC	AACCTGCCTG
15	CACCTAGGTG	ATTCAAAAGC	TTTATTGCTC	ACACAAAGCC	TGTTTGGGG	TCTCTTCACA	CAGACCATGT
	GACATTGGT	GCCGTAACTC	AGATGGGGA	ACCTCCCTG	GGAGATCAGT	CCCCGTCTAT	CCTGCTCTT
	GCTCCATGAG	AAAAGATCCAC	CTATGACCTC	TGGCCTCAG	ACCAACAGC	CCAAGGAACA	TCTCACCAAT
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25	TTTCTCTGC	AATACCGCTT	GACCCCAATA	CAAACTAAC	AATGGTTCCA	AATAGCCTGA	AAACGGCACT
	TTCAATTCT	CCATCCCACA	AGATCTAAAT	AATTCTGTC	GTAAAATGGA	CAAATGGTCT	GAGGTGCC
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	TCCTCTTTC	CCTCCTGCC	GTCCCCCTAG	TCCCAACCCC	AAAGTTCGCT	GAGTCTTCC	AATCTTCTT
	TTCTACTGAC	CCATCTGACC	TCTCCCTCT	TCCCCAGACT	GCTCTCTCT	AGGTCGCTCC	CCGCCAGGCT
30	GAATCAGGCT	CCAATTCTTC	CTCAGCGTCC	GCTCCTCCAC	CCTATAATCC	TTCTATCACC	TCCCCCTCTC
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	AGTTAGTATT	TAGCCTTTT	TTCATCAAAT	ATGAATACCT	AGCCCACCTC	ATGGCTCATT	TGGCAGCAAC
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5	CTTAAACTCT	CCT CCTAAA	ATTCCAGAGC	AAGTCACTAA	ACCCTAGATA	CTGAGAAATA	TTTTCCATC
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	ATGCTCCCTA	TCTT CCCAC	ATTTCTGAAG	GACAATGCCT	GTTAGAGCAA	TTGAATGCAA	ATAGTCAATT
	GAATAAGCAT	TTA TCATT	CTCAATAAGT	GCTTGTCAA	TTGAATATT	CTTAAATAAT	ATATTAAGA
10	ACAAGAAGAA	CAC ACCACAA	TGTTTTAAC	CCTCAGAAAA	AATTCTGAGG	TAATCAGAAA	AATCTCCCTT
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	AAAAGCACAG	CTC GAAAGG	AAGCTAGTAG	ATTATCACC	TTATCTGGTC	ATTGGATGTA	GGACCCCAAGG
	TAAATAAACT	ACTA TGGGGT	TAATGTGTCT	AGCTAGAGCA	GGAAGTAACT	TAAGGAAGTA	GAGAATGAAT
15	CAGCAGATGT	GGA AACTCCT	CGCCACTAA	AAAACCTACC	TTCTCTTGA	TTTCTGCCT	GAAAATAGAA
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	ACTCTCAAAA	CTG CTTTTG	AAGTATATTA	GGTATTGTT	AGGTGGACCC	TATCTGTGTC	AAAGGAGATT
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25	GATTTTGTA	CCCI AAGTTT	AAATTGGCT	TTCTTTTTT	TTTTTTGTA	CTCAATAAAA	CATCAAGCTC
	ATTTTATTATT	GC GAAGAGCG	AAACAACAA	GCTTCCACAG	CGTGGAGGG	GACCGAGTG	GGTTGCCAA
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	CATTCTTTT	GA AAAAAGCA	GAATATAAT	AAGTAGATAA	CTTAAAAAAA	ACTCTTGAG	CAGAAAGAAT
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	CCGGGGTCAA	GATT TGAAGT	CTCAATGGAA	AGAATAATCA	GTGGTTGGAG	AAA ACTGTCA	TTCTTCTTT
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	GTTATACATA	GCTA ATGAAG	TTCTTGCA	TCAACAATCC	CCACCCCCCT	CACACACTTT	GTCTTCTGG
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	CAATTAGGGA	CTGATAAATA	ATATTTTGT	AATTGCCAGT	GTAAATGGAC	AGGGGGCAAC	CTTTACATAC
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	CAACAATGGG	AGA AGGACCA	AAAAATGATA	AACCCCCGTC	CCTTAATAAG	CTCGTATTGT	AATTGAGATTG
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	CATAACATAC	CAC ACAGAG	CATTGTCCAC	CCCCACAAC	TGAAGATGTT	CCATAAGTCC	CTCTGGGTGC
	TCTGACATT	CCAT 3GAAAT	ATCTGCAAAT	GAAATACAA	ATTATATT	GATGTATACT	CTTAAACCAC
30	ACATTATAG	CCTTGAGGT	GGTGTCTACA	ACTTTCTAA	TAATCAGAAAT	AAAACACATA	TGTCTACTAA
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	TTTCTATGG	TTTG 3TAATT	TTTATACCTG	CTTITCTGCT	GAGCTATTAG	ATAAAACAT	TTAATATTAA
	CTATGTAT	TTTT TAAAGT	ATTGTTGCTG	CTTAATTAAAC	TATTGATGCT	TATATTAAAT	GTTATAGCCT
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25	CCTAACATAC	AGAAGAAAAC	AAATAGGGAA	TAACATTAG	ACATCTTCAT	TCGTTAAAAA	TCTACCAGAT
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	GACATTATA	AAAATATACC	TTTGTGTGTT	TGCAATTATG	CTTTTATTAG	TTCAAAACGT	TTGGCCTCAT
	GGAAGTTTT	CATC GTGGAA	ACCACATATT	TCTGAAAAAA	TATCTGACAA	TATACAAACC	TTCCATTCA
30	TTTTTACTCT	CCAA TCTAC	CATGTTTCA	AAAACAACT	GTAGTAAAAA	CACTCAGAAC	TTTATTCTGG
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	CAAGTTTTT	AAAGTCCCTAC	CACACTTGA	TTGAATGAAG	AAGTATGGAA	GATTATAATA	TATTCAATGC
	AAGTAAAAAT	ATCACAAATCC	TTAAGAACTC	TTAAGAAGC	ACTGAATCCC	ATAGGGATGA	AAGTGATTA
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	CTCATTCAAA	AGCACAGAGC	TAAGGGTTGA	AACCAGGCAG	TTGATATCC	GAGCCCACTC	CCTTACCTGC
	TACTCCAAAC	CATCATTCT	TTTGTGTTA	TGCCCCGAGA	TTCTTGTTC	TACCCAAGTT	TCCTGTACTC
50	TTCTTGCCCT	CTTC'CCCG	AGACATCCTT	GACCATCACA	GCTCTCCACT	GAGATAACTG	TGTCCTGGGT
	TCTGAGACAT	GGGG GCTGGA	AGGGACCCCA	GGGACAGTGA	GCAGTAGGG	GAGGATGCAG	TGAGAACAGA
	CCCTGGATCC	CCGG'GCATA	GGCAGGGAGA	AAAGTGGACAA	AGGAAAAAAC	AAGCAAGGCA	GGTGGAGCCA
	TGCCTAGGTA	AAAGTGTATCC	CTAAGCCACA	GTTCCCAGAA	GTTCTGATT	CAAAGCAAA	TTTTCTCTAA
55	GGTCAAAGGG	CAAATGTGATT	ATTCTAAATT	CTAAACTGAT	TATTTCTAAA	TTGAGAAAGC	TTCAGGGAGA
	GATCCAATA	TTCGAAGGAT	AAGAGAAATG	AGGAGTGGAA	GAGATAGGTG	AGTAACAGTA	ACTTAAATGT
	AGACTATATA	TAATATATAA	TATATGTAGA	GTATATATAT	ATAATTACAA	TATATTATAT	ATGTGGAATA
60	TATATATTAT	TTATATATAT	TTATATATT	TATATATATA	GATATTTTA	TATTTTATAT	ATAAAATATAG
	ATATTTTTAT	ATTTATATA	TAATATAGA	TATTTTTATA	TATATTATAT	ATAAAATATAT	GTAAAATACT
	GTGAAAGAAG	AATA GAATCT	TGAGACCTCA	AATTCACTAT	GCCAAAGGG	AAAGTAAGCT	TGGGAAATGA
	GTCATGCAA	AACTGCCCTC	CTTTGTCTCC	CAAATACCTG	TAATTCACA	TGCTTACTTT	ATCTTATATA
	AAATGTAGAT	GTACTGAGCA	TGAGATCCAT	GCATAATTTC	CCTCTAGTCC	CTTCTTTITA	CATGTAAGT
65	GTAGACTCAC	TGAGTGTTC	AGAGCCTGC	CACAATGTAA	ACACTTGCT	CATTGCCAAC	CCATCTTTCG
	TTTATTTCT	CCCCCTCCCG	CTTGCTCTT	CCCCCTCTAA	GATGGAAGTT	CCCAAAACTC	TCTTGGAAA
	AAGCGCAGGT	CACAGATCCT	ACAGTGATTT	GTGTTCTTT	TACCTGGGAC	AAAATAAAC	TCTAATCTGT
	TGAGATATGC	TTCAGTTACT	TTTGGTTTA	CAATATGTAC	ATGTATGTAT	ATAATTATA	TGTATATAAT
70	ATATGTACTT	GTTTAACCA	GAGGTATGTT	ATTCAAAATC	CATTATCCT	TACAATTACC	TGCATTCTCC
	CACAGTATTT	TCTG'GTCCC	TGCCCCCGAG	GTTGTCACTG	CAAATCAGGT	ACATGGATAC	TGGGAGCTGA
	TGGGCTCCCC	TCTG'GCTACC	TGGGCTGCTG	AAGGGGCCAT	AGACAGACCC	AGCTTCCCTC	TCGTGGAGAG
	GCCCTGGGCC	AGCC CTGCGT	GGGAGTGGGA	TTACAACCAG	ACTATAGCTT	CTTCACCTGC	TTTTTCCCTAT
75	CAGGATTTC	TAAGAGGCAA	TTGCTTGT	TTTGAGGGTG	GGGGCAAATC	AGGGGGAGTT	GAAGAGGAAA
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	TCTGCTAAC	TCTAAGTTAC	CTTGCAAG	TCTTAGGTAG	AGGGAGGAAA	TCCCAATAAA	GATTCCACCC
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5	TAGAGAATGG	CATTTTTGT	TTGATCAAA	CCTAAATATA	TTTGATGAAA	ATGTGTCTGG	TTCTAAGTTT
	ATTCCCCAGA	AAGCAGTGT	TACTCACTT	GAATTATAG	ACATCTTATA	ATATCTGAGT	CGAGTAGGAG
	CTCCGGCTC	TACCTCACTC	TTTCTCCCA	CACCCAGGGG	GAAGTGTAGG	GTTCTCAGAC	TTTAGAATAA
	AGAGGAATCA	CCTC GACAAC	TCACCTAAAA	TGCACATCTT	CAGGTCTCAT	ACTCAGAGGC	TCTGACTCAA
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	AGACCCGTG	GTTCGTGCTC	AGCTATAGGT	ACCAGAATT	TGATCAAAT	TTACTATCAT	TGTGACACTT
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	TTTGCTTCC	TATTGGCAG	CATCTTATCT	TGAAGTTCC	GCTTTCTGCT	TGGGACCTA	AAAACTAACT
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25	TTGGAAATGA	TTGGATTAAC	CGGATAACAA	TGAATATT	AATACAGTGA	TTTGGCCAGG	AGCAGTGGCT
	CATGCCIGTA	ATCC CAGCAT	TTGGGGAGGC	TGAGGCGGGT	GGATCACCTA	AGGCCGGGAG	TTCCAGACCA
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	TGTAATCCCA	GCAACTCGGG	AGGCTGAGGC	AGGAGAATTG	CTTGAACCCG	GGAGGCAGAG	GTGCACTGTA
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	GACCACCTG	GCCATGGTGA	AACCCATT	CTACTAAAAAA	TACAAAAATT	AGCCAGGTAT	GGTGGTGGGC
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25	CTCTCAGAGT	TCACAGAATT	GAAGAATGTT	GGGCCTTGG	TTACACTTTG	TTTAAGGGGA	ATGCTGTGGC
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	ATGAGATGTT	CTCTTATCAT	TTTTCATCT	ATCTTATAAT	CTTGGTGTCT	GACTTAGACA	CTCATTTCC
	TTTTGTACG	TGACCATGTA	AAAGTTCAAG	TCAAGAAAAA	CTTGTTTTGA	CATTGTTTT	GCTGAGTGT
	GGGTCCCTAA	AAGA ATT	GCTTGCCTT	TGAAAAGTTC	AGCATGATAT	TGTGTAATT	TTTCATGGCT
45	AATGATT	AGAACAGTTG	TGATGTGTTT	AGGTGTTTTA	AGAATATGAA	GCATTCACTG	GTTTAAGTTG
	GTTGTTATAA	AATG AAAGAA	TATGAAGGAA	AGCCTTCTTG	TCTTAAACAA	CACTGATTCA	CAAATAAGCA
	GCTTCTCTCA	AAAT GTTGTA	ATTACAAAAA	TTCCAAGGC	AATATAATAA	ACTCCTGTC	GGTGCTATGT
	CTAGAAACTT	AACAGCCCCA	AAGAAAGTCC	TGACAAGGC	AAAATATAT	ATATATATAC	AAATTGTGGA
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50	GCTTGACACT	TGACTCTTTT	GACGAGGCTG	AGGGAAAACA	CTCAGTTCA	TAGATTGCTG	GTACGGATGT
	AAAATAGTGA	CATC CCTATA	GAGAGGAATT	TGGCAATATC	TAGCAAAGT	GCTTATGCAT	TTATTCTTG
	ACCTAGTAAT	CCCG CTTCTA	GGATTAGTGG	TGAAGATACA	CCTCAACAA	AAAATATAT	ATACATTAGG
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	CTGAATAAAC	TATGGTATAT	CTGTACAATA	AACTGCAATT	CACTTATGTT	GTAAATTGTT	TCCAAAATC
55	CAGAGCCAAA	GAGI ATTGTT	TATGCTCTCT	TTAGTATAAG	AAAGGGAAA	TAAGATATGT	GTGCATCTGT
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	GTAGAAATAG	AATGAAAGTG	AATTAGGCTT	CTTGAGTAT	ATGTTTATAT	ATAGTTTGA	CTTTTGAATT
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	ATTCAATACT	TTAGCTTGGA	GAACCATTC	GAGTTCTAA	CTCATTGTAT	TGCCAAAAAT	AGAAAACAGC
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50	TGGTCTCAAA	CTCTAACCT	CAGGTGATCC	ACCCGCTT	GCCTCCAAA	GTGCTCGAT	TACAGGTGTG
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	ACTCATTCCA	GCATTAAGTC	AAAAATCAA	GTTCAAAGTC	TCATCTGAGA	CAAGGCAAGT	CCCTTCTGCC
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	CCTCCCATG	CAGG TGGGG	TTATGGGAAC	TACAATTCA	GATGAGATT	GGGTGGGGAC	ACAGCCATAC
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	ATAGGTCTAT	GTTCAGCAAT	CTGCTACTCC	ATACAGAGAT	TTGAGTTCAC	TTGGAATTT	AGTGCTGCTT
	ATATGTGACC	AGTIACTCTG	TTTACTTAT	CTATGCCCTA	AACATTACTA	TACTTACTAA	CTCCAAGATG
	CCTGGTCTCA	ACTTGACAAA	AATAACCCAA	GTTGGGAAAT	CCTTATGTGA	ATATGTAGAT	AGTCACAATT
60	GCTGGTTGAT	GATGATCTGT	CTTTCTGT	ATTTGAGAAA	ATGGAGATAA	AATGGACCAA	TCCAATAAT
	GGATTAAACA	TGGGAATAGG	TGAGAGAGAG	AGAGGAATAC	ATGGTGGCTC	TCAGTGTCTG	GCTTAGGCAG
	TAACACCTTT	CGTTATAAAA	GACGGAAAAT	AAAAAAAGAA	TAATTGGTGT	CTAGGGAAA	ATAATGAGCT
	CAAGTTTAA	CACTCTGAGT	TCGGGATGT	GAGACATCCA	GGCGCATTAA	TCCAAGAGGC	AGTTGGAAGC
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	TTGTCCCAGA	TAAAAGAAAAA	AAAAAAAAAG	CATTTTTTT	ACACAAAAAC	ATATACATGA	AAGTTCATAG
	AAAGTGTATT	CATAAAAAC	TGGAAAAAAC	TGAGATGTCT	TTATTGAGTG	AATGCTTAGG	CAAACGGTGG

	TCTATCCATA	CAATGGAATT	ATGCTTAGCA	ATAAAGAGAA	AAGAACATT	GATACATGCA	ATAACACAGA
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5	TATTTACTTA	ACATTTAAA	AATAGCAAAA	TCATAGAGAT	GGAGAACAGA	TTAATGGGTA	CTGTGTTTG
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	ATTCTATGTC	TTGGITGTAG	TCGTGATTG	AGGAATCTAC	ATGTGATAAA	ATTGTATGGG	TCTACATACG
	CATACACACA	AGAGCATATA	AAACTGGTGA	CATGTGAGA	AGCTCCGAC	ATTGTGCCAA	CATCAGTATC
	CTAGTTCAA	TATCAGACTA	CAGTTATACA	AAACATTGTC	ATTGAGGGAA	ACTGGTAAA	GGGAACACAG
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	ATGATAGACT	GGAT TAAAGAA	AATGTGGCAC	ATATACACCA	TGGAATACTA	TGCAGCCATA	AAAAATGATG
75	AGTTCATGTC	CTTTGTAGGG	ACATGGAGGA	AGCTGGAAAC	CATCACTCTC	AGCAAACAT	CACAAGGACA
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	GGGAACATCA	CCC ACTGGGG	CCTGTTGTGG	GATGAGGGGA	GTGGGGAGGG	ATAGCATTAG	GAGATATACC

	TAATGTTAAA	TGATGAGTTA	ATGGGTGCAG	CACACCAACA	TAGCACATGT	ATACATATGT	AACAAACCTG
	CACGTTGTG	ACATGTACCC	TAAAACCTAA	AGTATAATAA	AAAATATAT	ATATATATAT	AAAACAAC
	AAAATAAAC	TTCI TTTTCT	GCAGGATCAG	TCCATCACCA	CACACACAGG	CTGTGTTTA	TGTTGTTCCC
	CAGCTTAAGA	GATCGTTCTC	CAGATCCCAC	TGCTCCTTCC	AGTTGTCA	TCAGTTCTCC	ACTTCTTTT
5	GCTGATAAAC	TACT'CTAACT	AGTTACATAT	GATTCTGTG	CCCAGGTCCC	CTCCCTCAGT	TGTTTGAAAC
	ATAATCATTT	ATATCATT	TCATTTCAC	TCTAATIGCA	CAACCAAAAA	CTCCCTTTT	TTTAGATGG
	AGTCTCACT	TGTCACCTAG	GCTGGAGTGC	AGTGGCATGA	TCTCGGCTCA	CTCCAACCTC	CGCCTCACGG
	GTTCAAGTGA	TCCC CCTGCC	TTAGCCTCT	GAATAGCTGG	GATTACAC	ATGCACCAC	ACACCTGGCT
	AATTGCTTG	TTTITGTTG	TGTGTGTG	TGTTTTTTT	TTTTTTGGA	CAGAGTCTCA	CTCTGTTGCC
10	CAGGCTAGAC	TGCA GTGGCA	TGATCTCAGC	TCACTGCAAC	CTCCACCTCC	TGGGTCAAG	CGATTCTCCT
	GCCTCAGCCT	CCCC AGTAGC	TGGGACTACA	GGCATGCACC	ACCATGCCAG	GCTAATT	TTGTATTTC
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	TGGACCTCCC	AAAATGCTGG	GATTACAGAC	TTGAGCTACT	GCGCCGGCT	ATTGTGTGTT	TTTAGTAAAG
	ACGGGGTTTC	ACCA TGTTGT	CCAGGCTGGT	CTCAAACCTC	TGACCTCAAG	TGATCGCTC	GCCTCAGGGC
15	CTCAAAGTGC	TGGC ATTACA	GGAGTGGAGCC	ACCATGCCTG	GCCATAAAAC	TGCCCTTGT	TAATATGACT
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	TGTCTTCTC	TCTG ITCCCTC	TATCTGTTTC	CAGTACTG	GCCCTGGCTT	CTTTTACCT	CTTTTATATG
	CTCTTCCAGT	CTCAAGGCTCC	TTTGGGGATT	TGAAGGTATG	TTGCATTITG	CTATTCAATG	AATAATGACA
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	AGTTCATCTA	CTGTGAGGA	AATTGGACAA	ACATTGAC	TGGTATAACC	AAATACAGTT	GAACCTTTGG
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	AGAATTAGTA	AAAC TAAATC	AAGGATACAC	AGGTAGATT	GAATTTCAGA	TAAACAAACAA	ATACTTTTT
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	TTCCCTCCAG	TTTT TATCC	TGGCCCAGAT	CTGCAATGAA	CACACGACAG	AATCCAGGGG	GGATGAAGAT
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	GTTTGTCTC	GTGGGGCTGA	CATGAGGTT	ACTGTGACCA	CTGTTGTTA	ACCCCATAGT	CTCCTGGAAA
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	GCTGCACCC	TCAACTCGTC	ATTTACATTA	GGTATTCTC	CTAATGCTAT	CCCTCCCCCA	GTCCCCCACC
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	GAGCAGTATT	TTCC TTCAAC	CATGAGTGT	TGCAGGTTT	TCTTTTCTT	TTTGAGATGG	AGTCTCACTC
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	CTAAACTAA	AAAAA	AAAATTCCC	AATGAAATAT	AAAACTAAAG	TGCTAAACTG	TGATAGACTG
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50	TGGACTCCTT	CTCTCAGCCA	AAGGAATACC	AAAGTAAACC	TGAAA	TTTGGCCA	GGATTGGGG
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	GCATTGACAC	TAACACACAG	ATCTTAAGAC	TGACAAGCCA	GACTCTTGT	AGCAGAGAGC	CAGGCCCTGG
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	AGCTTCCC	GTAC CTGGGA	TTACAGATCC	ATGCCACTAT	GCCCAGCTAA	TTTTGTATT	TTTTGTAGAG
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	CTAGGTGCAA	TTCAATTAA	CATGAATTAA	TGAATTAAACA	CGCTCTCAA	GTTTAGTGCT	TTTCACAGA
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	ACCTATTATC	ATTTTTTG	GACAGGTTCT	CGCTGTCTCA	CCCTGGCTGG	AGTGGAGTGG	CATGACCACG
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	TGCTTGCTTG	CTTAAATACA	TTTCTCTTT	TCTGAGAAGG	CTTGAGTCCA	AAACTCTAG	TTACCTGTTG
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	TAAAGATTTT	AAAG CCTTCA	GATGCTGGTT	CAAGGTGAGA	AATGTGATTG	GGAGCAAATC	ATTAAACTTC
	TTGAAGTCTT	ATAGGGCAGT	TATGAATACT	TAATGTTAAC	ATATGTAAG	CTCTCTGCC	CTGTATACAG
10	TAAATGCTAG	TTAG CTATTA	TGATCACTAC	TAAAATGGGG	ATGACATAAA	CCTCATAAGG	TTTAAGTAT
	TATGCAAGAT	ACT ATACAAA	GTCCAGTAAA	TATCACATT	AATTGAATCC	ATGATGTCCG	ATTATTTAG
	CTACTTCAA	GAGAGAAAAA	AATGCTGCA	GTTTACTGT	TCTTATAGAG	AGCAAGGCAG	ATCCCAATTC
	CCAATGTGGT	AAAC ITGAAA	TTTTGCATT	TGAATCAACA	AAACACTTTC	TCCTTCTTT	CCTACTATTT
	ACAACTGGT	AAG CTATAC	TCCCCAAAT	CTGGAATTCT	CCTTTCTT	TCTTTTCCCT	CCTACCAAGA
15	CCGCAGGATC	TTTACTTGG	CTATAAGGGG	TAACACCTAA	GTAGTACAAG	TTCTCTGTAT	TACTTTTATA
	CTCTGTCACA	GATI CCCC	GTTCCTCAT	CTCCATGTGA	ATTTAGTTAA	ATTCTCAGCA	TTCTGATCCT
	TACTATACAA	GGTA AAATGAA	TATAAAAACA	AAACGAAACA	AAAACCTTT	CCTATTACAA	TAAGGCCCCA
	ACCTAATATT	TAGT GATATA	TATTAATGTG	AAACAAGGAAC	TAACGAAGAC	TGGGAAGAAA	TTCACAGACT
	TGAGAGAAGA	AATG GCAGGA	TTTCTGGGA	ACAATTTCAT	GTAACTGCAA	AGGTGGTAAA	AGGTCAAATA
20	GAATGAAGAT	GGAGAATACC	GGATTTTCTT	ACAAAATGAT	TTCCCAGGAG	ATCTCATCAA	ATGCACGAGG
	ATACCTTCTC	AGTTT CACCT	AGTGAGTAA	AGACTGGTAA	CATAGCTCAC	TTACAATTG	GATAAAACAAA
	ACTAAACAAA	CAAC ATCAA	ATTCAGAAA	AAATAATAGC	AAAACAGAAA	TCAAACACTC	AAATTTTTGG
	TCCCTCTGTT	TATT CATTT	TGGTACTCA	GTGAATGTTA	ATTAACCAAG	AAACTTAAAAA	GTTATTTCAA
	TTATGAACCT	CTTC AATCCT	TCATCAATT	TTTGAGTAT	TCTGGCTTA	AAAACATCTC	TTTCTTCTAC
25	AAACCTCTGA	AAG AGATGAA	CACCTCCACC	TACACCAAA	TAATGTGCTT	TGCTGGCCAA	AAGTACACGT
	CCATTTTAC	TTAA CAGTCT	AAGGAAAGTC	TGGTCAAAT	TACTATAATA	ATCTGGTTG	AAATGGTTT
	CTGAGGTGAG	AATC AGATCA	TATTTACAA	AAAGTTTTTC	ACTACTTAGT	ACAAGCTTAC	AAAACACTAGA
	CCACTCACC	GAA AAAATC	GGCATTATA	TAGTTGTGTT	ACTTTGGTT	TCCTGCATCT	TTTCACATCT
	GGCTCATTTA	CATCATTTTC	TTCATCTTC	AAAGTGGAGT	TAGCTACTAC	ATTAGGTAAG	GTTACTTCAT
	CAATCACCAT	ACTGTTATAA	TCTTGAAAGT	GAATTTCCTT	GGACCCCTCC	TTGAATGCAG	TTATACCTAG
30	TAAACCTGAT	CCACAACCAA	GATCCAAGAC	TTTTTCCCA	GCAAATTCA	CTTGGCCTT	TGTGAAATAA
	GCCAGGAGGT	CAA GGTACA	TTCCCAGATT	TTAAGCCTC	CCTCATAAAC	ACCTGTAATC	AGATCAGAGT
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	TGATAACTTA	ACAT GCTGGA	AACTGGTAA	TGTTCTATG	ACTTTATTT	CTAACATCTT	CTTAAATCT
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	CAAGT GATCC	TGAC GCAAGT	CAAATTGTT	TGCAAGACAT	TTTCTGTCCC	TCTCTCTCC	TTTTGACTT
	TCTGAGACTG	ACAC CTCTT	TGAGGAATCC	AGGGTCAAAG	CTCCATCTCT	AATGGGTGTT	AATTCAATT
	CCAGATGGTC	TTCT ATAGTG	AAATTAAAACT	GAAAGGTCA	CCTCTTATTA	AATGCACACA	ATCTTAAAT
	TCAGATTCTT	CAAC ITCTGG	ATAGAATTG	ATGATACACA	CAAATCTGCC	TCAATTATTC	AATTAGTTT
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	CATACAGCTG	CTTT TCTTA	AAAAGTTGTG	GGGAAGAGAG	AGAGATAAGA	GATTGGACAA	CTCATACACAA
	CCTTAAGGGT	TCCA AAGTGG	GAGAAGAAAA	TCAACTATAA	AAACAAACAG	AAGAACAAACA	GCAACCACCA
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	GTGTGTAAAT	TCAT CCAAGA	CTTCACTCCA	AAACATTAGT	CGAGAACAGC	AGCCCTAAAGT	GTATAGAAGT
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	GGCTTGGAGT	CACT TCCGGC	TGCAAGTCCC	GGAAACAATC	CGACCCAGA	AGTGGGGACT	TCTGGCCCTC
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	CTGGGCTTG	GC GG GTCTGG	TTTGAAGTC	TCCTGTTGA	CGAAAGTATG	TCTCAGGAAG	GTGCGGTCCC
	AGCTAGCGCG	GTTC CCCTGG	AAGAATTAAG	TAGCTGGCA	GAGGAGCTAT	GCCGCCGGGA	ACTGCCGTCC
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	GAACCTTCT	CTTC GTCCC	TTCA GACCA	CCGCCAGGCT	GGGTTATATT	ACCGCGGCCT	GAACCCCCCTC
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5	TAAGAATTAA	AGGC'CATAGT	TCTGTGGT	GAAATCTTA	AAAGATGTT	AGTAAATAAA	AATGATTTC
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	CAGGCTGGAG	TCTITCTGAA	AGAGTTCTTC	CGCTTGTGT	TGGTTCAA	CTGTTGGATT	TGAGGCGCTT
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	CAGTCAAATA	AAGT TGGTAA	GATAGGTATG	TAAGTAATAT	GAAAAAAGAT	AGAAGGTGAT	GAGTGA
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5	TGTTTTGTT	TGTTGT	GGGGGACAGG	GTCTGCTT	GTCACAAAAA	CTGGAGTGT	GTGGTGCAGA
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	GCTCACCCAT	GTGACTTCAG	TGACTTCAT	CACACTGGC	TGTTGGCAGA	GGCAGAAGTA	CTTGAGAAAAG
20	CCATGTGCA	CATCCAGCAG	GTTCACCTA	TCTCAGATAC	CTGATGCCAG	TGGTTTCAGG	GTTCATAAGA
	GTAGCAAAAG	TGTGAGCAGG	TCGCTGTGT	CTAGCACTT	TCAAGTTCT	GCTTGCCTTA	ATTTTATTAT
	TGTCCCCCGG	GCCACAGCAG	GTCATAGCGT	TTAGCCCAGA	GTCATTGAG	AAAAGTGTGG	ATTCAACAAAG
	GGCAGTCATT	GTGCCATT	TTATAAATAA	TCTACCACAG	ACTGAGTAA	AGCCTTGCAT	GAATACCATG
	GATATTAAATT	TGAATTCTTC	CTTTTTAGAT	TTCTTTCTC	TAGCAATT	TTTGTCTATT	TTGGATTAGA
25	ATTATATCTG	TAGAATATT	CAGTTATAAT	AGGTACAAAC	TTTTATTCCA	CTGAACATCT	TTAGTTTAT
	TTAGGTCTAC	TGGTAGGTAT	AAACTTCAGA	AGTTAATATT	CAATATTAT	AAAACCCATT	AACAAGTGTG
	ACACTTAAT	AGTITAAATA	ATTCTTTGA	CACAACTGTT	TCCAAGTTGT	GTTACGTATT	TTAATTCAAT
	CAAATGTTGA	AATTGTTAG	TAGATAGTT	TAATTATAGG	AGAAACCTAC	CCCCATGACA	TTTGGATGTC
	TTAAAAGTTC	TGTIATCTT	CTTTGAGTT	ATTCACTT	TATTGGATAT	CTGCTCTGTT	ATTTCCAGTA
30	TGGACCATGC	ATTICATGCC	AATACTTGGA	AGTTTATAAT	TAAGTAAGTT	TGTTTGTAT	TTTTTACTTT
	TTAGAAAATG	TTTICCATAT	TCCCCAATCT	TAATTATTCA	TGATTCTTA	GATTGCATT	AAAACATT
	GTGTGAATT	AATGTTCACT	GACACTGCTG	TCTGATAATC	CAGATATTCT	ACATGTAGCT	CTCAAGCCAA
	ATTGGACTTC	TTAACCCCTGT	GGCCTCTAA	ATTTAAAAAA	ATGTTCTTC	TAGTTAGCTA	GTACTTCAGA
	AATAATGGC	CATCGGCCAG	ACTAGAACCT	AACCACTTT	CTTCTGCTAC	TGTTGTTAA	CCAGCTATCA
35	AGTATCCTAT	TTCTAGGATT	AGATAAATTG	ATAACTATAA	TTAAACTGA	ATATAATCTT	TTCAATTAGGT
	ACTTTTAAGT	TGTTCACACT	TAATTCCATT	TGTACAGTAA	TTTAACCTT	CTGAAACTGA	AGCATTAA
	AGGGTCACCA	GGGATAGTGC	CTGTAGCATT	CATCAGATT	TTAGGGTGA	GAGGAGATGT	GGTTGAGATG
	AAAAATGGT	TAAC AATATC	TACTTTATAC	ACATACATAA	AAACATTAAAG	GTCAGTGTAT	TTTCAGGCT
	TAGGTACTTT	TCTGTACTA	CCAGGACATT	AAAGTGCCT	TCAGTGGTA	AGAGTGTGC	CTGGGAGCTG
40	TATCACATGT	GCTAAATCC	ATTCTTGGAA	TCATTACTC	CTTCTGAGCC	CTTGGGCTAT	TTGGTTAATT
	TCTCTGAACG	TTAGTTGCT	CATCTGAAAA	TGGAAATAAT	AATAGCAACT	TCTTGACAGG	GTATAGTGA
	GAATTGAGTT	CATCACTGTG	AAATGCTTAG	AAATGTGCAT	GACACATAGT	TAATACTCAA	GGAATTAGCC
	ACATCACTAT	CATCATCACT	GATTATCTTC	CACTCTTACC	CTCTTCCAGT	TCATTTCCTG	CCCAGCAGAA
	TGATCTTTA	AAAAGTAAAT	CAGATCATGT	TACTCTATTG	CTTGAAGTCT	ATCCCATTTG	ATTAAGAATA
45	ACAACCTAAT	CCTCTGTGGA	TGCTGCCCTC	TTCACCAAGCC	TGTCTCATGC	TGCTCTCCCT	ACTCTTAGTT
	CCTCAACAT	ACCAAACTCT	CCTGTCCCG	AGTCTTTCG	TGGTTTTTCC	ATCTGCCTAG	GATGCTCTC
	TCTCCTATT	TGTGTACCTT	GCTAACTCCT	GCTTACTGTC	TTTCAGTTCT	CAGCTTAAGA	GTTATATCTT
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	TTTACACAGA	AAAAAAATT	GCAACTTATT	TAACAAATA	TAACTGCTTC	AGAGGTAAC	TGGGCACATC
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	TATATCCAT	AATTACTTT	CACCCAGAGC	ATTGTTATTAG	ATTCTTAAC	GCTGTCATTG	CCTCTGGGGT
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	TTTTCTTCA	CCAA'CGCATT	GCGACCTTA	GGGATACAAG	TATGTTGTG	CATGTATATG	TATGTATCAG
	TCTTTAAAT	TTGATAGT	CATACATTG	TTTTATT	GAAAAGTTAG	AGTGGTGAAT	TGGTATCCCA

	TTTATGAAAC	ATTATATTCT	AAAAATTGT	AGTACGATTA	TTGGGAATTA	TAACTCATTT	TCCTGTAA
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5	ACTCTGTAC	CCAAGCTGGA	GTGCAGTGGT	ATGACCTTG	CTCACTGCAG	CCTCTGCCTC	ACGGGTTCAA
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	GCCTTGGCCT	CCCAAAAGTGC	TGGGATTACA	GGTGTGAGCC	ACCGCGCCA	GCCTATATGT	AATAATT
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10	GCTGATACAG	GGAA'TTCCTT	TGTACCTCG	CTCTCCCTG	CCAGTCAGCT	ATGGGGGTGA	AAGTGTAGGG
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	AACTTTTTC	TTCTGCTTC	TCTCTTTAT	CTCACCTGCC	CCTCCCCTTG	TATCCCTTCT	TCCTTTTCC
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15	TTGTTGGGT	ATCCATATAC	AATGGCAGGA	AGGGTGT	CTTCTTCTT	TTTATCTTAT	AGATTCTAT
	TCTCAACACC	AACCTCTCC	TTTTTCAGTT	TCCTCTTGC	TTCTCTTGAC	ACCACAGAGT	TTGAGCTAG
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	ACCTCTTAAT	AGTA'CACAT	TGGGTGTTAG	GTGCTGGGA	GGACACCAAT	CTTCAAGCCA	TATCATCTCA
	CTTGGAAAAAA	AGTCAAAATA	AAACCAGTAG	ATTTAATTAA	TATTACACTA	TTTATAGAAG	CATGTGATGT
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	GCTTCCCGGG	TTCA CGCCAT	TCCCCCTGCC	CAGCCTCCCG	AGTAGCTGGG	ACTACAGGCG	CCTGCCACCG
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	TTATATTACC	CACA CTTCT	TTGTTGGCAT	TAAGATGCAA	ACTTTGTTT	AAACAGTTGA	GTAAATCAA
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	GAATGAGAGA	GAAATTTAA	AGTAAGCAAA	CAAATAAGTT	GTGTGTCAACC	ACTCATTCA	TCATTAAACA
	AGTATTTC	GAGTACTTAT	TCTGTGCCAG	GAAATGTTGT	AGGTGCCCTC	AACAACCTAG	AGTCTAGCCT
	GAGACACAAG	TAAC'AGGT	ATTATTATAG	AATGGTATGA	TCTTGGAGG	ACTGGGTATT	GGCTGGCTCA
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	GGTGGGAGA	TTGCTTGAGC	TAGGAGTTCG	AGACCAAGGCT	GGCCAACATG	GTGAAACCCCC	GTCTCTACTA
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5	TCTGCTGAGG	AAAATGGACT	ATTTTCAAAT	ATTTTAATA	AGGGTCAAAA	TGAGGGATC	GCATTTTC
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	GCCCCCAGG	GCTCGCTGGG	CCAGCTCTG	TCCCAACCAC	CTGCTGCTT	AACCTGGCCA	ATAGGAAGAT
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5	ATCCATTCTC	TCTG CCAAG	TTGCTCTGTA	TGTGTTCGTC	AGTGTTCATG	CGAATTCTTG	CTTGAGGAAA
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	CTAAACTATA	TGCCATAAAC	CTCAAGTTAT	TCATTTTATT	TTGTTTCTAT	TTTGGGGTGA	AGATTCAAGT
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	GGACTGAATT	ACTCTCCAAG	TTGAGAGATG	TCTTGGGTT	AAATTAAAAG	CCCTACCTAA	AACTGAGGTG
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25	GATCATGTTC	ACTG CAATGC	TGGACACTAC	AGGTATCTGT	CCCTGGGCCA	GCAGGGACCT	CTGAAGCCTT
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	ACTTCTCAAG	CTCCACCACT	TCCTAAATCT	TAAGAACCTT	AATTGACAGT	TTCAATTGAA	GGTGTGTTT
	GTAGACTTAA	CACCCAGTGA	AAGCCCAGCC	ATCATGACAA	ATCCTGAAT	GTTCCTTAA	GAAAATGATG
	CTGGTCATCG	CAGC TTCAGC	ATCTCCTGTT	TTTGATGCT	TGGCTCCCTC	TGCTGATCTC	AGTTTCTGG
	CTTTCTCTC	CTCAGCCCC	TCTCACCCCT	TTGCTGTCCT	GTGTAGTGAT	TTGGTGAGAA	ATCGTTGCTG
30	CACCCCTCCC	CCAGC ACCAT	TTATGAGTCT	CAAGTTTAT	TATTGCAATA	AAAGTGCTT	ATGCCGAAT TC
	GCCGCCGCCA	TGGGAGTGCA	GGTGGAAACC	ATCTCCCCAG	GAGACGGGCG	CACCTTCCCC	AAGCGCGGCC
	AGACCTCGCT	GGTGC ACTAC	ACCGGGATGC	TTGAAGATGG	AAAGAAATT	GATTCTCCC	GGGACAGAAA
	CAAGCCCTT	AAGT ITATGC	TAGGCAAGCA	GGAGGTGATC	CGAGGCTGGG	AAGAAGGGGT	TGCCCATG
	AGTGTGGGTC	AGAC AGCCAA	ACTGACTATA	TCTCCAGATT	ATGCCCTATGG	TGCCACTGGG	CACCCAGGCA
35	TCATCCCACC	ACATGCCACT	CTCGTCTCG	ATGTGGAGCT	TCTAAAACCTG	GAATGACAGG	AATGGCCTCC
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	ATATGGAGCT	TTTCTGTATG	TTCCACTCCA	CTTGTATAG	ACATCTGCC	TGACTGAATG	TGTTCTGTC
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	ATGCCATAAA	CCTCAAGTTA	TTCA	AAGCTTCTAC	CCTAGTCTGG	TGCTACACTT	ACATTGCTTA
40	TGGTTATTTT	TGTGGCTCT	GTTATAACTA	TTATAGCACC	AGGTCTATGA	CCAGGAGAAT	TAGACTGGCA
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	TGTTCTACCA	CCTG AACTAG	GCTGGCCACA	GGAATTATAA	AAGCTGAGAA	ATTCTTAAT	AAATGAAACC
	AGGCAACATC	ATTCAAGGCT	CATATGTA	AAATCCATGCC	TTCTTTCTC	CCAATCTCCA	TTCCCAAAC
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	GAAGAGTAAG	AGG ATCAAGA	CTTCTTGTG	CTCAAATACC	ACTGTTCTCT	TCTCTACCCCT	GCCCTAACCA
	GGAGCTTGTG	ACCCC AAAC	CTGAGGTGAT	TTATGCTTA	ATCAAGCAA	CTTCCCTCTT	CAGAAAAGAT
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	ATGAACATAG	AAAATATCAA	AACTGAATT	TTCCCTGTAA	ATTCCCCGTT	TTGACGACGC	ACTTGAGGCC
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	AAAAAAATCA	TCTTTTATC	CTGGAAAGGAG	GAAGGAAGGT	GAGACAAAAG	GGAGAGAGGG	AGGAAAGCCT
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	TCACCATTAT	AAGCAATGCA	ACAATGAACA	TCTGTATAAA	TAATATTCA	TTTCTCTCAC	CCTTTATTTC
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	TGGATGAAGC	AGGJACATTA	AAATGGCACC	AGACATTCT	GTCATCCTCC	CCTCCTTCA	TTTACTTATT
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	CATGCCGTC	TTCC GGGAG	GGACCAAAGG	CGGGCAGGAT	ATAACTGACT	TCACCATGCA	ATTTGTGCT
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40	GCCTTAGGGT	AGTGCTAAGA	GGATCTCTG	TCCATCAGCC	AGGACAGTCA	GCTCTCTCCT	TTCAGGGCCA
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	CCACGGCCAC	ATTGTTCT	AAGAAACCT	CTGTCATTG	CTCCCCACATT	CTGATGAGCA	ACCGCTTCCC
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	AGTGTCTGTA	AAAC AGCCTA	GTTTTAATA	GCTATGGAAT	CAATTCAATT	TGGACTGGTG	TGCTCTTCTT
45	AAATCAAGTC	CTT AATTAA	GACTGAAAAT	ATATAAGCTC	AGATTATT	AATGGGAATA	TTTATAAAATG
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	TAAAGATGGA	GTTC T GTGA	CTGACTCTG	ATATCAAGAT	ACTGGGAGCC	AAATTAAAAA	TCAGAAGGCT
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	TCTACCCATA	TTACAGATGG	GCAAATTAA	GCATAAGAAA	ACTAAGAAAT	ATGCACAATA	GCAGTTGAAA
	CAAGAAGCCA	CAG ACCTAGG	ATTTCATGAT	TTCATTCAA	CTGTTGCCT	TCTGCTTTA	AGTTGCTGAT
	GAAC TCTAA	TCAAATAGCA	TAAGTTCTG	GGACCTCAGT	TTTATCATTT	TCAAAATGGA	GGGAATAATA
	CCTAAGCCTT	CCTG CCGCAA	CAGTTTTA	TGCTAATCAG	GGAGGT CATT	TTGGTAAAT	ACTTCTGAA
50	GCCGAGCCTC	AAGA TGAGG	CAAAGCACGA	AATGTTATT	TTTAATT	ATTTATATAT	GTATTTATAA
	ATATATTAA	GATAATTATA	ATATACTATA	TTTATGGAA	CCCCTTCATC	CTCTGAGTGT	GACCAGGCAT
	CCTCCACAA	AGCA GACAGT	GTTTCTGG	ATAAGTAAGT	TTGATTTCAT	TAATACAGGG	CATTTGGTC
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55	GCATTCTGT	TTCA TTCAAT	TCCACCTGCA	ATCAAGTCCT	ACAAGCTAA	ATTAGATGAA	CTCAACTTTG
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	CAGAGAGGGA	GTC ATTTCAT	TGGCGTTGA	GTCAGCAAAG	AAGTCAAGAT	GGCCAAAGTT	CCAGACATGT
60	TTGAAGACCT	GAAC AACTGT	TACAGTAAA	ATGAAGAAGA	CAGTTCC	ATTGATCATC	TGTCTCTGAA
	TCAGAAATCC	TTCT ATCATG	TAAGCTATGG	CCC ACTCCAT	GAAGGCTGA	TGGATCAATC	TGTGTCTCTG
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5	ATGATCAGTA	CCTACGGCT	GCTGCATTAC	ATAATCTGGA	TGAAGCAGTG	AAATTGACA	TGGGTGCTTA
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	GCCCAAGATG	AAGACCAACC	AGTGTGCTG	AAGGAGATGC	CTGAGATACC	AAAAACCATC	ACAGGTAGTG
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	TGTGAGAAAC	CTTGTGAGA	CAGAGAACAG	GGAATTAAAT	GTGTATACA	TATCC	CAGCTGCGGC
	ATCCTCTGTC	TCAGAGTCTT	GGTGTCTCTG	TTCTTTCCC	CTCGGGGTCT	CCCTGGGTCT	CCCCAAGTCC
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	GTCTCTGCT	CAGI CTGTCC	TTCACTCTGT	GTGTGTGTG	GTCTCTCT	CTCTCTCTCC	TTCCCTTCCA
	CTCCCTCTTC	CTCC'GCCCTC	CACCTCTCCA	GGCCCCGTG	TTGTCCTCC	GTCCGGCTT	TCTCTGCC
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5	CCCTCTCCGC	CCAGGTGCGC	TGCGGCCCGG	GCTTCTGCG	CCCACCCGGC	GGGCTCCTGG	GAGGGCGTCT
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50	GCCTGAAGAG	CTCCCAGGCC	AAACACTTCA	CCCCACGCGC	CACAGTCCCC	CTGTGAATAT	GCAGCCCCGA
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	CATTATCTCC	CCCTAGTTAG	AGACAGTCT	TCCTGAGGC	CTGGGGGCA	TCTGTGCCTT	ATTTATACTT
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	CGGATTCTTG	GGTC TCCAAG	AAGTCTGTC	ACAGACTTCT	GCCCTGGCTC	TTCCCCATCT	AGGCCTGGGC
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 (SEQ. ID NO:3004)

Human Adenosine A₁ Receptor Nucleic Acid and Antisense Oligonucleotide Fragments

5'-ATGCCGCCCT CCATCTCAGC TTTCCAGGCC GCCTACATCG GCATCGAGGT GCTCATCGCC CTGGTCTCTG
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5	CTCCTTCTT	CCCTGAGCTT	TCCGGGGAGG	AGCCTGGAGT	GTAATTACCT	GTCATCTGGG	CCACCAGCTC
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	AGTACCCCCC	TGAGAGCATG	TGGGGGAAGG	CCTGCTGTC	ATGTGAATCC	CTCAATACCC	CTAGTATCTG
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10	TCTGGGAAG	GACCAACCCA	TGCCCTGCCA	AGCCTGGAGC	CCCTGTGTTG	GGGGGCAAGG	TGGGGGAGCC
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	GCTGTGGACC	GCTA.CCTCCG	GGTCAAGATC	CCTCTCCGGT	ACAAGATGGT	GGTGACCCCC	CGGAGGGCGG
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50	GGGCCTGGC	AGCC'AACGGC	AGCATGGGG	AGCCCCTGAT	CAAGTGCAG	TTCGAGAAGG	TCATCAGCAT
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	GAGATACCCA	CAGAGTGTG	TCCCTCCACT	AGGAGTTAAC	TACCTACAC	CTCTGGGCC	TGCAGGAGGC
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	TGACCATCCC	ATGAGCAGTC	CAGAGCTCA	GGGCTGGGCA	GGTCCTGGGG	AGGCTGAGAC	TGCAGAGGAG
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 20 AGCCCGTGTAT CAACTGGAG TTCGAGAAGG TCATCAGCAT GGAGTACATG GTCTACTTCA ACTTCTTTGT
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 CTCAACAAAAGA AGG'GTGCGC CTCCTCCGGC GACCCGAGA AGTACTATGG GAAGGAGCTG AAGATGCCA
 AGTCGCTGGC CCTCATCTC TTCCCTTTG CCCTCAGCTG GCTGCCTTIG CACATCCTCA ACTGCATCAC
 CCTCTCTGC CCCTCTGCCA ACAAGCCCAG CATCCTTAC TACATTGCCA TCTCCTCAC GCACGGCAAC
 25 TCGGCCATGA ACCCATTGT CTATGCCCTC CGCATCCAGA AGTCCCGCT CACCTTCCTT AAGATTGGA
 ATGACCATT CCCTG'GCCAG CCTGCACCTC CCATTGACGA GGATCTCCA GAAGAGAGGC CTGATGACTA G-3'
(FRAG. NO:)(SEQ. ID NO: 2432)**
 5'-CGCATTGTTG TTITAATAAA AGAATCTGGA AGATAAAATAG TCTTGAAGAG AGACAAAGGA AGGAAAATTT
 AAATCCTTAG ATTCAAGCAG AAGAATTCCA TGTGAAGGT TTGGGTGTT GTTGTGTTG TTTGGTGTGT
 TTTTGTGTTT TTG'TTTT TGTTTTTGAGATGGAG TCTCGCTGT TTACCGGGAG CGACAGAGCC
 30 GCACGGCCGA GTCCAGTCCC AGCCAGCTAC CATCCCTCTG GAGCTTACCG GCCGGCCTTG GCTTCCCCAG
 GAATCCTTGG AGCTAGCGGC TGCTGAAGGC GTCGAGGTGT GGGGGCACTT GGACAGAACAA GTCAGGCAGC
 CGGGAGCTCT GCCAGCTTG GTGACCTTGG TGCTTGCCT CGTCCCCCTT GGTGCCGTC TGCTGATGTG
 CCCAGCTGT GCCG GCCATG CGGCCCTCCA TCTCAGCTTT CCAGGCCGCC TACATCGGCA TCGAGGTGCT
 CATGCCCTG GTCTGTGCG CGGGAACGT GCTGGTGTAC TGGCGGTGA AGGTGAACCA GGCGCTGGG
 35 GATGCCACCT TCTGCTTCAT CGTGTGCGTG GCGGTGGCTG ATGTGGCCGT GGGTGCCTG GTCATCCCC
 TCGCCATCCT CATCAACATT GGGCCACAGA CCTACTTCCA CACCTGCCTC ATGGTGCCT GTCCGGTCT
 CATCCTCACC CAGAGCTCA TCCCTGCCCT GCTGGCAATT GCTGTGGACC GCTACCTCCG GGTCAAGATC
 CCTCTCCGGT ACAAGATGGT GGTGACCCCC CGGAGGGCGG CGTGGCCAT AGCCGCTGC TGGATCCTCT
 CCTTCGTGGT GGGACTGACC CCTATGTTG GCTGGAACAA TCTGAGTGC GTGGAGCGGG CCTGGCAGC
 40 CAACGGCAGC ATGC GGGAGC CCGTGATCAA GTCGAGTTC GAGAAGGTCA TCAGCATGGA GTACATGGTC
 TACTTCAACT TCTTGTGTG GGTGCTGCC CCGCTTCTCC TCATGGTCCCT CATCTACCTG GAGGTCTTCT
 ACCTAATCCG CAAGCAGCTC AACAGAAGG TGTGGCCCTC CTCCGGCAGC CCGCAGAAGT ACTATGGAA
 GGAGCTGAAG ATCGCCAAGT CGTGGCCCT CATCTCTTC CTCTTGCCTC TCAGCTGGCT GCCTTGCAC
 45 ATCCTCAACT GCATCACCT CTTCTGCCG TCCGCCACA AGCCCAGCAT CCTTACCTAC ATTGCCATCT
 CCTCCCTAACG ATTTGAAATG ACCATTTCG CTGCGAGCT GCACCTCCCA TTGACGAGGA TCTCCAGAA
 GAGAGGCCCTG ATGAGCTAGAC CCCGCCCTCC GCTCCACCG CCCACATCCA GTGGGTCTC AGTCCAGTCC
 TCACATGCCG GCTGCTCCCAG GGGTCTCCCT GAGCTGGCC CAGCTGGCT GTTGGCTGGG GGATGGGG
 50 AGGCTCTGAA GAGATACCCA CAGAGTGTGG TCCCTCCACT AGGAGTTAAC TACCTACAC TCCCGTCA
 TGCAAGGAGG CTGGAGGGC AAGGGTCTTA CGGAGGGACC AGGTGCTAG AGGCAACAGT GTTCTGAGCC
 CCCACCTGCC TGACCATCCC ATGAGCAGTC CAGAGCTCA GGGCTGGCA GGTCTGGGG AGGCTGAGAC
 TGCAGAGGAG CCAC'CTGGGC TGGGAGAAGG TGCTTGGCT TCTGCGGTGA GGCAGGGAG TCTGCTTGT
 TTAGATGTG TGCGCAGC CCCAGGACCA AGCTTAAGGA GAGGAGAGCA TCTGCTCTGA GACGGATGGA
 AGGAGAGAGG TTGAGGATGC ACTGGCTGT TCTGTAGGAG AGACTGGCCA GA -3'
 55 **(FRAG. NO:)**(SEQ. ID NO: 2422)**
 5'-ATGAGTGTCA GAAGTGTGAA GGGTGCCTGT TCTGAATCCC AGAGCCTCT CTCCTCTGT GAGGCTGGCA
 GGTGAGGAAG GGT'TAACCT CACTGGAGG AATCCCTGGA GCTAGCGCT GCTGAAGGCG TCGAGGTGTG
 GGGGCACCTG GACAGAACAG TCAGGCAGCC GGGAGCTCTG CCAGCTTGG TGACCTTGGG CCGGGCTGGG
 AGCGCTGCCG CGGC AGCCGG AGGACTATGA GCTGCCGCG GTTGTCCAGA GCCCAGCCCA GCCCTACCGC
 60 CGCGGCCCGG AGC'CTGTT CCTGGAACCT TGGGCACTGC CTCTGGGACC CCTGCCGGCC AGCAGGCAGG
 ATGGTCTTG CCTCGTGCCTC CTGGTGCCTC GTCTGCTGAT GTGCCAGCC TGTGCCCGCC ATGCCGCCCT****

CCATCTCAGC TTT'CAGGCC GCCTACATCG GCATCGAGGT GCTCATCGCC CTGGTCTCTG TGCCCCGGAA
 CGTGCTGGT ATC'GGGCGG TGAAAGGTGAA CCAGGCGCTG CCGGATGCCA CCTCTGCTT CATCGTGTG
 CTGGCGGTGG CTGATGTGGC CGTGGGTGCC CTGGTCATCC CCCTCGCCAT CCTCATCAAC ATTGGGCCAC
 5 AGACCTACTT CCACACCTGC CTCATGGTT CCGTCCGGT CCTCATCCTC ACCCAGAGCT CCATCCTGGC
 CCTGCTGGCA ATTGCTGTGG ACCGCTACCT CCGGGTCAAG ATCCCTCTC GGTACAAGAT GGTGGTGACC
 CCCCGGAGGG CGG CGGTGGC CATAGCCGGC TGCTGGATCC TCTCTTCTCG GTGGGGACTG ACCCTATGT
 TTGGCTGGAA CAA'CTGAGT GCGGTGGAGC GGGCCTGGGC AGCCAACGGC AGCATGGGG AGCCCGTGAT
 CAAGTGCAGAG TTCGAGAAGG TCATCAGCAT GGAGTACATG GTCTACTTCA ACTTCTTGT GTGGGTGCTG
 10 CCCCGCTTC TCCICATGGT CCTCATCTAC CTGGAGGTCT TCTACCTAAT CCGCAAGCAG CTCAACAAGA
 AGGTGTCGGC CTCC'TCCGGC GACCCGCAGA AGTACTATGG GAAGGAGCTG AAGATGCCA AGTCGCTGGC
 CCTCATCCTC TTCC TCTTTG CCCTCAGCTG GCTGCCTTG CACATCCTCA ACTGCATCAC CCTCTTCTGC
 CCGTCCTGCC ACAAGGCCAG CATCCTTACC TACATTGCCA TCTTCCTCAC GCACGGCAAC TCGGCCATGA
 15 ACCCCATTGT CTATGCCCTC CGCATCCAGA AGTCCCGCT CACCTTCCTT AAGATTGGA ATGACCATT
 CCGCTGCCAG CCTC'CACCTC CCATTGACGA GGATCTCCC GAAGAGAGGC CTGATGACTA GACCCCGCT
 TCCGCTCCA CCACCCCACA TCCAGTGGGG TCTCAGTCCA GTCTCACAT GCCGCTGTC CCAGGGGTCT
 CCCTGAGCCT GCCC CAGCTG GGCTGTTGGC TGGGGCATG GGGGAGGCTC TGAAGAGATA CCCACAGAGT
 GTGGTCCTC CACTAGGAGT TAACTACCT ACACCTCTGG GCCCTCGAGG AGGCCCTGGGA GGGCAAGGGT
 CCTACGAGG GACCAGGTGT CTAGAGGCAA CAGTGTCTG AGCCCCCACC TGCCGTACCA TCCCATGAGC
 20 AGTCCAGCGC TTCAAGGGCTG GGCAGGTCCT GGGGAGGCTG AGACTCGAGA GGAGCCACCT GGGCTGGGAG
 AAGGTGCTT GGC'TCTGCG GTGAGGCAGG GGAGTCTGCT TGTCTTAGAT GTTGGTGGTG CAGCCCCAGG
 ACCAACGTTA AGGAAGAGGAG AGCATCTGCT CTGAGACGGA TGGAAAGGAGA GAGGTTGAGG ATGCACTGGC
 CTGTTCTGTA GGAGAGACTG GCCAGAGGC GCTAAGGGGC AGGAATCAAG GAGGCTCCGT TCCCACCTCT
 GAGGACTCTG GACC'CCAGGC CATACCAAGGT GCTAGGGTGC CTGCTCTCT TGCCCTGGGC CAGCCCAGGA
 25 TTGTACGTGG GAGAGGCAGA AAGGGTAGGT TCAGTAATCA TTTCTGATGA TTTGCTGGAG TGCTGGCTCC
 ACGCCCTGGG GAGT'GAGCTT GGTGCGGTAG GTGCTGGCT CAAACAGCCA CGAGGTGGTA GCTCTGAGCC
 CTCCCTCTG CCCTGAGCTT TCCGGGGAGG AGCTGGAGT GTAATTACCT GTCATCTGGG CCACCAAGCTC
 CACTGGCCCC CGTIGCCGGG CCTGGACTGT CCTAGGTGAC CCCATCTCTG CTGCTCTGG GCCTGATGGA
 GAGGAGAACAA CTAGACATGC CAACTCGGGA GCATTCTGCC TGCCCTGGAA CGGGGTGGAC GAGGGAGTGT
 CTGTAAGGAC TCAC TGTGA CTGTAGGCGC CCCTGGGGTG GGTTCAGCAG GCTGCAGCAG GCAGAGGAGG
 30 AGTACCCCCC TGAC AGCATG TGGGGGAAGG CCTGCTGTC ATGTGAATCC CTCATAACCC CTAGTATCTG
 GCTGGTTTT CAGGGCTTT GGAAGCTCTG TTGCAAGGTGT CGGGGGGTCT AGGACTTTAG GGATCTGGGA
 TCTGGGGAAG GACC'AACCCA TGCCCTGCCA AGCCTGGAGC CCCTGTGTG GGGGCAAGG TGGGGAGGCC
 TGGAGCCCC GTGTGGAGG GCGAGGCGGG GGAGCCTGGA GCCCCCTGTG GGGAGGGCGA GGCGGGGGAT
 CCTGGAGCCC CTGTGTCGGG GGGCGAGGGA GGGGAGGTGG CGTCGGTTG ACCTCTGAA CATGAGTGT
 35 AACTCCAGGA CTTC CTTCCA AGCCCTTCCC TCTGTTGGAA ATTGGGTGTG CCCTGGCTCC CAAGGGAGGC
 CCATGTACT AATAA AAAAC TGTGAACCC -3' (FRAG. NO:) (SEQ. ID NO: 2421)
 5'-ATGCCGCCCT CCATCTCAGC TTTCAGGCC GCCTACATCG GCATCGAGGT GCTCATCGCC CTGGTCTCTG
 TGCCCGGGAA CGTC CTGGTG ATCTGGGCC TGAAAGGTGAA CCAGGCGCTG CCGGATGCCA CCTCTGCTT
 40 CATCGCTCTG CTGGCGGTGG CTGATGTGCC CGTGGGTGCC CTGGTCATCC CCCTCGCCAT CCTCATCAAC
 ATTGGGCCAC AGACCTACTT CCACACCTGC CTCATGGTT CCTGTCCGGT CCTCATCCTC ACCCAGAGCT
 CCATCCTGGC CCTGCTGGCA ATTGCTGTGG ACCGCTACCT CGGGGTCAAG ATCCCTCTCC GGTACAAGAT
 GGTGGTGACC CCCGGAGGG CGGCGGTGGC CATAGCCGGC TGCTGGATCC TCTCTTCTCG GGTGGGACTG
 CCCCTATGT TTGGCTGGAA CAATCTGAGT CGGGTGGAGC GGGCCTGGGC AGCCAACGGC AGCATGGGG
 AGCCCGTGAT CAAC TGCAG TGCGAGAAGG TCATCAGCAT GGAGTACATG GTCTACTTCA ACTTCTTGT
 45 GTGGGTGCTG CCCCCGCTTC TCCTCATGGT CCTCATCTAC TGAGGCTCTG TCTACCTAAT CCGCAAGCAG
 CTCAACAAAGA AGGTGTCGGC CCTCTCGGGC GACCCCGAGA AGTACTATGG GAAGGAGCTG AAGATGCCA
 AGTCGCTGGC CCTCATCCTC TTCCCTTTG CCTCTCAGCTG GCTGCCTTG CACATCCTCA ACTGCATCAC
 CCTCTCTGTC CGCTCTGCC ACAAGCCAG CATCCTTAC TACATTGCCA TCTTCCTCAC GCACGGCAAC
 TCGGCCATGA ACCCCATTGT CTATGCCCTC CGCATCCAGA AGTCCCGCT CACCTTCCTT AAGATTGGA
 50 ATGACCATTT CCGC'GCCAG CCTGCACCTC CCATTGACGA GGATCTCCA GAAGAGAGGC CTGATGACTA G
 (FRAG NO:) (SEQ. ID NO: 2420)
 5'-GAT GGA GGG CGG CAT GGC GGG-3' (FRAG. NO: 1657) (SEQ ID NO:2412)
 5'-G CGG GTC GCC GC-3' (FRAG. NO: 1658) (SEQ ID NO:2413)
 5'-GGC GGG CBC BGG C-3' (FRAG. NO: 1659) (SEQ ID NO:2414)
 55 5'-GGC GGG CBC-3' (FRAG. NO: 1660) (SEQ ID NO:2415)
 5'-GC GGC CTG G-3' (FRAG. NO: 1661) (SEQ ID NO:2416)
 5'-GGB GGG CGG C-3' (FRAG. NO: 1662) (SEQ ID NO:2417)
 5'-GBT GGB GGG-3' (FRAG. NO: 1663) (SEQ ID NO:2418)
 5'-GG CTG GGC-3' (FRAG. NO: 1664) (SEQ ID NO:2419)
 60 5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG.1) (SEQ. ID NO: 11)
 5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG.2) (SEQ. ID NO:12)

	5'-GGC CTG GAA AGC' TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 3) (SEQ. ID NO: 13)
	5'-GC CTG GAA AGC' TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 4) (SEQ. ID NO: 14)
	5'-C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 5) (SEQ. ID NO: 15)
	5'-CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 6) (SEQ. ID NO: 16)
5	5'-TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 7) (SEQ. ID NO: 17)
	5'-G GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 8) (SEQ. ID NO: 18)
	5'-GAA AGC TGA GAT' GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 9) (SEQ. ID NO: 19)
	5'-AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 10) (SEQ. ID NO: 20)
10	5'-A AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 11) (SEQ. ID NO: 21)
	5'-AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 12) (SEQ. ID NO: 22)
	5'-GC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 13) (SEQ. ID NO: 23)
	5'-C TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 14) (SEQ. ID NO: 24)
	5'-TGA GAT GGA GGC CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 15) (SEQ. ID NO: 25)
15	5'-GA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 16) (SEQ. ID NO: 26)
	5'-A GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 17) (SEQ. ID NO: 27)
	5'-GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 18) (SEQ. ID NO: 28)
	5'-AT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 19) (SEQ. ID NO: 29)
	5'-T GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 20) (SEQ. ID NO: 30)
	5'-GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 21) (SEQ. ID NO: 31)
20	5'-GA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 22) (SEQ. ID NO: 32)
	5'-A GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 23) (SEQ. ID NO: 33)
	5'-GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 24) (SEQ. ID NO: 34)
	5'-GG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 25) (SEQ. ID NO: 35)
	5'-G CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 26) (SEQ. ID NO: 36)
25	5'-CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 27) (SEQ. ID NO: 37)
	5'-GG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 28) (SEQ. ID NO: 38)
	5'-G CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 29) (SEQ. ID NO: 39)
	5'-CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 30) (SEQ. ID NO: 40)
	5'-AT GGC GGG CAC AGG CTG GGC-3' (FRAG 31) (SEQ. ID NO: 41)
30	5'-T GGC GGG CAC AGG CTG GGC-3' (FRAG 32) (SEQ. ID NO: 42)
	5'-GGC GGG CAC AGC CTG GGC-3' (FRAG 33) (SEQ. ID NO: 43)
	5'-GC GGG CAC AGG CTG GGC-3' (FRAG 34) (SEQ. ID NO: 44)
	5'-C GGG CAC AGG CTG GGC-3' (FRAG 35) (SEQ. ID NO: 45)
	5'-GGG CAC AGG CTG GGC-3' (FRAG 36) (SEQ. ID NO: 46)
35	5'-GG CAC AGG CTG GGC-3' (FRAG 37) (SEQ. ID NO: 47)
	5'-G CAC AGG CTG GGC-3' (FRAG 38) (SEQ. ID NO: 48)
	5'-CAC AGG CTG GGC-3' (FRAG 39) (SEQ. ID NO: 49)
	5'-AC AGG CTG GGC-3' (FRAG 40) (SEQ. ID NO: 50)
	5'-C AGG CTG GGC-3' (FRAG 41) (SEQ. ID NO: 51)
40	5'-AGG CTG GGC-3' (FRAG 42) (SEQ. ID NO: 52)
	5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 43) (SEQ. ID NO: 53)
	5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 44) (SEQ. ID NO: 54)
	5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 45) (SEQ. ID NO: 55)
	5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 46) (SEQ. ID NO: 56)
45	5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 47) (SEQ. ID NO: 57)
	5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 48) (SEQ. ID NO: 58)
	5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 49) (SEQ. ID NO: 59)
	5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 50) (SEQ. ID NO: 60)
	5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 51) (SEQ. ID NO: 61)
50	5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 52) (SEQ. ID NO: 62)
	5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 53) (SEQ. ID NO: 63)
	5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 54) (SEQ. ID NO: 64)
	5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 55) (SEQ. ID NO: 65)
	5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 56) (SEQ. ID NO: 66)
55	5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 57) (SEQ. ID NO: 67)
	5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 58) (SEQ. ID NO: 68)
	5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 59) (SEQ. ID NO: 69)
	5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 60) (SEQ. ID NO: 70)
	5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 61) (SEQ. ID NO: 71)
60	5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG CA-3' (FRAG 62) (SEQ. ID NO: 72)
	5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG C-3' (FRAG 63) (SEQ. ID NO: 73)
	5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CGG -3' (FRAG 64) (SEQ. ID NO: 74)

5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG CG -3' (FRAG 65) (SEQ. ID NO: 75)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG C -3' (FRAG 66) (SEQ. ID NO: 76)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GGG -3' (FRAG 67) (SEQ. ID NO: 77)
5'-GGC GGC CTG GAA AGC TGA GAT GGA GG -3' (FRAG 68) (SEQ. ID NO: 78)
5 5'-GGC GGC CTG GAA AGC TGA GAT GGA G -3' (FRAG 69) (SEQ. ID NO: 79)
5'-GGC GGC CTG GAA AGC TGA GAT GGA -3' (FRAG 70) (SEQ. ID NO: 80)
5'-GGC GGC CTG GAA AGC TGA GAT GG -3' (FRAG 71) (SEQ. ID NO: 81)
5'-GGC GGC CTG GAA AGC TGA GAT G -3' (FRAG 72) (SEQ. ID NO: 82)
5'-GGC GGC CTG GAA AGC TGA GAT -3' (FRAG 73) (SEQ. ID NO: 83)
10 5'-GGC GGC CTG GAA AGC TGA GA-3' (FRAG 74) (SEQ. ID NO: 84)
5'-GGC GGC CTG GAA AGC TGA G-3' (FRAG 75) (SEQ. ID NO: 85)
5'-GGC GGC CTG GAA AGC TGA-3' (FRAG 76) (SEQ. ID NO: 86)
5'-GGC GGC CTG GAA AGC TG-3' (FRAG 77) (SEQ. ID NO: 87)
5'-GGC GGC CTG GAA AGC T-3' (FRAG 78) (SEQ. ID NO: 88)
15 5'-GGC GGC CTG GAA AGC-3' (FRAG 79) (SEQ. ID NO: 89)
5'-GGC GGC CTG GAA AG-3' (FRAG 80) (SEQ. ID NO: 90)
5'-GGC GGC CTG GAA A-3' (FRAG 81) (SEQ. ID NO: 91)
5'-GGC GGC CTG GAA-A-3' (FRAG 82) (SEQ. ID NO: 92)
5'-GGC GGC CTG GA- \cdot (FRAG 83) (SEQ. ID NO: 93)
20 5'-GGC GGC CTG G-3' (FRAG 84) (SEQ. ID NO: 94)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 85) (SEQ. ID NO: 95)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 86) (SEQ. ID NO: 96)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 87) (SEQ. ID NO: 97)
25 5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 88) (SEQ. ID NO: 98)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 89) (SEQ. ID NO: 99)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 90) (SEQ. ID NO: 100)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 91) (SEQ. ID NO: 101)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 92) (SEQ. ID NO: 102)
30 5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 93) (SEQ. ID NO: 103)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 94) (SEQ. ID NO: 104)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 95) (SEQ. ID NO: 105)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 96) (SEQ. ID NO: 106)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 97) (SEQ. ID NO: 107)
35 5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 98) (SEQ. ID NO: 108)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 99) (SEQ. ID NO: 109)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 100) (SEQ. ID NO: 110)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 101) (SEQ. ID NO: 111)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 102) (SEQ. ID NO: 112)
40 5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 103) (SEQ. ID NO: 113)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG CA-3' (FRAG 104) (SEQ. ID NO: 114)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG C-3' (FRAG 105) (SEQ. ID NO: 115)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CGG -3' (FRAG 106) (SEQ. ID NO: 116)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG CG -3' (FRAG 107) (SEQ. ID NO: 117)
45 5'-GC GGC CTG GAA AGC TGA GAT GGA GGG C -3' (FRAG 108) (SEQ. ID NO: 118)
5'-GC GGC CTG GAA AGC TGA GAT GGA GGG -3' (FRAG 109) (SEQ. ID NO: 119)
5'-GC GGC CTG GAA AGC TGA GAT GGA GG -3' (FRAG 110) (SEQ. ID NO: 120)
5'-GC GGC CTG GAA AGC TGA GAT GGA G -3' (FRAG 111) (SEQ. ID NO: 121)
5'-GC GGC CTG GAA AGC TGA GAT GGA -3' (FRAG 112) (SEQ. ID NO: 122)
50 5'-GC GGC CTG GAA AGC TGA GAT GG -3' (FRAG 113) (SEQ. ID NO: 123)
5'-GC GGC CTG GAA AGC TGA GAT G -3' (FRAG 114) (SEQ. ID NO: 124)
5'-GC GGC CTG GAA AGC TGA GAT -3' (FRAG 115) (SEQ. ID NO: 125)
5'-GC GGC CTG GAA AGC TGA GA-3' (FRAG 116) (SEQ. ID NO: 126)
5'-GC GGC CTG GAA AGC TGA G-3' (FRAG 117) (SEQ. ID NO: 127)
55 5'-GC GGC CTG GAA AGC TGA-3' (FRAG 118) (SEQ. ID NO: 128)
5'-GC GGC CTG GAA AGC TG-3' (FRAG 119) (SEQ. ID NO: 129)
5'-GC GGC CTG GAA AGC T-3' (FRAG 120) (SEQ. ID NO: 130)
5'-GC GGC CTG GAA AGC-3' (FRAG 121) (SEQ. ID NO: 131)
5'-GC GGC CTG GAA AG-3' (FRAG 122) (SEQ. ID NO: 132)
60 5'-GC GGC CTG GAA A-3' (FRAG 123) (SEQ. ID NO: 133)
5'-GC GGC CTG GAA-3' (FRAG 124) (SEQ. ID NO: 134)
5'-GC GGC CTG GA-3' (FRAG 125) (SEQ. ID NO: 135)

5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 126) (SEQ. ID NO: 136)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 127) (SEQ. ID NO: 137)
5 5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 128) (SEQ. ID NO: 138)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 129) (SEQ. ID NO: 139)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 130) (SEQ. ID NO: 140)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 131) (SEQ. ID NO: 141)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 132) (SEQ. ID NO: 142)
10 10 5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 133) (SEQ. ID NO: 143)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 134) (SEQ. ID NO: 144)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 135) (SEQ. ID NO: 145)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 136) (SEQ. ID NO: 146)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 137) (SEQ. ID NO: 147)
15 15 5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 138) (SEQ. ID NO: 148)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 139) (SEQ. ID NO: 149)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 140) (SEQ. ID NO: 150)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 141) (SEQ. ID NO: 151)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 142) (SEQ. ID NO: 152)
20 20 5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT G -3' (FRA 143) (SEQ. ID NO: 153)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 144) (SEQ. ID NO: 154)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG CA-3' (FRAG 145) (SEQ. ID NO: 155)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG C-3' (FRAG 146) (SEQ. ID NO: 156)
25 25 5'-C GGC CTG GAA AGC TGA GAT GGA GGG CGG -3' (FRAG 147) (SEQ. ID NO: 157)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG CG -3' (FRAG 148) (SEQ. ID NO: 158)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG C -3' (FRAG 149) (SEQ. ID NO: 159)
5'-C GGC CTG GAA AGC TGA GAT GGA GGG -3' (FRAG 150) (SEQ. ID NO: 160)
5'-C GGC CTG GAA AGC TGA GAT GGA GG -3' (FRAG 151) (SEQ. ID NO: 161)
5'-C GGC CTG GAA AGC TGA GAT GGA G -3' (FRAG 152) (SEQ. ID NO: 162)
30 30 5'-C GGC CTG GAA AGC TGA GAT GGA -3' (FRAG 153) (SEQ. ID NO: 163)
5'-C GGC CTG GAA AGC TGA GAT GG -3' (FRAG 154) (SEQ. ID NO: 164)
5'-C GGC CTG GAA AGC TGA GAT G -3' (FRAG 155) (SEQ. ID NO: 165)
5'-C GGC CTG GAA AGC TGA GAT -3' (FRAG 156) (SEQ. ID NO: 166)
5'-C GGC CTG GAA AGC TGA GA-3' (FRAG 157) (SEQ. ID NO: 167)
35 35 5'-C GGC CTG GAA AGC TGA G-3' (FRAG 158) (SEQ. ID NO: 168)
5'-C GGC CTG GAA AGC TGA-3' (FRAG 159) (SEQ. ID NO: 169)
5'-C GGC CTG GAA AGC TG-3' (FRAG 160) (SEQ. ID NO: 170)
5'-C GGC CTG GAA AGC T-3' (FRAG 161) (SEQ. ID NO: 171)
5'-C GGC CTG GAA AGC-3' (FRAG 162) (SEQ. ID NO: 172)
40 40 5'-C GGC CTG GAA AG-3' (FRAG 163) (SEQ. ID NO: 173)
5'-C GGC CTG GAA A-3' (FRAG 164) (SEQ. ID NO: 174)
5'-C GGC CTG GAA-3' (FRAG 165) (SEQ. ID NO: 175)
5'-GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 166) (SEQ. ID NO: 176)
45 45 5'-GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 167) (SEQ. ID NO: 177)
5'-GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 168) (SEQ. ID NO: 178)
5'-GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 169) (SEQ. ID NO: 179)
5'-GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 170) (SEQ. ID NO: 180)
5'-GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 171) (SEQ. ID NO: 181)
50 50 5'-GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 172) (SEQ. ID NO: 182)
5'-GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 173) (SEQ. ID NO: 183)
5'-GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 174) (SEQ. ID NO: 184)
5'-GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 175) (SEQ. ID NO: 185)
5'-GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 176) (SEQ. ID NO: 186)
55 55 5'-GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 177) (SEQ. ID NO: 187)
5'-GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 178) (SEQ. ID NO: 188)
5'-GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 179) (SEQ. ID NO: 189)
5'-GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC G -3' (FRAG 180) (SEQ. ID NO: 190)
5'-GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 181) (SEQ. ID NO: 191)
60 60 5'-GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 182) (SEQ. ID NO: 192)
5'-GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 183) (SEQ. ID NO: 193)
5'-GGC CTG GAA AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 184) (SEQ. ID NO: 194)

5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG CA-3' (FRAG 185) (SEQ. ID NO: 195)
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG C-3' (FRAG 186) (SEQ. ID NO: 196)
5'- GGC CTG GAA AGC TGA GAT GGA GGG CGG -3' (FRAG 187) (SEQ. ID NO: 197)
5'- GGC CTG GAA AGC TGA GAT GGA GGG CG -3' (FRAG 188) (SEQ. ID NO: 198)
5 5'- GGC CTG GAA AGC TGA GAT GGA GGG C -3' (FRAG 189) (SEQ. ID NO: 199)
5'- GGC CTG GAA AGC TGA GAT GGA GGG -3' (FRAG 190) (SEQ. ID NO: 200)
5'- GGC CTG GAA AGC TGA GAT GGA GG -3' (FRAG 191) (SEQ. ID NO: 201)
5'- GGC CTG GAA AGC TGA GAT GGA G -3' (FRAG 192) (SEQ. ID NO: 202)
5'- GGC CTG GAA AGC TGA GAT GGA -3' (FRAG 193) (SEQ. ID NO: 203)
10 10 5'- GGC CTG GAA AGC TGA GAT GG -3' (FRAG 194) (SEQ. ID NO: 204)
5'- GGC CTG GAA AGC TGA GAT G -3' (FRAG 195) (SEQ. ID NO: 205)
5'- GGC CTG GAA AGC TGA GAT -3' (FRAG 196) (SEQ. ID NO: 206)
5'- GGC CTG GAA AGC TGA GA-3' (FRAG 197) (SEQ. ID NO: 207)
5'- GGC CTG GAA AGC TGA G-3' (FRAG 198) (SEQ. ID NO: 208)
15 15 5'- GGC CTG GAA AGC TGA-3' (FRAG 199) (SEQ. ID NO: 209)
5'- GGC CTG GAA AGC TG-3' (FRAG 200) (SEQ. ID NO: 210)
5'- GGC CTG GAA AGC T-3' (FRAG 201) (SEQ. ID NO: 211)
5'- GGC CTG GAA AGC-3' (FRAG 202) (SEQ. ID NO: 212)
5'- GGC CTG GAA AG-3' (FRAG 203) (SEQ. ID NO: 213)
20 20 5'- GGC CTG GAA A-3' (FRAG 204) (SEQ. ID NO: 214)
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 205) (SEQ. ID NO:
215)
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 206) (SEQ. ID NO: 216)
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 207) (SEQ. ID NO: 217)
25 25 5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 208) (SEQ. ID NO: 218)
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 209) (SEQ. ID NO: 219)
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 210) (SEQ. ID NO: 220)
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 211) (SEQ. ID NO: 221)
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 212) (SEQ. ID NO: 222)
30 30 5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 213) (SEQ. ID NO: 223)
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 214) (SEQ. ID NO: 224)
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 215) (SEQ. ID NO: 225)
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 216) (SEQ. ID NO: 226)
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 217) (SEQ. ID NO: 227)
35 35 5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 218) (SEQ. ID NO: 228)
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 219) (SEQ. ID NO: 229)
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 220) (SEQ. ID NO: 230)
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 221) (SEQ. ID NO: 231)
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 222) (SEQ. ID NO: 232)
40 40 5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 223) (SEQ. ID NO: 233)
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG CA-3' (FRAG 224) (SEQ. ID NO: 234)
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG C-3' (FRAG 225) (SEQ. ID NO: 235)
5'- GC CTG GAA AGC TGA GAT GGA GGG CGG -3' (FRAG 226) (SEQ. ID NO: 236)
5'- GC CTG GAA AGC TGA GAT GGA GGG CG -3' (FRAG 227) (SEQ. ID NO: 237)
45 45 5'- GC CTG GAA AGC TGA GAT GGA GGG C -3' (FRAG 228) (SEQ. ID NO: 238)
5'- GC CTG GAA AGC TGA GAT GGA GGG -3' (FRAG 229) (SEQ. ID NO: 239)
5'- GC CTG GAA AGC TGA GAT GGA GG -3' (FRAG 230) (SEQ. ID NO: 240)
5'- GC CTG GAA AGC TGA GAT GGA G -3' (FRAG 231) (SEQ. ID NO: 241)
5'- GC CTG GAA AGC TGA GAT GGA -3' (FRAG 232) (SEQ. ID NO: 242)
50 50 5'- GC CTG GAA AGC TGA GAT GG -3' (FRAG 233) (SEQ. ID NO: 243)
5'- GC CTG GAA AGC TGA GAT G -3' (FRAG 234) (SEQ. ID NO: 244)
5'- GC CTG GAA AGC TGA GAT -3' (FRAG 235) (SEQ. ID NO: 245)
5'- GC CTG GAA AGC TGA GA-3' (FRAG 236) (SEQ. ID NO: 246)
5'- GC CTG GAA AGC TGA G-3' (FRAG 237) (SEQ. ID NO: 247)
55 55 5'- GC CTG GAA AGC TA-3' (FRAG 238) (SEQ. ID NO: 248)
5'- GC CTG GAA AGC TG-3' (FRAG 239) (SEQ. ID NO: 249)
5'- GC CTG GAA AGC T-3' (FRAG 240) (SEQ. ID NO: 250)
5'- GC CTG GAA AGC T-1' (FRAG 241) (SEQ. ID NO: 251)
5'- GC CTG GAA AG-3' (FRAG 242) (SEQ. ID NO: 252)
60 60 5'- C CTG GAA AGC TGA GAT GG A GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 243) (SEQ. ID NO: 253)
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 244) (SEQ. ID NO: 254)
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 245) (SEQ. ID NO: 255)

5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 246) (SEQ. ID NO: 256)
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 247) (SEQ. ID NO: 257)
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 248) (SEQ. ID NO: 258)
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 249) (SEQ. ID NO: 259)
5 5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 250) (SEQ. ID NO: 260)
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 251) (SEQ. ID NO: 261)
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-C-3' (FRAG 252) (SEQ. ID NO: 262)
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 253) (SEQ. ID NO: 263)
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 254) (SEQ. ID NO: 264)
10 5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 255) (SEQ. ID NO: 265)
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 256) (SEQ. ID NO: 266)
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 257) (SEQ. ID NO: 267)
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 258) (SEQ. ID NO: 268)
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 259) (SEQ. ID NO: 269)
15 5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 260) (SEQ. ID NO: 270)
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 261) (SEQ. ID NO: 271)
5'- C CTG GAA AGC TGA GAT GGA GGG CGG CA-3' (FRAG 262) (SEQ. ID NO: 272)
5'- C CTG GAA AGC TGA GAT GGA GGG CGG C-3' (FRAG 263) (SEQ. ID NO: 273)
5'- C CTG GAA AGC TGA GAT GGA GGG CGG -3' (FRAG 264) (SEQ. ID NO: 274)
20 5'- C CTG GAA AGC TGA GAT GGA GGG CG -3' (FRAG 265) (SEQ. ID NO: 275)
5'- C CTG GAA AGC TGA GAT GGA GGG C -3' (FRAG 266) (SEQ. ID NO: 276)
5'- C CTG GAA AGC TGA GAT GGA GGG -3' (FRAG 267) (SEQ. ID NO: 277)
5'- C CTG GAA AGC TGA GAT GGA GG -3' (FRAG 268) (SEQ. ID NO: 278)
5'- C CTG GAA AGC TGA GAT GGA G -3' (FRAG 269) (SEQ. ID NO: 279)
25 5'- C CTG GAA AGC TGA GAT GGA -3' (FRAG 270) (SEQ. ID NO: 280)
5'- C CTG GAA AGC TGA GAT GG -3' (FRAG 271) (SEQ. ID NO: 281)
5'- C CTG GAA AGC TGA GAT G -3' (FRAG 272) (SEQ. ID NO: 282)
5'- C CTG GAA AGC TGA GAT -3' (FRAG 273) (SEQ. ID NO: 283)
5'- C CTG GAA AGC TGA GA-3' (FRAG 274) (SEQ. ID NO: 284)
30 5'- C CTG GAA AGC TGA G-3' (FRAG 275) (SEQ. ID NO: 285)
5'- C CTG GAA AGC TGA-3' (FRAG 276) (SEQ. ID NO: 286)
5'- C CTG GAA AGC TG-3' (FRAG 277) (SEQ. ID NO: 287)
5'- C CTG GAA AGC T 3' (FRAG 278) (SEQ. ID NO: 288)
5'- C CTG GAA AGC-3' (FRAG 279) (SEQ. ID NO: 289)
35 5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 280) (SEQ. ID NO: 290)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 281) (SEQ. ID NO: 291)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 282) (SEQ. ID NO: 292)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 283) (SEQ. ID NO: 293)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 284) (SEQ. ID NO: 294)
40 5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 285) (SEQ. ID NO: 295)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 286) (SEQ. ID NO: 296)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 287) (SEQ. ID NO: 297)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 288) (SEQ. ID NO: 298)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-C-3' (FRAG 289) (SEQ. ID NO: 299)
45 5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 290) (SEQ. ID NO: 300)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 291) (SEQ. ID NO: 301)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 292) (SEQ. ID NO: 302)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 293) (SEQ. ID NO: 303)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 294) (SEQ. ID NO: 304)
50 5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 295) (SEQ. ID NO: 305)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 296) (SEQ. ID NO: 306)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 297) (SEQ. ID NO: 307)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 298) (SEQ. ID NO: 308)
5'- CTG GAA AGC TGA GAT GGA GGG CGG CA-3' (FRAG 299) (SEQ. ID NO: 309)
55 5'- CTG GAA AGC TGA GAT GGA GGG CGG C-3' (FRAG 300) (SEQ. ID NO: 310)
5'- CTG GAA AGC TGA GAT GGA GGG CGG -3' (FRAG 301) (SEQ. ID NO: 311)
5'- CTG GAA AGC TGA GAT GGA GGG CG -3' (FRAG 302) (SEQ. ID NO: 312)
5'- CTG GAA AGC TGA GAT GGA GGG C -3' (FRAG 303) (SEQ. ID NO: 313)
5'- CTG GAA AGC TGA GAT GGA GGG -3' (FRAG 304) (SEQ. ID NO: 314)
60 5'- CTG GAA AGC TGA GAT GGA GG -3' (FRAG 305) (SEQ. ID NO: 315)
5'- CTG GAA AGC TGA GAT GGA G -3' (FRAG 306) (SEQ. ID NO: 316)
5'- CTG GAA AGC TGA GAT GGA -3' (FRAG 307) (SEQ. ID NO: 317)

- 5'- CTG GAA AGC TGA GAT GG -3' (FRAG 308) (SEQ. ID NO: 318)
5'- CTG GAA AGC TGA GAT G -3' (FRAG 309) (SEQ. ID NO: 319)
5'- CTG GAA AGC TGA GAT -3' (FRAG 310) (SEQ. ID NO: 320)
5'- CTG GAA AGC TGA GA-3' (FRAG 311) (SEQ. ID NO: 321)
5 5'- CTG GAA AGC TGA G-3' (FRAG 312) (SEQ. ID NO: 322)
5'- CTG GAA AGC TGA A-3' (FRAG 313) (SEQ. ID NO: 323)
5'- CTG GAA AGC TG 3' (FRAG 314) (SEQ. ID NO: 324)
5'- CTG GAA AGC T-3' (FRAG 315) (SEQ. ID NO: 325)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 316) (SEQ. ID NO: 326)
10 5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 317) (SEQ. ID NO: 327)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 318) (SEQ. ID NO: 328)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 319) (SEQ. ID NO: 329)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 320) (SEQ. ID NO: 330)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 321) (SEQ. ID NO: 331)
15 5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 322) (SEQ. ID NO: 332)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 323) (SEQ. ID NO: 333)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 324) (SEQ. ID NO: 334)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 325) (SEQ. ID NO: 335)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 326) (SEQ. ID NO: 336)
20 5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 327) (SEQ. ID NO: 337)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 328) (SEQ. ID NO: 338)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 329) (SEQ. ID NO: 339)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 330) (SEQ. ID NO: 340)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 331) (SEQ. ID NO: 341)
25 5'- TG GAA AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 332) (SEQ. ID NO: 342)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 333) (SEQ. ID NO: 343)
5'- TG GAA AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 334) (SEQ. ID NO: 344)
5'- TG GAA AGC TGA GAT GGA GGG CGG CA-3' (FRAG 335) (SEQ. ID NO: 345)
5'- TG GAA AGC TGA GAT GGA GGG CGG C-3' (FRAG 336) (SEQ. ID NO: 346)
30 5'- TG GAA AGC TGA GAT GGA GGG CGG -3' (FRAG 337) (SEQ. ID NO: 347)
5'- TG GAA AGC TGA GAT GGA GGG CG -3' (FRAG 338) (SEQ. ID NO: 348)
5'- TG GAA AGC TGA GAT GGA GGG C -3' (FRAG 339) (SEQ. ID NO: 349)
5'- TG GAA AGC TGA GAT GGA GGG -3' (FRAG 340) (SEQ. ID NO: 350)
5'- TG GAA AGC TGA GAT GGA GG -3' (FRAG 341) (SEQ. ID NO: 351)
35 5'- TG GAA AGC TGA GAT GGA G -3' (FRAG 342) (SEQ. ID NO: 352)
5'- TG GAA AGC TGA GAT GGA -3' (FRAG 343) (SEQ. ID NO: 353)
5'- TG GAA AGC TGA GAT GG -3' (FRAG 344) (SEQ. ID NO: 354)
5'- TG GAA AGC TGA GAT G -3' (FRAG 345) (SEQ. ID NO: 355)
5'- TG GAA AGC TGA GAT -3' (FRAG 346) (SEQ. ID NO: 356)
40 5'- TG GAA AGC TGA GA-3' (FRAG 347) (SEQ. ID NO: 357)
5'- TG GAA AGC TGA G-3' (FRAG 348) (SEQ. ID NO: 358)
5'- TG GAA AGC TGA 3' (FRAG 349) (SEQ. ID NO: 359)
5'- TG GAA AGC TG-3 (FRAG 350) (SEQ. ID NO: 360)
5'- G GAA AGC TGA C AT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 351) (SEQ. ID NO: 361)
45 5'- G GAA AGC TGA C AT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 352) (SEQ. ID NO: 362)
5'- G GAA AGC TGA C AT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 353) (SEQ. ID NO: 363)
5'- G GAA AGC TGA C AT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 354) (SEQ. ID NO: 364)
5'- G GAA AGC TGA C AT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 355) (SEQ. ID NO: 365)
5'- G GAA AGC TGA C AT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 356) (SEQ. ID NO: 366)
50 5'- G GAA AGC TGA C AT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 357) (SEQ. ID NO: 367)
5'- G GAA AGC TGA C AT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 358) (SEQ. ID NO: 368)
5'- G GAA AGC TGA C AT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 359) (SEQ. ID NO: 369)
5'- G GAA AGC TGA C AT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 360) (SEQ. ID NO: 370)
5'- G GAA AGC TGA C AT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 361) (SEQ. ID NO: 371)
55 5'- G GAA AGC TGA C AT GGA GGG CGG CAT GGC GGG C-3' (FRAG 362) (SEQ. ID NO: 372)
5'- G GAA AGC TGA C AT GGA GGG CGG CAT GGC GGG -3' (FRAG 363) (SEQ. ID NO: 373)
5'- G GAA AGC TGA C AT GGA GGG CGG CAT GGC GG-3' (FRAG 364) (SEQ. ID NO: 374)
5'- G GAA AGC TGA C AT GGA GGG CGG CAT GGC G-3' (FRAG 365) (SEQ. ID NO: 375)
5'- G GAA AGC TGA C AT GGA GGG CGG CAT GGC -3' (FRAG 366) (SEQ. ID NO: 376)
60 5'- G GAA AGC TGA C AT GGA GGG CGG CAT GG -3' (FRAG 367) (SEQ. ID NO: 377)
5'- G GAA AGC TGA C AT GGA GGG CGG CAT G -3' (FRAG 368) (SEQ. ID NO: 378)
5'- G GAA AGC TGA C AT GGA GGG CGG CAT -3' (FRAG 369) (SEQ. ID NO: 379)

5'- G GAA AGC TGA GAT GGA GGG CGG CA-3' (FRAG 370) (SEQ. ID NO: 380)
5'- G GAA AGC TGA GAT GGA GGG CGG C-3' (FRAG 371) (SEQ. ID NO: 381)
5'- G GAA AGC TGA GAT GGA GGG CGG -3' (FRAG 372) (SEQ. ID NO: 382)
5'- G GAA AGC TGA GAT GGA GGG CG -3' (FRAG 373) (SEQ. ID NO: 383)
5 5'- G GAA AGC TGA GAT GGA GGG C -3' (FRAG 374) (SEQ. ID NO: 384)
5'- G GAA AGC TGA GAT GGA GGG -3' (FRAG 375) (SEQ. ID NO: 385)
5'- G GAA AGC TGA GAT GGA GG -3' (FRAG 376) (SEQ. ID NO: 386)
5'- G GAA AGC TGA GAT GGA G G -3' (FRAG 377) (SEQ. ID NO: 387)
5'- G GAA AGC TGA GAT GGA -3' (FRAG 378) (SEQ. ID NO: 388)
10 5'- G GAA AGC TGA GAT GG -3' (FRAG 379) (SEQ. ID NO: 389)
5'- G GAA AGC TGA GAT G -3' (FRAG 380) (SEQ. ID NO: 390)
5'- G GAA AGC TGA GAT -3' (FRAG 381) (SEQ. ID NO: 391)
5'- G GAA AGC TGA G A-3' (FRAG 382) (SEQ. ID NO: 392)
5'- G GAA AGC TGA G I-3' (FRAG 383) (SEQ. ID NO: 393)
15 5'- G GAA AGC TGA -3' (FRAG 384) (SEQ. ID NO: 394)
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 385) (SEQ. ID NO: 395)
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 386) (SEQ. ID NO: 396)
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 387) (SEQ. ID NO: 397)
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 388) (SEQ. ID NO: 398)
20 5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 389) (SEQ. ID NO: 399)
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 390) (SEQ. ID NO: 400)
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 391) (SEQ. ID NO: 401)
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 392) (SEQ. ID NO: 402)
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 393) (SEQ. ID NO: 403)
25 5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 394) (SEQ. ID NO: 404)
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 395) (SEQ. ID NO: 405)
5'- GAA AGC TGA GAT GGA GGG CGG C-3' (FRAG 396) (SEQ. ID NO: 406)
5'- GAA AGC TGA GAT GGA GGG CGG -3' (FRAG 397) (SEQ. ID NO: 407)
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 398) (SEQ. ID NO: 408)
30 5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC G -3' (FRAG 399) (SEQ. ID NO: 409)
5'- GAA AGC TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 400) (SEQ. ID NO: 410)
5'- GAA AGC TGA GAT GGA GGG CGG CAT GG -3' (FRAG 401) (SEQ. ID NO: 411)
5'- GAA AGC TGA GAT GGA GGG CGG CAT G -3' (FRAG 402) (SEQ. ID NO: 412)
5'- GAA AGC TGA GAT GGA GGG CGG CAT -3' (FRAG 403) (SEQ. ID NO: 413)
35 5'- GAA AGC TGA GAT GGA GGG CGG CA-3' (FRAG 404) (SEQ. ID NO: 414)
5'- GAA AGC TGA GAT GGA GGG CGG C-3' (FRAG 405) (SEQ. ID NO: 415)
5'- GAA AGC TGA GAT GGA GGG CGG -3' (FRAG 406) (SEQ. ID NO: 416)
5'- GAA AGC TGA GAT GGA GGG CG -3' (FRAG 407) (SEQ. ID NO: 417)
5'- GAA AGC TGA GAT GGA GGG C -3' (FRAG 408) (SEQ. ID NO: 418)
40 5'- GAA AGC TGA GAT GGA GGG -3' (FRAG 409) (SEQ. ID NO: 419)
5'- GAA AGC TGA GAT GGA GG -3' (FRAG 410) (SEQ. ID NO: 420)
5'- GAA AGC TGA GAT GGA G -3' (FRAG 411) (SEQ. ID NO: 421)
5'- GAA AGC TGA GAT GGA -3' (FRAG 412) (SEQ. ID NO: 422)
5'- GAA AGC TGA GAT GG -3' (FRAG 413) (SEQ. ID NO: 423)
45 5'- GAA AGC TGA GAT G -3' (FRAG 414) (SEQ. ID NO: 424)
5'- GAA AGC TGA GAT -3' (FRAG 415) (SEQ. ID NO: 425)
5'- GAA AGC TGA G A-3' (FRAG 416) (SEQ. ID NO: 426)
5'- GAA AGC TGA G -3' (FRAG 417) (SEQ. ID NO: 427)
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 418) (SEQ. ID NO: 428)
50 5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 419) (SEQ. ID NO: 429)
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 420) (SEQ. ID NO: 430)
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 421) (SEQ. ID NO: 431)
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 422) (SEQ. ID NO: 432)
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 423) (SEQ. ID NO: 433)
55 5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3'(FRAG 424) (SEQ. ID NO: 434)
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 425) (SEQ. ID NO: 435)
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 426) (SEQ. ID NO: 436)
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 427) (SEQ. ID NO: 437)
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 428) (SEQ. ID NO: 438)
60 5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 429) (SEQ. ID NO: 439)
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 430) (SEQ. ID NO: 440)
5'- AA AGC TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 431) (SEQ. ID NO: 441)

- 5'- AA AGC TGA GAT' GGA GGG CGG CAT GGC G-3' (FRAG 432) (SEQ. ID NO: 442)
 5'- AA AGC TGA GAT' GGA GGG CGG CAT GGC -3' (FRAG 433) (SEQ. ID NO: 443)
 5'- AA AGC TGA GAT' GGA GGG CGG CAT GG -3' (FRAG 434) (SEQ. ID NO: 444)
 5'- AA AGC TGA GAT' GGA GGG CGG CAT G -3' (FRAG 435) (SEQ. ID NO: 445)
- 5 5'- AA AGC TGA GAT' GGA GGG CGG CAT -3' (FRAG 436) (SEQ. ID NO: 446)
 5'- AA AGC TGA GAT' GGA GGG CGG CA-3' (FRAG 437) (SEQ. ID NO: 447)
 5'- AA AGC TGA GAT' GGA GGG CGG C-3' (FRAG 438) (SEQ. ID NO: 448)
 5'- AA AGC TGA GAT' GGA GGG CGG -3' (FRAG 439) (SEQ. ID NO: 449)
 5'- AA AGC TGA GAT' GGA GGG CG -3' (FRAG 440) (SEQ. ID NO: 450)
- 10 10 5'- AA AGC TGA GAT' GGA GGG C -3' (FRAG 441) (SEQ. ID NO: 451)
 5'- AA AGC TGA GAT' GGA GGG -3' (FRAG 442) (SEQ. ID NO: 452)
 5'- AA AGC TGA GAT' GGA GG -3' (FRAG 443) (SEQ. ID NO: 453)
 5'- AA AGC TGA GAT' GGA G G -3' (FRAG 444) (SEQ. ID NO: 454)
 5'- AA AGC TGA GAT' GGA G -3' (FRAG 445) (SEQ. ID NO: 455)
- 15 15 5'- AA AGC TGA GAT' GG -3' (FRAG 446) (SEQ. ID NO: 456)
 5'- AA AGC TGA GAT' G -3' (FRAG 447) (SEQ. ID NO: 457)
 5'- AA AGC TGA GAT' -3' (FRAG 448) (SEQ. ID NO: 458)
 5'- AA AGC TGA GA-3' (FRAG 449) (SEQ. ID NO: 459)
- 20 20 5'- A AGC TGA GAT' GGA GGG CG G CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 450) (SEQ. ID NO: 460)
 5'- A AGC TGA GAT' GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 451) (SEQ. ID NO: 461)
 5'- A AGC TGA GAT' GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 452) (SEQ. ID NO: 462)
 5'- A AGC TGA GAT' GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 453) (SEQ. ID NO: 463)
 5'- A AGC TGA GAT' GGA GGG CGG CAT GGC GGG CAC AGG CT -3' (FRAG 454) (SEQ. ID NO: 464)
 5'- A AGC TGA GAT' GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 455) (SEQ. ID NO: 465)
- 25 25 5'- A AGC TGA GAT' GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 456) (SEQ. ID NO: 466)
 5'- A AGC TGA GAT' GGA GGG CGG CAT GGC GGG CAC AG -3' (FRAG 457) (SEQ. ID NO: 467)
 5'- A AGC TGA GAT' GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 458) (SEQ. ID NO: 468)
 5'- A AGC TGA GAT' GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 459) (SEQ. ID NO: 469)
 5'- A AGC TGA GAT' GGA GGG CGG CAT GGC GGG CA-3' (FRAG 460) (SEQ. ID NO: 470)
- 30 30 5'- A AGC TGA GAT' GGA GGG CGG CAT GGC GGG C -3' (FRAG 461) (SEQ. ID NO: 471)
 5'- A AGC TGA GAT' GGA GGG CGG CAT GGC GGG -3' (FRAG 462) (SEQ. ID NO: 472)
 5'- A AGC TGA GAT' GGA GGG CGG CAT GGC GG-3' (FRAG 463) (SEQ. ID NO: 473)
 5'- A AGC TGA GAT' GGA GGG CGG CAT GGC G -3' (FRAG 464) (SEQ. ID NO: 474)
 5'- A AGC TGA GAT' GGA GGG CGG CAT GGC -3' (FRAG 465) (SEQ. ID NO: 475)
- 35 35 5'- A AGC TGA GAT' GGA GGG CGG CAT GG -3' (FRAG 466) (SEQ. ID NO: 476)
 5'- A AGC TGA GAT' GGA GGG CGG CAT G -3' (FRAG 467) (SEQ. ID NO: 477)
 5'- A AGC TGA GAT' GGA GGG CGG CAT -3' (FRAG 468) (SEQ. ID NO: 478)
 5'- A AGC TGA GAT' GGA GGG CGG CA-3' (FRAG 469) (SEQ. ID NO: 479)
 5'- A AGC TGA GAT' GGA GGG CGG C-3' (FRAG 470) (SEQ. ID NO: 480)
- 40 40 5'- A AGC TGA GAT' GGA GGG CGG -3' (FRAG 471) (SEQ. ID NO: 481)
 5'- A AGC TGA GAT' GGA GGG CG -3' (FRAG 472) (SEQ. ID NO: 482)
 5'- A AGC TGA GAT' GGA GGG C -3' (FRAG 473) (SEQ. ID NO: 483)
 5'- A AGC TGA GAT' GGA GGG -3' (FRAG 474) (SEQ. ID NO: 484)
 5'- A AGC TGA GAT' GGA GG -3' (FRAG 475) (SEQ. ID NO: 485)
- 45 45 5'- A AGC TGA GAT' GGA G -3' (FRAG 476) (SEQ. ID NO: 486)
 5'- A AGC TGA GAT' GGA -3' (FRAG 477) (SEQ. ID NO: 487)
 5'- A AGC TGA GAT' GG -3' (FRAG 478) (SEQ. ID NO: 488)
 5'- A AGC TGA GAT' G -3' (FRAG 479) (SEQ. ID NO: 489)
 5'- A AGC TGA GAT' -3' (FRAG 480) (SEQ. ID NO: 490)
- 50 50 5'- AGC TGA GAT' GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 481) (SEQ. ID NO: 491)
 5'- AGC TGA GAT' GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 482) (SEQ. ID NO: 492)
 5'- AGC TGA GAT' GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 483) (SEQ. ID NO: 493)
 5'- AGC TGA GAT' GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 484) (SEQ. ID NO: 494)
 5'- AGC TGA GAT' GGA GGG CGG CAT GGC GGG CAC AGG CT -3' (FRAG 485) (SEQ. ID NO: 495)
- 55 55 5'- AGC TGA GAT' GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 486) (SEQ. ID NO: 496)
 5'- AGC TGA GAT' GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 487) (SEQ. ID NO: 497)
 5'- AGC TGA GAT' GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 488) (SEQ. ID NO: 498)
 5'- AGC TGA GAT' GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 489) (SEQ. ID NO: 499)
 5'- AGC TGA GAT' GGA GGG CGG CAT GGC GGG CAC AGG CA-3' (FRAG 490) (SEQ. ID NO: 500)
- 60 60 5'- AGC TGA GAT' GGA GGG CGG CAT GGC GGG CA-3' (FRAG 491) (SEQ. ID NO: 501)
 5'- AGC TGA GAT' GGA GGG CGG CAT GGC GGG C -3' (FRAG 492) (SEQ. ID NO: 502)
 5'- AGC TGA GAT' GGA GGG CGG CAT GGC GGG -3' (FRAG 493) (SEQ. ID NO: 503)

(1) (2) (3) (4) (5) (6) (7) (8) (9) (10) (11) (12) (13) (14) (15) (16) (17) (18) (19) (20) (21) (22) (23) (24) (25) (26) (27) (28) (29) (30) (31) (32) (33) (34) (35) (36) (37) (38) (39) (40) (41) (42) (43) (44) (45) (46) (47) (48) (49) (50) (51) (52) (53) (54) (55) (56) (57) (58) (59) (60)

5'- AGC TGA GAT G₃A GGG CGG CAT GGC GG-3' (FRAG 494) (SEQ. ID NO: 504)
 5'- AGC TGA GAT G₃A GGG CGG CAT GGC G-3' (FRAG 495) (SEQ. ID NO: 505)
 5'- AGC TGA GAT G₃A GGG CGG CAT GGC -3' (FRAG 496) (SEQ. ID NO: 506)
 5'- AGC TGA GAT G₃A GGG CGG CAT GG -3' (FRAG 497) (SEQ. ID NO: 507)
 5 5'- AGC TGA GAT G₃A GGG CGG CAT G -3' (FRAG 498) (SEQ. ID NO: 508)
 5'- AGC TGA GAT G₃A GGG CGG CAT -3' (FRAG 499) (SEQ. ID NO: 509)
 5'- AGC TGA GAT G₃A GGG CGG CA-3' (FRAG 500) (SEQ. ID NO: 510)
 5'- AGC TGA GAT G₃A GGG CGG C-3' (FRAG 501) (SEQ. ID NO: 511)
 5'- AGC TGA GAT G₃A GGG CGG -3' (FRAG 502) (SEQ. ID NO: 512)
 10 10 5'- AGC TGA GAT G₃A GGG CG -3' (FRAG 503) (SEQ. ID NO: 513)
 5'- AGC TGA GAT G₃A GGG C -3' (FRAG 504) (SEQ. ID NO: 514)
 5'- AGC TGA GAT G₃A GGG -3' (FRAG 505) (SEQ. ID NO: 515)
 5'- AGC TGA GAT G₃A GG -3' (FRAG 506) (SEQ. ID NO: 516)
 5'- AGC TGA GAT G₃A G -3' (FRAG 507) (SEQ. ID NO: 517)
 15 15 5'- AGC TGA GAT G₃A -3' (FRAG 508) (SEQ. ID NO: 518)
 5'- AGC TGA GAT G₃G -3' (FRAG 509) (SEQ. ID NO: 519)
 5'- AGC TGA GAT G -3' (FRAG 510) (SEQ. ID NO: 520)
 5'- GC TGA GAT G₃A GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 511) (SEQ. ID NO: 521)
 5'- GC TGA GAT G₃A GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 512) (SEQ. ID NO: 522)
 20 20 5'- GC TGA GAT G₃A GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 513) (SEQ. ID NO: 523)
 5'- GC TGA GAT G₃A GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 514) (SEQ. ID NO: 524)
 5'- GC TGA GAT G₃A GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 515) (SEQ. ID NO: 525)
 5'- GC TGA GAT G₃A GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 516) (SEQ. ID NO: 526)
 5'- GC TGA GAT G₃A GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 517) (SEQ. ID NO: 527)
 25 25 5'- GC TGA GAT G₃A GGG CGG CAT GGC GGG CAC AG-3' (FRAG 518) (SEQ. ID NO: 528)
 5'- GC TGA GAT G₃A GGG CGG CAT GGC GGG CAC A-3' (FRAG 519) (SEQ. ID NO: 529)
 5'- GC TGA GAT G₃A GGG CGG CAT GGC GGG CAC-3' (FRAG 520) (SEQ. ID NO: 530)
 5'- GC TGA GAT G₃A GGG CGG CAT GGC GGG CA-3' (FRAG 521) (SEQ. ID NO: 531)
 5'- GC TGA GAT G₃A GGG CGG CAT GGC GGG C-3' (FRAG 522) (SEQ. ID NO: 532)
 30 30 5'- GC TGA GAT G₃A GGG CGG CAT GGC GGG -3' (FRAG 523) (SEQ. ID NO: 533)
 5'- GC TGA GAT G₃A GGG CGG CAT GGC GG-3' (FRAG 524) (SEQ. ID NO: 534)
 5'- GC TGA GAT G₃A GGG CGG CAT GGC G-3' (FRAG 525) (SEQ. ID NO: 535)
 5'- GC TGA GAT G₃A GGG CGG CAT GGC -3' (FRAG 526) (SEQ. ID NO: 536)
 5'- GC TGA GAT G₃A GGG CGG CAT GG -3' (FRAG 527) (SEQ. ID NO: 537)
 35 35 5'- GC TGA GAT G₃A GGG CGG CAT G -3' (FRAG 528) (SEQ. ID NO: 538)
 5'- GC TGA GAT G₃A GGG CGG CAT -3' (FRAG 529) (SEQ. ID NO: 539)
 5'- GC TGA GAT G₃A GGG CGG CA-3' (FRAG 530) (SEQ. ID NO: 540)
 5'- GC TGA GAT G₃A GGG CGG C-3' (FRAG 531) (SEQ. ID NO: 541)
 5'- GC TGA GAT G₃A GGG CGG -3' (FRAG 532) (SEQ. ID NO: 542)
 40 40 5'- GC TGA GAT G₃A GGG CG -3' (FRAG 533) (SEQ. ID NO: 543)
 5'- GC TGA GAT G₃A GGG C -3' (FRAG 534) (SEQ. ID NO: 544)
 5'- GC TGA GAT G₃A GGG -3' (FRAG 535) (SEQ. ID NO: 545)
 5'- GC TGA GAT G₃A GG -3' (FRAG 536) (SEQ. ID NO: 546)
 5'- GC TGA GAT G₃A G -3' (FRAG 537) (SEQ. ID NO: 547)
 45 45 5'- GC TGA GAT G₃A -3' (FRAG 538) (SEQ. ID NO: 548)
 5'- GC TGA GAT GG -3' (FRAG 539) (SEQ. ID NO: 549)
 5'- C TGA GAT G₃A GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 540) (SEQ. ID NO: 550)
 5'- C TGA GAT G₃A GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 541) (SEQ. ID NO: 551)
 50 50 5'- C TGA GAT G₃A GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 542) (SEQ. ID NO: 552)
 5'- C TGA GAT G₃A GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 543) (SEQ. ID NO: 553)
 5'- C TGA GAT G₃A GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 544) (SEQ. ID NO: 554)
 5'- C TGA GAT G₃A GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 545) (SEQ. ID NO: 555)
 5'- C TGA GAT G₃A GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 546) (SEQ. ID NO: 556)
 5'- C TGA GAT G₃A GGG CGG CAT GGC GGG CAC AG-3' (FRAG 547) (SEQ. ID NO: 557)
 55 55 5'- C TGA GAT G₃A GGG CGG CAT GGC GGG CAC A-3' (FRAG 548) (SEQ. ID NO: 558)
 5'- C TGA GAT G₃A GGG CGG CAT GGC GGG CAC-3' (FRAG 549) (SEQ. ID NO: 559)
 5'- C TGA GAT G₃A GGG CGG CAT GGC GGG CA-3' (FRAG 550) (SEQ. ID NO: 560)
 5'- C TGA GAT G₃A GGG CGG CAT GGC GGG C-3' (FRAG 551) (SEQ. ID NO: 561)
 5'- C TGA GAT G₃A GGG CGG CAT GGC GGG -3' (FRAG 552) (SEQ. ID NO: 562)
 60 60 5'- C TGA GAT G₃A GGG CGG CAT GGC GG-3' (FRAG 553) (SEQ. ID NO: 563)
 5'- C TGA GAT G₃A GGG CGG CAT GGC G-3' (FRAG 554) (SEQ. ID NO: 564)
 5'- C TGA GAT G₃A GGG CGG CAT GGC -3' (FRAG 555) (SEQ. ID NO: 565)

5'- C TGA GAT GGA GGG CGG CAT GG -3' (FRAG 556) (SEQ. ID NO: 566)
 5'- C TGA GAT GGA GGG CGG CAT G -3' (FRAG 557) (SEQ. ID NO: 567)
 5'- C TGA GAT GGA GGG CGG CAT -3' (FRAG 558) (SEQ. ID NO: 568)
 5'- C TGA GAT GGA GGG CGG CA-3' (FRAG 559) (SEQ. ID NO: 569)
 5 5'- C TGA GAT GGA GGG CGG C-3' (FRAG 560) (SEQ. ID NO: 570)
 5'- C TGA GAT GGA GGG CGG -3' (FRAG 561) (SEQ. ID NO: 571)
 5'- C TGA GAT GGA GGG CG -3' (FRAG 562) (SEQ. ID NO: 572)
 5'- C TGA GAT GGA GGG C -3' (FRAG 563) (SEQ. ID NO: 573)
 5'- C TGA GAT GGA GGG -3' (FRAG 564) (SEQ. ID NO: 574)
 10 5'- C TGA GAT GGA GG -3' (FRAG 565) (SEQ. ID NO: 575)
 5'- C TGA GAT GGA G -3' (FRAG 566) (SEQ. ID NO: 576)
 5'- C TGA GAT GGA -3' (FRAG 567) (SEQ. ID NO: 577)
 5'- TGA GAT GGA CGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 568) (SEQ. ID NO: 578)
 5'- TGA GAT GGA CGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 569) (SEQ. ID NO: 579)
 15 5'- TGA GAT GGA CGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 570) (SEQ. ID NO: 580)
 5'- TGA GAT GGA CGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 571) (SEQ. ID NO: 581)
 5'- TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 572) (SEQ. ID NO: 582)
 5'- TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 573) (SEQ. ID NO: 583)
 5'- TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 574) (SEQ. ID NO: 584)
 20 5'- TGA GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 575) (SEQ. ID NO: 585)
 5'- TGA GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 576) (SEQ. ID NO: 586)
 5'- TGA GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 577) (SEQ. ID NO: 587)
 5'- TGA GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 578) (SEQ. ID NO: 588)
 5'- TGA GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 579) (SEQ. ID NO: 589)
 25 5'- TGA GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 580) (SEQ. ID NO: 590)
 5'- TGA GAT GGA GGG CGG CAT GGC GG-3' (FRAG 581) (SEQ. ID NO: 591)
 5'- TGA GAT GGA GGG CGG CAT GGC G-3' (FRAG 582) (SEQ. ID NO: 592)
 5'- TGA GAT GGA GGG CGG CAT GGC -3' (FRAG 583) (SEQ. ID NO: 593)
 5'- TGA GAT GGA GGG CGG CAT GG -3' (FRAG 584) (SEQ. ID NO: 594)
 30 5'- TGA GAT GGA GGG CGG CAT G -3' (FRAG 585) (SEQ. ID NO: 595)
 5'- TGA GAT GGA GGG CGG CAT -3' (FRAG 586) (SEQ. ID NO: 596)
 5'- TGA GAT GGA GGG CGG CA-3' (FRAG 587) (SEQ. ID NO: 597)
 5'- TGA GAT GGA GGG CGG C-3' (FRAG 588) (SEQ. ID NO: 598)
 5'- TGA GAT GGA GGG CGG -3' (FRAG 589) (SEQ. ID NO: 599)
 35 5'- TGA GAT GGA GGG CG -3' (FRAG 590) (SEQ. ID NO: 600)
 5'- TGA GAT GGA GGG C -3' (FRAG 591) (SEQ. ID NO: 601)
 5'- TGA GAT GGA GGG -3' (FRAG 592) (SEQ. ID NO: 602)
 5'- TGA GAT GGA GG -3' (FRAG 593) (SEQ. ID NO: 603)
 5'- TGA GAT GGA G -3' (FRAG 594) (SEQ. ID NO: 604)
 40 5'- GA GAT GGA GCG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 595) (SEQ. ID NO: 605)
 5'- GA GAT GGA GCG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 596) (SEQ. ID NO: 606)
 5'- GA GAT GGA GCG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 597) (SEQ. ID NO: 607)
 5'- GA GAT GGA GCG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 598) (SEQ. ID NO: 608)
 5'- GA GAT GGA GCG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 599) (SEQ. ID NO: 609)
 45 5'- GA GAT GGA GCG CGG CAT GGC GGG CAC AGG C-3' (FRAG 600) (SEQ. ID NO: 610)
 5'- GA GAT GGA GCG CGG CAT GGC GGG CAC AGG -3' (FRAG 601) (SEQ. ID NO: 611)
 5'- GA GAT GGA GCG CGG CAT GGC GGG CAC AG-3' (FRAG 602) (SEQ. ID NO: 612)
 5'- GA GAT GGA GCG CGG CAT GGC GGG CAC A-3' (FRAG 603) (SEQ. ID NO: 613)
 5'- GA GAT GGA GCG CGG CAT GGC GGG CAC-3' (FRAG 604) (SEQ. ID NO: 614)
 50 5'- GA GAT GGA GCG CGG CAT GGC GGG CA-3' (FRAG 605) (SEQ. ID NO: 615)
 5'- GA GAT GGA GCG CGG CAT GGC GGG C-3' (FRAG 606) (SEQ. ID NO: 616)
 5'- GA GAT GGA GCG CGG CAT GGC GGG -3' (FRAG 607) (SEQ. ID NO: 617)
 5'- GA GAT GGA GCG CGG CAT GGC GG-3' (FRAG 608) (SEQ. ID NO: 618)
 5'- GA GAT GGA GCG CGG CAT GGC G-3' (FRAG 609) (SEQ. ID NO: 619)
 55 5'- GA GAT GGA GCG CGG CAT GGC -3' (FRAG 610) (SEQ. ID NO: 620)
 5'- GA GAT GGA GCG CGG CAT GG -3' (FRAG 611) (SEQ. ID NO: 621)
 5'- GA GAT GGA GCG CGG CAT G -3' (FRAG 612) (SEQ. ID NO: 622)
 5'- GA GAT GGA GCG CGG CAT -3' (FRAG 613) (SEQ. ID NO: 623)
 5'- GA GAT GGA GCG CGG CA-3' (FRAG 614) (SEQ. ID NO: 624)
 60 5'- GA GAT GGA GCG CGG C-3' (FRAG 615) (SEQ. ID NO: 625)
 5'- GA GAT GGA GCG CGG -3' (FRAG 616) (SEQ. ID NO: 626)
 5'- GA GAT GGA GCG CG -3' (FRAG 617) (SEQ. ID NO: 627)

5'- GA GAT GGA GCG C -3' (FRAG 618) (SEQ. ID NO: 628)
 5'- GA GAT GGA GCG -3' (FRAG 619) (SEQ. ID NO: 629)
 5'- GA GAT GGA GC -3' (FRAG 620) (SEQ. ID NO: 630)
 5'- A GAT GGA GGC CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 621) (SEQ. ID NO: 631)
 5 5'- A GAT GGA GGC CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 622) (SEQ. ID NO: 632)
 5'- A GAT GGA GGC CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 623) (SEQ. ID NO: 633)
 5'- A GAT GGA GGC CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 624) (SEQ. ID NO: 634)
 5'- A GAT GGA GGC CGG CAT GGC GGG CAC AGG CT-3' (FRAG 625) (SEQ. ID NO: 635)
 5'- A GAT GGA GGC CGG CAT GGC GGG CAC AGG C-3' (FRAG 626) (SEQ. ID NO: 636)
 10 5'- A GAT GGA GGC CGG CAT GGC GGG CAC AGG -3' (FRAG 627) (SEQ. ID NO: 637)
 5'- A GAT GGA GGC CGG CAT GGC GGG CAC AG-3' (FRAG 628) (SEQ. ID NO: 638)
 5'- A GAT GGA GGC CGG CAT GGC GGG CAC A-3' (FRAG 629) (SEQ. ID NO: 639)
 5'- A GAT GGA GGC CGG CAT GGC GGG CAC-3' (FRAG 630) (SEQ. ID NO: 640)
 5'- A GAT GGA GGC CGG CAT GGC GGG CA-3' (FRAG 631) (SEQ. ID NO: 641)
 15 5'- A GAT GGA GGC CGG CAT GGC GGG C-3' (FRAG 632) (SEQ. ID NO: 642)
 5'- A GAT GGA GGC CGG CAT GGC GGG -3' (FRAG 633) (SEQ. ID NO: 643)
 5'- A GAT GGA GGC CGG CAT GGC GG-3' (FRAG 634) (SEQ. ID NO: 644)
 5'- A GAT GGA GGC CGG CAT GGC G-3' (FRAG 635) (SEQ. ID NO: 645)
 5'- A GAT GGA GGC CGG CAT GGC -3' (FRAG 636) (SEQ. ID NO: 646)
 20 5'- A GAT GGA GGC CGG CAT GG -3' (FRAG 637) (SEQ. ID NO: 647)
 5'- A GAT GGA GGC CGG CAT G -3' (FRAG 638) (SEQ. ID NO: 648)
 5'- A GAT GGA GGC CGG CAT -3' (FRAG 639) (SEQ. ID NO: 649)
 5'- A GAT GGA GGC CGG CA-3' (FRAG 640) (SEQ. ID NO: 650)
 5'- A GAT GGA GGC CGG C-3' (FRAG 641) (SEQ. ID NO: 651)
 25 5'- A GAT GGA GGC CGG -3' (FRAG 642) (SEQ. ID NO: 652)
 5'- A GAT GGA GGC CG -3' (FRAG 643) (SEQ. ID NO: 653)
 5'- A GAT GGA GGC C -3' (FRAG 644) (SEQ. ID NO: 654)
 5'- A GAT GGA GGC -3' (FRAG 645) (SEQ. ID NO: 655)
 5'- GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 646) (SEQ. ID NO: 656)
 30 5'- GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 647) (SEQ. ID NO: 657)
 5'- GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 648) (SEQ. ID NO: 658)
 5'- GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 6) (SEQ. ID NO: 659)
 5'- GAT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 650) (SEQ. ID NO: 660)
 5'- GAT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 651) (SEQ. ID NO: 661)
 35 5'- GAT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 652) (SEQ. ID NO: 662)
 5'- GAT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 653) (SEQ. ID NO: 663)
 5'- GAT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 654) (SEQ. ID NO: 664)
 5'- GAT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 655) (SEQ. ID NO: 665)
 5'- GAT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 656) (SEQ. ID NO: 666)
 40 5'- GAT GGA GGG CGG CAT GGC GGG C-3' (FRAG 657) (SEQ. ID NO: 667)
 5'- GAT GGA GGG CGG CAT GGC GGG -3' (FRAG 658) (SEQ. ID NO: 668)
 5'- GAT GGA GGG CGG CAT GGC GG-3' (FRAG 659) (SEQ. ID NO: 669)
 5'- GAT GGA GGG CGG CAT GGC G-3' (FRAG 660) (SEQ. ID NO: 670)
 5'- GAT GGA GGG CGG CAT GGC -3' (FRAG 661) (SEQ. ID NO: 671)
 45 5'- GAT GGA GGG CGG CAT GG -3' (FRAG 662) (SEQ. ID NO: 672)
 5'- GAT GGA GGG CGG CAT G -3' (FRAG 663) (SEQ. ID NO: 673)
 5'- GAT GGA GGG CGG CAT -3' (FRAG 664) (SEQ. ID NO: 674)
 5'- GAT GGA GGG CGG CA-3' (FRAG 665) (SEQ. ID NO: 675)
 5'- GAT GGA GGG CGG C-3' (FRAG 666) (SEQ. ID NO: 676)
 50 5'- GAT GGA GGG CGG -3' (FRAG 667) (SEQ. ID NO: 677)
 5'- GAT GGA GGG CG -3' (FRAG 668) (SEQ. ID NO: 678)
 5'- GAT GGA GGG C -3' (FRAG 669) (SEQ. ID NO: 679)
 5'- AT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 670) (SEQ. ID NO: 680)
 5'- AT GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 671) (SEQ. ID NO: 681)
 55 5'- AT GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 672) (SEQ. ID NO: 682)
 5'- AT GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 673) (SEQ. ID NO: 683)
 5'- AT GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 674) (SEQ. ID NO: 684)
 5'- AT GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 675) (SEQ. ID NO: 685)
 5'- AT GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 676) (SEQ. ID NO: 686)
 60 5'- AT GGA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 677) (SEQ. ID NO: 687)
 5'- AT GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 678) (SEQ. ID NO: 688)
 5'- AT GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 679) (SEQ. ID NO: 689)

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5' AT GGA GGG CGG CAT GGC GGG CA-3' (FRAG 680) (SEQ. ID NO: 690)
 5' AT GGA GGG CGG CAT GGC GGG C-3' (FRAG 681) (SEQ. ID NO: 691)
 5' AT GGA GGG CGG CAT GGC GGG -3' (FRAG 682) (SEQ. ID NO: 692)
 5' AT GGA GGG CGG CAT GGC GG-3' (FRAG 683) (SEQ. ID NO: 693)
 5 5' AT GGA GGG CGG CAT GGC G-3' (FRAG 684) (SEQ. ID NO: 694)
 5' AT GGA GGG CGG CAT GGC -3' (FRAG 685) (SEQ. ID NO: 695)
 5' AT GGA GGG CGG CAT GG -3' (FRAG 686) (SEQ. ID NO: 696)
 5' AT GGA GGG CGG CAT G -3' (FRAG 687) (SEQ. ID NO: 697)
 5' AT GGA GGG CGG CAT -3' (FRAG 688) (SEQ. ID NO: 698)
 10 5' AT GGA GGG CGG CA-3' (FRAG 689) (SEQ. ID NO: 699)
 5' AT GGA GGG CGG C-3' (FRAG 690) (SEQ. ID NO: 700)
 5' AT GGA GGG CGG -3' (FRAG 691) (SEQ. ID NO: 701)
 5' AT GGA GGG CGG -3' (FRAG 692) (SEQ. ID NO: 702)
 5' T GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 693) (SEQ. ID NO: 703)
 15 5' T GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 694) (SEQ. ID NO: 704)
 5' T GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 695) (SEQ. ID NO: 705)
 5' T GGA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 696) (SEQ. ID NO: 706)
 5' T GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 697) (SEQ. ID NO: 707)
 5' T GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 698) (SEQ. ID NO: 708)
 20 5' T GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 699) (SEQ. ID NO: 709)
 5' T GGA GGG CGG CAT GGC GGG CAC AG -3' (FRAG 700) (SEQ. ID NO: 710)
 5' T GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 701) (SEQ. ID NO: 711)
 5' T GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 702) (SEQ. ID NO: 712)
 25 5' T GGA GGG CGG CAT GGC GGG CA-3' (FRAG 703) (SEQ. ID NO: 713)
 5' T GGA GGG CGG CAT GGC GGG C-3' (FRAG 704) (SEQ. ID NO: 714)
 5' T GGA GGG CGG CAT GGC GGG -3' (FRAG 705) (SEQ. ID NO: 715)
 5' T GGA GGG CGG CAT GGC GG-3' (FRAG 706) (SEQ. ID NO: 716)
 5' T GGA GGG CGG CAT GGC G-3' (FRAG 707) (SEQ. ID NO: 717)
 5' T GGA GGG CGG CAT GGC -3' (FRAG 708) (SEQ. ID NO: 718)
 30 5' T GGA GGG CGG CAT GG -3' (FRAG 709) (SEQ. ID NO: 719)
 5' T GGA GGG CGG CAT G -3' (FRAG 710) (SEQ. ID NO: 720)
 5' T GGA GGG CGG CAT -3' (FRAG 711) (SEQ. ID NO: 721)
 5' T GGA GGG CGG CA-3' (FRAG 712) (SEQ. ID NO: 722)
 5' T GGA GGG CGG C-3' (FRAG 713) (SEQ. ID NO: 723)
 35 5' T GGA GGG CGG -3' (FRAG 714) (SEQ. ID NO: 724)
 5' GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 715) (SEQ. ID NO: 725)
 5' GGA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 716) (SEQ. ID NO: 726)
 5' GGA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 717) (SEQ. ID NO: 727)
 5' GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 718) (SEQ. ID NO: 728)
 40 5' GGA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 719) (SEQ. ID NO: 729)
 5' GGA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 720) (SEQ. ID NO: 730)
 5' GGA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 721) (SEQ. ID NO: 731)
 5' GGA GGG CGG CAT GGC GGG CAC AG -3' (FRAG 722) (SEQ. ID NO: 732)
 5' GGA GGG CGG CAT GGC GGG CAC A-3' (FRAG 723) (SEQ. ID NO: 733)
 45 5' GGA GGG CGG CAT GGC GGG CAC-3' (FRAG 724) (SEQ. ID NO: 734)
 5' GGA GGG CGG CAT GGC GGG CA-3' (FRAG 725) (SEQ. ID NO: 735)
 5' GGA GGG CGG CAT GGC GGG C-3' (FRAG 726) (SEQ. ID NO: 736)
 5' GGA GGG CGG CAT GGC GGG -3' (FRAG 727) (SEQ. ID NO: 737)
 5' GGA GGG CGG CAT GGC GG-3' (FRAG 728) (SEQ. ID NO: 738)
 50 5' GGA GGG CGG CAT GGC G-3' (FRAG 729) (SEQ. ID NO: 739)
 5' GGA GGG CGG CAT GGC -3' (FRAG 730) (SEQ. ID NO: 740)
 5' GGA GGG CGG CAT GG -3' (FRAG 731) (SEQ. ID NO: 741)
 5' GGA GGG CGG CAT G -3' (FRAG 732) (SEQ. ID NO: 742)
 5' GGA GGG CGG CAT -3' (FRAG 733) (SEQ. ID NO: 743)
 55 5' GGA GGG CGG CA-3' (FRAG 734) (SEQ. ID NO: 744)
 5' GGA GGG CGG C-3' (FRAG 735) (SEQ. ID NO: 745)
 5' GA GGG CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 736) (SEQ. ID NO: 746)
 5' GA GGG CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 737) (SEQ. ID NO: 747)
 5' GA GGG CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 738) (SEQ. ID NO: 748)
 60 5' GA GGG CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 739) (SEQ. ID NO: 749)
 5' GA GGG CGG CAT GGC GGG CAC AGG CT-3' (FRAG 740) (SEQ. ID NO: 750)
 5' GA GGG CGG CAT GGC GGG CAC AGG C-3' (FRAG 741) (SEQ. ID NO: 751)

5' - GA GGG CGG CAT GGC GGG CAC AGG -3' (FRAG 742) (SEQ. ID NO: 752)
 5' - GA GGG CGG CAT GGC GGG CAC AG-3' (FRAG 743) (SEQ. ID NO: 753)
 5' - GA GGG CGG CAT GGC GGG CAC A-3' (FRAG 744) (SEQ. ID NO: 754)
 5' - GA GGG CGG CAT GGC GGG CAC-3' (FRAG 745) (SEQ. ID NO: 755)
 5 5' - GA GGG CGG CAT GGC GGG CA-3' (FRAG 746) (SEQ. ID NO: 756)
 5' - GA GGG CGG CAT GGC GGG C-3' (FRAG 747) (SEQ. ID NO: 757)
 5' - GA GGG CGG CAT GGC GGG -3' (FRAG 748) (SEQ. ID NO: 758)
 5' - GA GGG CGG CAT GGC GG-3' (FRAG 749) (SEQ. ID NO: 759)
 5' - GA GGG CGG CAT GGC G-3' (FRAG 750) (SEQ. ID NO: 760)
 10 5' - GA GGG CGG CAT GGC -3' (FRAG 751) (SEQ. ID NO: 761)
 5' - GA GGG CGG CAT GG -3' (FRAG 752) (SEQ. ID NO: 762)
 5' - GA GGG CGG CAT G -3' (FRAG 753) (SEQ. ID NO: 763)
 5' - GA GGG CGG CAT -3' (FRAG 754) (SEQ. ID NO: 764)
 5' - GA GGG CGG CA-3' (FRAG 755) (SEQ. ID NO: 765)
 15 5' - A GGG CGG CA'' GGC GGG CAC AGG CTG GGC-3' (FRAG 756) (SEQ. ID NO: 766)
 5' - A GGG CGG CA'' GGC GGG CAC AGG CTG GG-3' (FRAG 757) (SEQ. ID NO: 767)
 5' - A GGG CGG CA'' GGC GGG CAC AGG CTG G-3' (FRAG 758) (SEQ. ID NO: 768)
 5' - A GGG CGG CA'' GGC GGG CAC AGG CTG -3' (FRAG 759) (SEQ. ID NO: 769)
 5' - A GGG CGG CA'' GGC GGG CAC AGG CT-3' (FRAG 760) (SEQ. ID NO: 770)
 20 5' - A GGG CGG CA'' GGC GGG CAC AGG C-3' (FRAG 761) (SEQ. ID NO: 771)
 5' - A GGG CGG CA'' GGC GGG CAC AGG -3' (FRAG 762) (SEQ. ID NO: 772)
 5' - A GGG CGG CA'' GGC GGG CAC AG-3' (FRAG 763) (SEQ. ID NO: 773)
 5' - A GGG CGG CA'' GGC GGG CAC A-3' (FRAG 764) (SEQ. ID NO: 774)
 5' - A GGG CGG CA'' GGC GGG CAC-3' (FRAG 765) (SEQ. ID NO: 775)
 25 5' - A GGG CGG CA'' GGC GGG CA-3' (FRAG 766) (SEQ. ID NO: 776)
 5' - A GGG CGG CA'' GGC GGG C-3' (FRAG 767) (SEQ. ID NO: 777)
 5' - A GGG CGG CA'' GGC GGG -3' (FRAG 768) (SEQ. ID NO: 778)
 5' - A GGG CGG CA'' GGC GG-3' (FRAG 769) (SEQ. ID NO: 779)
 5' - A GGG CGG CA'' GGC G-3' (FRAG 770) (SEQ. ID NO: 780)
 30 5' - A GGG CGG CA'' GGC -3' (FRAG 771) (SEQ. ID NO: 781)
 5' - A GGG CGG CA'' GG -3' (FRAG 772) (SEQ. ID NO: 782)
 5' - A GGG CGG CA'' G -3' (FRAG 773) (SEQ. ID NO: 783)
 5' - A GGG CGG CA'' -3' (FRAG 774) (SEQ. ID NO: 784)
 5' - GGG CGG CAT 3GC GGG CAC AGG CTG GGC-3' (FRAG 775) (SEQ. ID NO: 785)
 35 5' - GGG CGG CAT 3GC GGG CAC AGG CTG GG-3' (FRAG 776) (SEQ. ID NO: 786)
 5' - GGG CGG CAT 3GC GGG CAC AGG CTG G-3' (FRAG 777) (SEQ. ID NO: 787)
 5' - GGG CGG CAT 3GC GGG CAC AGG CTG -3' (FRAG 778) (SEQ. ID NO: 788)
 5' - GGG CGG CAT 3GC GGG CAC AGG CT-3' (FRAG 779) (SEQ. ID NO: 789)
 5' - GGG CGG CAT 3GC GGG CAC AGG C-3' (FRAG 780) (SEQ. ID NO: 790)
 40 5' - GGG CGG CAT 3GC GGG CAC AGG -3' (FRAG 781) (SEQ. ID NO: 791)
 5' - GGG CGG CAT 3GC GGG CAC AG-3' (FRAG 782) (SEQ. ID NO: 792)
 5' - GGG CGG CAT 3GC GGG CAC A-3' (FRAG 783) (SEQ. ID NO: 793)
 5' - GGG CGG CAT 3GC GGG CAC-3' (FRAG 784) (SEQ. ID NO: 794)
 5' - GGG CGG CAT 3GC GGG CA-3' (FRAG 785) (SEQ. ID NO: 795)
 45 5' - GGG CGG CAT 3GC GGG C-3' (FRAG 786) (SEQ. ID NO: 796)
 5' - GGG CGG CAT 3GC GGG -3' (FRAG 787) (SEQ. ID NO: 797)
 5' - GGG CGG CAT 3GC GG-3' (FRAG 788) (SEQ. ID NO: 798)
 5' - GGG CGG CAT 3GC G-3' (FRAG 789) (SEQ. ID NO: 799)
 5' - GGG CGG CAT 3GC -3' (FRAG 790) (SEQ. ID NO: 800)
 50 5' - GGG CGG CAT 3G -3' (FRAG 791) (SEQ. ID NO: 801)
 5' - GGG CGG CAT 3 -3' (FRAG 792) (SEQ. ID NO: 802)
 5' - GG CGG CAT G 3C GGG CAC AG G CTG GGC-3' (FRAG 793) (SEQ. ID NO: 803)
 5' - GG CGG CAT G 3C GGG CAC AGG CTG GG-3' (FRAG 794) (SEQ. ID NO: 804)
 5' - GG CGG CAT G 3C GGG CAC AGG CTG G-3' (FRAG 795) (SEQ. ID NO: 805)
 55 5' - GG CGG CAT G 3C GGG CAC AGG CTG -3' (FRAG 796) (SEQ. ID NO: 806)
 5' - GG CGG CAT G 3C GGG CAC AGG CT-3' (FRAG 797) (SEQ. ID NO: 807)
 5' - GG CGG CAT G 3C GGG CAC AGG C-3' (FRAG 798) (SEQ. ID NO: 808)
 5' - GG CGG CAT G 3C GGG CAC AGG -3' (FRAG 799) (SEQ. ID NO: 809)
 5' - GG CGG CAT G 3C GGG CAC AG-3' (FRAG 800) (SEQ. ID NO: 810)
 60 5' - GG CGG CAT G 3C GGG CAC A-3' (FRAG 801) (SEQ. ID NO: 811)
 5' - GG CGG CAT G 3C GGG CAC-3' (FRAG 802) (SEQ. ID NO: 812)
 5' - GG CGG CAT G 3C GGG CA-3' (FRAG 803) (SEQ. ID NO: 813)

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5' - GG CGG CAT GGC GGG C-3' (FRAG 804) (SEQ. ID NO: 814)
 5' - GG CGG CAT GGC GGG -3' (FRAG 805) (SEQ. ID NO: 815)
 5' - GG CGG CAT GGC GG-3' (FRAG 806) (SEQ. ID NO: 816)
 5' - GG CGG CAT GGC G-3' (FRAG 807) (SEQ. ID NO: 817)
 5 5' - GG CGG CAT GGC -3' (FRAG 808) (SEQ. ID NO: 818)
 5' - GG CGG CAT GG -3' (FRAG 809) (SEQ. ID NO: 819)
 5' - G CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 810) (SEQ. ID NO: 820)
 5' - G CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 811) (SEQ. ID NO: 821)
 5' - G CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 812) (SEQ. ID NO: 822)
 10 5' - G CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 813) (SEQ. ID NO: 823)
 5' - G CGG CAT GGC GGG CAC AGG CT-3' (FRAG 814) (SEQ. ID NO: 824)
 5' - G CGG CAT GGC GGG CAC AGG C-3' (FRAG 815) (SEQ. ID NO: 825)
 5' - G CGG CAT GGC GGG CAC AGG -3' (FRAG 816) (SEQ. ID NO: 826)
 5' - G CGG CAT GGC GGG CAC AG-3' (FRAG 817) (SEQ. ID NO: 827)
 15 5' - G CGG CAT GGC GGG CAC A-3' (FRAG 818) (SEQ. ID NO: 828)
 5' - G CGG CAT GGC GGG CAC-3' (FRAG 819) (SEQ. ID NO: 829)
 5' - G CGG CAT GGC GGG CA-3' (FRAG 820) (SEQ. ID NO: 830)
 5' - G CGG CAT GGC GGG C-3' (FRAG 821) (SEQ. ID NO: 831)
 5' - G CGG CAT GGC GGG -3' (FRAG 822) (SEQ. ID NO: 832)
 20 5' - G CGG CAT GGC GG-3' (FRAG 823) (SEQ. ID NO: 833)
 5' - G CGG CAT GGC G-3' (FRAG 824) (SEQ. ID NO: 834)
 5' - G CGG CAT GGC -3' (FRAG 825) (SEQ. ID NO: 835)
 5' - CGG CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 826) (SEQ. ID NO: 836)
 5' - CGG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 827) (SEQ. ID NO: 837)
 25 5' - CGG CAT GGC GGG CAC AGG CTG G-3' (FRAG 828) (SEQ. ID NO: 838)
 5' - CGG CAT GGC GGG CAC AGG CTG -3' (FRAG 829) (SEQ. ID NO: 839)
 5' - CGG CAT GGC GGG CAC AGG CT-3' (FRAG 830) (SEQ. ID NO: 840)
 5' - CGG CAT GGC GGG CAC AGG C-3' (FRAG 831) (SEQ. ID NO: 841)
 5' - CGG CAT GGC GGG CAC AGG -3' (FRAG 832) (SEQ. ID NO: 842)
 30 5' - CGG CAT GGC GGG CAC AG-3' (FRAG 833) (SEQ. ID NO: 843)
 5' - CGG CAT GGC GGG CAC A-3' (FRAG 834) (SEQ. ID NO: 844)
 5' - CGG CAT GGC GGG CAC-3' (FRAG 835) (SEQ. ID NO: 845)
 5' - CGG CAT GGC GGG CA-3' (FRAG 836) (SEQ. ID NO: 846)
 5' - CGG CAT GGC GGG C-3' (FRAG 837) (SEQ. ID NO: 847)
 35 5' - CGG CAT GGC GGG -3' (FRAG 838) (SEQ. ID NO: 848)
 5' - CGG CAT GGC GG-3' (FRAG 839) (SEQ. ID NO: 849)
 5' - CGG CAT GGC G-3' (FRAG 840) (SEQ. ID NO: 850)
 5' - GG CAT GGC GGG CAC AGG C TG GGC-3' (FRAG 841) (SEQ. ID NO: 851)
 5' - GG CAT GGC GGG CAC AGG CTG GG-3' (FRAG 842) (SEQ. ID NO: 852)
 40 5' - GG CAT GGC GGG CAC AGG CTG G-3' (FRAG 843) (SEQ. ID NO: 853)
 5' - GG CAT GGC GGG CAC AGG CTG -3' (FRAG 844) (SEQ. ID NO: 854)
 5' - GG CAT GGC GGG CAC AGG CT-3' (FRAG 845) (SEQ. ID NO: 855)
 5' - GG CAT GGC GGG CAC AGG C-3' (FRAG 846) (SEQ. ID NO: 856)
 5' - GG CAT GGC GGG CAC AGG -3' (FRAG 847) (SEQ. ID NO: 857)
 45 5' - GG CAT GGC GGG CAC AG-3' (FRAG 848) (SEQ. ID NO: 858)
 5' - GG CAT GGC GGG CAC A-3' (FRAG 849) (SEQ. ID NO: 859)
 5' - GG CAT GGC GGG CAC-3' (FRAG 850) (SEQ. ID NO: 860)
 5' - GG CAT GGC GGG CA-3' (FRAG 851) (SEQ. ID NO: 861)
 5' - GG CAT GGC GGG C-3' (FRAG 852) (SEQ. ID NO: 862)
 50 5' - GG CAT GGC GGG -3' (FRAG 853) (SEQ. ID NO: 863)
 5' - GG CAT GGC GG-3' (FRAG 854) (SEQ. ID NO: 864)
 5' - G CAT GGC GGG CAC AGG CTG GGC-3' (FRAG 855) (SEQ. ID NO: 865)
 5' - G CAT GGC GGG CAC AGG CTG GG-3' (FRAG 856) (SEQ. ID NO: 866)
 5' - G CAT GGC GGG CAC AGG CTG G-3' (FRAG 857) (SEQ. ID NO: 867)
 55 5' - G CAT GGC GGG CAC AGG CTG -3' (FRAG 858) (SEQ. ID NO: 868)
 5' - G CAT GGC GGG CAC AGG CT-3' (FRAG 859) (SEQ. ID NO: 869)
 5' - G CAT GGC GGG CAC AGG C-3' (FRAG 860) (SEQ. ID NO: 870)
 5' - G CAT GGC GGG CAC AGG -3' (FRAG 861) (SEQ. ID NO: 871)
 5' - G CAT GGC GGG CAC AG-3' (FRAG 862) (SEQ. ID NO: 872)
 60 5' - G CAT GGC GGG CAC A-3' (FRAG 863) (SEQ. ID NO: 873)
 5' - G CAT GGC GGG CAC-3' (FRAG 864) (SEQ. ID NO: 874)
 5' - G CAT GGC GGG CA-3' (FRAG 865) (SEQ. ID NO: 875)

5'- G CAT GGC GCG C-3' (FRAG 866) (SEQ. ID NO: 876)
5'- G CAT GGC GCG -3' (FRAG 867) (SEQ. ID NO: 877)
5'- CAT GGC GGC CAC AGG CTG GGC-3' (FRAG 868) (SEQ. ID NO: 878)
5'- CAT GGC GGC CAC AGG CTG GG-3' (FRAG 869) (SEQ. ID NO: 879)
5 5'- CAT GGC GGC CAC AGG CTG G-3' (FRAG 870) (SEQ. ID NO: 880)
5'- CAT GGC GGC CAC AGG CTG -3' (FRAG 871) (SEQ. ID NO: 881)
5'- CAT GGC GGC CAC AGG CT-3' (FRAG 872) (SEQ. ID NO: 882)
5'- CAT GGC GGC CAC AGG C-3' (FRAG 873) (SEQ. ID NO: 883)
5'- CAT GGC GGC CAC AGG -3' (FRAG 874) (SEQ. ID NO: 884)
10 5'- CAT GGC GGC CAC AG-3' (FRAG 875) (SEQ. ID NO: 885)
5'- CAT GGC GGC CAC A-3' (FRAG 876) (SEQ. ID NO: 886)
5'- CAT GGC GGC CAC-3' (FRAG 877) (SEQ. ID NO: 887)
5'- CAT GGC GGC CA-3' (FRAG 878) (SEQ. ID NO: 888)
5'- CAT GGC GGC C-3' (FRAG 879) (SEQ. ID NO: 889)
15 5'- AT GGC GGG CAC AGG CTG GGC-3' (FRAG 880) (SEQ. ID NO: 890)
5'- AT GGC GGG CAC AGG CTG GG-3' (FRAG 881) (SEQ. ID NO: 891)
5'- AT GGC GGG CAC AGG CTG G-3' (FRAG 882) (SEQ. ID NO: 892)
5'- AT GGC GGG CAC AGG CTG -3' (FRAG 883) (SEQ. ID NO: 893)
5'- AT GGC GGG CAC AGG CT-3' (FRAG 884) (SEQ. ID NO: 894)
20 5'- AT GGC GGG CAC AGG C-3' (FRAG 885) (SEQ. ID NO: 895)
5'- AT GGC GGG CAC AGG -3' (FRAG 886) (SEQ. ID NO: 896)
5'- AT GGC GGG CAC AG-3' (FRAG 887) (SEQ. ID NO: 897)
5'- AT GGC GGG CAC A-3' (FRAG 888) (SEQ. ID NO: 898)
5'- AT GGC GGG CAC-3' (FRAG 889) (SEQ. ID NO: 899)
25 5'- AT GGC GGG CA-3' (FRAG 890) (SEQ. ID NO: 900)
5'- T GGC GGG CAC AGG CTG GGC-3' (FRAG 891) (SEQ. ID NO: 901)
5'- T GGC GGG CAC AGG CTG GG-3' (FRAG 892) (SEQ. ID NO: 902)
5'- T GGC GGG CAC AGG CTG G-3' (FRAG 893) (SEQ. ID NO: 903)
5'- T GGC GGG CAC AGG CTG -3' (FRAG 894) (SEQ. ID NO: 904)
30 5'- T GGC GGG CAC AGG CT-3' (FRAG 895) (SEQ. ID NO: 905)
5'- T GGC GGG CAC C-3' (FRAG 896) (SEQ. ID NO: 906)
5'- T GGC GGG CAC AGG -3' (FRAG 897) (SEQ. ID NO: 907)
5'- T GGC GGG CAC AG-3' (FRAG 898) (SEQ. ID NO: 908)
5'- T GGC GGG CAC A-3' (FRAG 899) (SEQ. ID NO: 909)
35 5'- T GGC GGG CAC-3' (FRAG 900) (SEQ. ID NO: 910)
5'- GGC GGG CAC AGG CTG GGC-3' (FRAG 901) (SEQ. ID NO: 911)
5'- GGC GGG CAC AGG CTG GG-3' (FRAG 902) (SEQ. ID NO: 912)
5'- GGC GGG CAC AGG CTG G-3' (FRAG 903) (SEQ. ID NO: 913)
5'- GGC GGG CAC AGG CTG -3' (FRAG 904) (SEQ. ID NO: 914)
40 5'- GGC GGG CAC AGG CT-3' (FRAG 905) (SEQ. ID NO: 915)
5'- GGC GGG CAC AGG C-3' (FRAG 906) (SEQ. ID NO: 916)
5'- GGC GGG CAC AGG -3' (FRAG 907) (SEQ. ID NO: 917)
5'- GGC GGG CAC AG-3' (FRAG 908) (SEQ. ID NO: 918)
5'- GGC GGG CAC A-3' (FRAG 909) (SEQ. ID NO: 919)
45 5'- GC GGG CAC AGG CTG GGC-3' (FRAG 910) (SEQ. ID NO: 920)
5'- GC GGG CAC AGG CTG GG-3' (FRAG 911) (SEQ. ID NO: 921)
5'- GC GGG CAC AGG CTG G-3' (FRAG 912) (SEQ. ID NO: 922)
5'- GC GGG CAC AGG CTG -3' (FRAG 913) (SEQ. ID NO: 923)
5'- GC GGG CAC AGG CT-3' (FRAG 914) (SEQ. ID NO: 924)
50 5'- GC GGG CAC AGG C-3' (FRAG 915) (SEQ. ID NO: 925)
5'- GC GGG CAC AGG -3' (FRAG 916) (SEQ. ID NO: 926)
5'- GC GGG CAC AG-3' (FRAG 917) (SEQ. ID NO: 927)
5'- C GGG CAC AGG CTG GGC-3' (FRAG 918) (SEQ. ID NO: 928)
5'- GGG CAC AGG CTG GG-3' (FRAG 919) (SEQ. ID NO: 929)
55 5'- C GGG CAC AGG CTG G-3' (FRAG 920) (SEQ. ID NO: 930)
5'- C GGG CAC AGG CTG -3' (FRAG 921) (SEQ. ID NO: 931)
5'- C GGG CAC AGG CT-3' (FRAG 922) (SEQ. ID NO: 932)
5'- C GGG CAC AGG C-3' (FRAG 923) (SEQ. ID NO: 933)
5'- C GGG CAC AGG -3' (FRAG 924) (SEQ. ID NO: 934)
60 5'- GGG CAC AGG CTC GGC-3' (FRAG 925) (SEQ. ID NO: 935)
5'- GGG CAC AGG CTC GG-3' (FRAG 926) (SEQ. ID NO: 936)
5'- GGG CAC AGG CTC G-3' (FRAG 927) (SEQ. ID NO: 937)

5' - GGG CAC AGG CTG -3' (FRAG 928) (SEQ. ID NO: 938)
 5' - GGG CAC AGG CT -3' (FRAG 929) (SEQ. ID NO: 939)
 5' - GGG CAC AGG C-3' (FRAG 930) (SEQ. ID NO: 940)
 5' - GG CAC AGG CTG GGC-3' (FRAG 931) (SEQ. ID NO: 941)
 5 5' - GG CAC AGG CTG GG-3' (FRAG 932) (SEQ. ID NO: 942)
 5' - GG CAC AGG CTG G-3' (FRAG 933) (SEQ. ID NO: 943)
 5' - GG CAC AGG CTG -3' (FRAG 934) (SEQ. ID NO: 944)
 5' - GG CAC AGG CT-3' (FRAG 935) (SEQ. ID NO: 945)
 5' - G CAC AGG CTG GC C-3' (FRAG 936) (SEQ. ID NO: 946)
 10 5' - G CAC AGG CTG GC -3' (FRAG 937) (SEQ. ID NO: 947)
 5' - G CAC AGG CTG G-3' (FRAG 938) (SEQ. ID NO: 948)
 5' - G CAC AGG CTG -3' (FRAG 939) (SEQ. ID NO: 949)
 5' -CAC AGG CTG GGC 3' (FRAG 940) (SEQ. ID NO: 950)
 5' -CAC AGG CTG GG-3' (FRAG 941) (SEQ. ID NO: 951)
 15 5' -CAC AGG CTG G-3' (FRAG 942) (SEQ. ID NO: 952)
 5' -AC AGG CTG GGC-3' (FRAG 943) (SEQ. ID NO: 953)
 5' -AC AGG CTG GG-3' (FRAG 944) (SEQ. ID NO: 954)
 5' -C AGG CTG GGC-3' (FRAG 945) (SEQ. ID NO: 955)
 5' -TTT TCC TTC CTT TGT CTC TCT TC (FRAG 946) (SEQ. ID NO: 956)
 20 5' -GCT CCC GGC TGC CTG (FRAG 947) (SEQ. ID NO: 957)
 5' -CTC GGC CGT GCG GCT CTG TCG CTC CCG GT (FRAG 948) (SEQ. ID NO: 958)
 5' -CCG CCG CCC TCC 3GG GGG TC (FRAG 949) (SEQ. ID NO: 959)
 5' -TGC TGC CGT TGG CTG CCC (FRAG 950) (SEQ. ID NO: 960)
 5' -CTT CTG CGG GTC 'GCC GG (FRAG 951) (SEQ. ID NO: 961)
 25 5' -TGC TGG GCT TGT 'GGC (FRAG 952) (SEQ. ID NO: 962)
 5' -GGC CTC TCT TCT GGG (FRAG 953) (SEQ. ID NO: 963)
 5' -CCT GGT CCC TCC GT (FRAG 954) (SEQ. ID NO: 964)
 5' -GGT GGC TCC TCT 'GC (FRAG 955) (SEQ. ID NO: 965)
 5' -GCT TGG TCC TGG 3GC TGC (FRAG 956) (SEQ. ID NO: 966)
 30 5' -TGC TCT CCT CTC CTT (FRAG 957) (SEQ. ID NO: 967)

Human Adenosine A2a Receptor Nucleic Acid and Antisense Oligonucleotide Fragments

5' -TGC TTT TCT TTT CTG GGC CTC TGT GGT CTG TTT TCT TCT G GCC CTG CTG GGG CGC TCT CC GCC GCC
 CGC CTG GCT CCC GGB GCC CBT GBT GGG CBT GCC GTG GTT CTT GCC CTC CTT TGG CTG CCG TGC CCG CTC
 CCC GGC CTC CTG GCG GGT GGC CGT TG GGC CCG TGT TCC CCT GGG -GCC TGG GGC TCC CTT CTC TC GCC
 35 CTT CTT GCT GGG CCT C TGC TGC TGC TGG TGC TGT GGC CCC C GTA CAC CGA GGA GCC CAT GAT GGG CAT
 GCC ACA GAC GAC AGG C GTB CBC CGB GGB GCC CBT GBT GGG CBT GCC BCB GBC GBC BGG C-3' (FRAG. NO.
 1665) (SEQ. ID NO:1680)
 5' -CTG GGC CTC-3' (FRAG 1666) (SEQ. ID NO: 1681)
 5' -TGC TTT TCT TTT CTG GGC CTC-3' (FRAG 958) (SEQ. ID NO: 968)
 40 5' -TGT GGT CTG TTT TTT TCT G-3' (FRAG 959) (SEQ. ID NO: 969)
 5' -GCC CTG CTG GGG CGC TCT CC-3' (FRAG 960) (SEQ. ID NO: 970)
 5' -GCC GCC CGC CTG GCT CCC-3' (FRAG 961) (SEQ. ID NO: 971)
 5' -GGB GCC CBT GBT GGG CBT GCC-3' (FRAG 962) (SEQ. ID NO: 972)
 5' -GTG GTT CTT GCC CTC CTT TGG CTG-3' (FRAG 963) (SEQ. ID NO: 973)
 45 5' -CCG TGC CCG CTC CCC GGC-3' (FRAG 964) (SEQ. ID NO: 974)
 5' -CTC CTG GCG GGT 'GGC CGT TG-3' (FRAG 965) (SEQ. ID NO: 975)
 5' -GGC CCG TGT TCC CCT GGG-3' (FRAG 966) (SEQ. ID NO: 976)
 5' -GCC TGG GGC TCC CTT CTC TC-3' (FRAG 967) (SEQ. ID NO: 977)
 5' -GCC CTT CTT GCT GGG CCT C-3' (FRAG 968) (SEQ. ID NO: 978)
 50 5' -TGC TGC TGC TGG 'TGC TGT GGC CCC C-3' (FRAG 969) (SEQ. ID NO: 979)
 5' -GTACACCGAGGGAGCCATGATGGGCATGCCACAGACGACAGGC-3' (FRAG 970) (SEQ. ID NO: 980)
 5' -GTBCBCCGBGGBGGCCCBTGBTGGGCBTGCCBCBGBGBCBGGC-3' (FRAG 971) (SEQ. ID NO: 981)

Human Adenosine A2b Receptor Nucleic Acid & Antisense Oligonucleotide Fragments

55 5' -GGC GCC GTG CCG CGT CTT GGT GGC GGC GG GTT CGC GCC CGC GCG GGG CCC CTC CGG TCC GTT CGC
 CGC CGC GGG CCC CTC CGG TCC CGG GTC GGG GCC CCC CGC GGC C GCC TCG GGG CTG GGG CGC TGG
 TGG CCG GG CCG CGC CTC CGC CTG CCG CTT CTG GCT GGG CCC CGG GCG CCC CCT CCC CTC TTG CTC GGG
 TCC CCG TG ACA GCG CGT CCT GTG TCT CCA GCA GCA TGG CCG GGC CAG CTG GGC CCC BCB GCG CGT CCT
 GTG TCT CCB GCB GCB TGG CCG GGC CBG CTG GGC CCC CCCAGCCCCG AGGCTCAGAA GCGGCAGGGC

	GAGGC CGCGGT	CCGG CGCGCTA	TGGCCATGCC	CGGCGGGTCT	CACCGGGCTG	CCCCTCGCCC	GGCGCGCCTT
	CGGTAGGGG	CGCC'CGGGC	CCAGCTGGCC	CGGCCATGCT	GCTGGAGACA	CAGGACCGCG	TGTACGTGGC
	GCTGGAGCTG	GTCATCGCCG	CGCTTCGGT	GGCGGGCAAC	GTGCTGGTGT	GCGCCGCGGT	GGGCACGGCG
5	AACACTCTGC	AGACGCCAC	CAACTACTTC	CTGGTGTCCC	TGGCTGCCG	CGACGTGGCC	GTGGGGCTCT
	TCGCCATCCC	CTTGCCCATC	ACCATCAGCC	TGGGCTTCTG	CACTGACTTC	TACGGCTGCC	TCTTCCTCGC
	CTGCTTCGTG	CTGGTGCTCA	CGCAGAGCTC	CATCTTCAGC	CTTCTGGCCG	TGGCAGTCGA	CAGATAACCTG
	GCCATCTGTG	TCCC3CTCAG	GTATAAAAGT	TTGGTCACGG	GGACCCGAGC	AAGAGGGGTC	ATTGCTGTCC
	TCTGGGTCTT	TGCCITTGGC	ATCGGATTGA	CTCCATTCCCT	GGGGTGGAAAC	AGTAAAGACA	GTGCCACCAA
10	CAACTGCACA	GAAC'CCTGGG	ATGGAACCAC	GAATGAAAGC	TGCTGCCTTG	TGAAGTGTCT	CTTTGAGAAT
	GTGGTCCCCA	TGACCTACAT	GGTATATTTC	AATTCTTTG	GGTGTGTTCT	GCCCCCACTG	CTTATAATGC
	TGGTGATCTA	CATTAAGATC	TTCCCTGGG	CCTGCAGGCA	GCTTCAGCGC	ACTGAGCTGA	TGGACCACTC
	GAGGACCAACC	CTCCAGCGGG	AGATCCATGC	AGCCAAGTCA	CTGGCCATGA	TTGTGGGGAT	TTTGCCCTG
	TGCTGGTTAC	CTGT3CATGC	TGTTAACCTGT	GTCACTCTT	TCCAGGCCAGC	TCAGGGTAAA	AATAAGCCA
15	AGTGGGCAAT	GAA'ATGGCC	ATTCTTCTGT	CACATGCCA	TTCAGTTGTC	AATCCCATTG	TCTATGCTTA
	CCGGAACCAGA	GAC'CTCCGCT	ACACTTTCA	CAAATTATC	TCCAGGTATC	TTCTCTGCCA	AGCAGATGTC
	AAGAGTGGGA	ATGGTCAGGC	TGGGGTACAG	CCTGCTCTCG	GTGTGGGCCT	ATGATCTAGG	CTCTCGCCCTC
	TTCCAGGAGA	AGATACAAAT	CCACAAGAAA	CAAAGAGGAC	ACGGCTGGTT	TTCATTGTGA	AAGATAGCTA
	CACCTCACAA	GGAAATGGAC	TGCCTCTCTT	GAGCACTTCC	CTGGAGCTAC	CACGTATCTA	GCTAATATGT
20	ATGTGTCAGT	AGTAGCACCA	AGGATTGACA	AATATATTTA	TGATCTATTTC	AGCTGCTTTT	ACTGTGTGGA
	TTATGCCAAC	AGCTITGAATG	GATTCTAAC	GACTCTTTTG	TTTTTAAAG	TCTGCCTTGT	TTATGGTGGA
	AAATTACTGTA	AACTIATTTA	CTGTGAAACA	GTGTGAACTA	TTATAATGCA	AATACTTTTT	AACTTAGAGG
	CAATGGAAAA	ATAA'AAGTTG	ACTGTACTAA	AAATGTATAC	TTGTTGCCAG	GAAGGTGACC	TCAAAAATTA
	AAAGTATAAT	TATTGGCCG	GGCATGGGG	CTCACACCTG	TAATTCCAGC	ACTTGGGAG	GCCAAGGCAG
25	GCGGATCACG	AGG'CAGGAG	TTCAAAACCA	GCCTGTCAA	TATAGTG	GGGCAATTG	TTAGTTATCC
	GCGGCCACCA	AGACGCCGCA	CGGCGCCTGG	ACCGGAGGGG	CCCCGCGCG	GCGCGAACCT	TGGGCTCGGG
	CGAGTGGGTG	GTGCTCCGCC	CAGCCCGAGA	CGGGCGGGCG	CGCGGGCCAA	TGGGTGCCGC	CTCTTGCCG
	CGGGGGGCC	CGACCCGTGG	GTCCC GGCCA	CCAGCGCCCC	AGCCCCGAGG	CTCAGAACGCG	GCAGGCGGAG
	GCGCGGTCCG	GGCCCTATGG	CCATGCCCGG	CGGGTCTCAC	GCGGCTGCC	CTCGCCCGGC	GCGCCTTCGG
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	GGAGCTGGTC	ATCGCCGCGC	TTTCGGTGGC	GGGCAACGTG	CTGGTGTGCG	CCGGGTGGG	CACGGCGAAC
	ACTCTGCAGA	CGCCCCACAA	CTACTTCTG	GTGCTCCCTGG	CTGCGGCCGA	CGTGGCCGTG	GGGCTCTTCG
	CCATCCCCCT	TGCCATCACC	ATCAGCCTGG	GCTCTGCAC	TGACTTCTAC	GGCTGCCTCT	TCCTCGCCCTG
	CTTCGTGCTG	GTGCTCACGC	AGAGCTCCAT	CTTCAGCCTT	CTGGCGTGG	CAGTCGACAG	ATACCTGGCC
35	ATCTGTGTCC	CGCTCAGGTA	TTAAAGTTTG	GTCACGGGGA	CCCGAGCAAG	AGGGTCATT	GCTGTCTCT
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	CTGCACAGAA	CCCTGGGATG	GAACCACGAA	TGAAAGCTGC	TGCCCTGTGA	AGTGTCTCTT	TGAGAATGTG
	GTCCCCATGA	GCTACATGGT	ATATTTCAT	TTCTTGGGT	GTGTTCTGCC	CCCACTGCTT	ATAATGCTGG
	TGATCTACAT	TAAGATCTTC	CTGGTGGCT	GCAGGCAGCT	TCAGCGCACT	GAGCTGATGG	ACCACTCGAG
40	GACCACCTC	CAGCGGGAGA	TCCATGCAGC	CAAGTCACTG	GCCATGATTG	TGGGGATT	TGCCCTGTGC
	TGGTTACCTG	TGCA'PGCTGT	TAACTGTGTC	ACTCTTTCC	AGCCAGCTCA	GGGAAAAAT	AAGCCAAGT
	GGGCAATGAA	TATC'GCCATT	CTTCTGTCAC	ATGCCAATT	AGTTGTCAAT	CCCATTGTCT	ATGCTTACCG
	GAACCGAGAC	TTCCGCTACA	CTTTTCACAA	AATTATCTCC	AGGTATCTTC	TCTGCCAAGC	AGATGTCAAG
	AGTGGGAATG	GTCA'GGCTGG	GGTACAGCCT	GCTCTCGGTG	TGGGCCTATG	ATCTAGGCTC	TCGCCTCTTC
45	CAGGAGAAGA	TACA AATCCA	CAAGAAACAA	AGAGGACACG	GCTGGTTTC	ATTGTGAAAG	ATAGCTACAC
	CTCACAAGGA	AATC GACTGC	CTCTCTTGAG	CACTCCCTG	GAGCTACCAC	GTATCTAGCT	AATATGTATG
	TGTCAGTAGT	AGGC TCCAAG	GATTGACAAA	TATATTATG	ATCTATTTCAG	CTGCTTTAC	TGTGTGGATT
	ATGCCAACAG	CTTGAATGGA	TTCTAACAGA	CTCTTTGTT	TTTAAAAGTC	TGCCTTGT	ATGGTGGAAA
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	CGCCCCGGGGC	CCAGCTGGCC	CGGCCATGCT	GCTGGAGACA	CAGGACCGCG	TGTACGTGGC	GCTGGAGCTG
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55	CTTTGCCATC	ACCA'PGAGCC	TGGGCTTCTG	CACTGACTTC	TACGGCTGCC	TCTTCCTCGC	CTGCTTCGTG
	CTGGTGCTCA	CGCA'GAGCTC	CATCTTCAGC	CTTCTGGCCG	TGGCAGTCGA	CAGATAACCTG	GCCATCTGTG
	TCCCGCTCAG	GTATAAAAGT	TTGGTCACGG	GGACCCGAGC	AAGAGGGGTC	ATTGCTGTCC	TCTGGGTCT
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	GAACCTGGG	ATGGAACCAC	GAATGAAAGC	TGCTGCCTTG	TGAAGTGTCT	CTTGAGAAT	GTGGTCCCCA
	TGAGCTACAT	GGTATATTTC	AATTCTTTG	GGTGTGTTCT	GCCCCCACTG	CTTATAATGC	TGGTGATCTA

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	TGGCTGCGGC	CGACGTGGCC	GTGGGGCTCT	TCGCCATCCC	CTTGCATC	ACCATCAGCC	TGGGCTTCTG
	CACTGACTTC	TACGGCTGCC	TCTTCCTCGC	CTGCTTCGTG	CTGGTGCTCA	CGCAGAGCTC	CATCTTCAGC
	CTTCTGGCCG	TGGCAGTCGA	CAGATAACCTG	GCCATCTGTG	TCCCCTTGGC	GTATAAAAGT	TTGGTCACGG
5	GGACCCGAGC	AAGAGGGGTC	ATTGCTGTCC	TCTGGGTCT	TGCCTTTGGC	ATCGGATTGA	CTCCATTCTC
	GGGGTGAAC	AGTA AAGACA	GTGCCACCAA	CAACTGCACA	GAACCCCTGGG	ATGGAACCAC	GAATGAAAGC
	TGCTGCCITG	TGAAGTGTCT	CTTGAGAAT	GTGGTCCCCA	TGAGCTACAT	GGTATATTTG	AATTCTTTG
	GGTGTGTTCT	GCCCCCACTG	CTTATAATGC	TGGTGTATCTA	CATTAAGATC	TTCCTGGTGG	CCTGCAGGCA
	GCTTCAGCGC	ACTGAGCTGA	TGGACCACCTC	GAGGACCACC	CTCCAGCGGG	AGATCCATGC	AGCCAAGTCA
10	CTGGCCATGA	TTGIGGGGAT	TTTGCCCTG	TGCTGGTTAC	CTGTGCATGC	TGTTAACTGT	GTCACTCTT
	TCCAGCCAGC	TCAGGGTAAA	AATAAGCCCA	AGTGGGCAAT	GAATATGCC	ATTCTCTGT	CACATGCCAA
	TTCAGTTGTC	AATCCCATTG	TCTATGCTTA	CCGGAACCGA	GACTTCCGCT	ACACTTTCA	CAAATTATC
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15	ACGGCTGGTT	TTCA TTGTGA	AAGATAGCTA	CACCTCACAA	GGAAATGGAC	TGCCCTCTTT	GAGCACTTCC
	CTGGAGCTAC	CACC TATCTA	GCTAATATGT	ATGTGTCAGT	AGTAGCACCA	AGGATTGACA	AATATATTAA
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	TATAGTG (FRAG. NO ____)	(SEQ. ID NO: 2424)					
	5'-GCGCGTCCTG-3'	(FRAG. NO: 1671)	(SEQ. ID NO:1686)				
	5'-GCT GGG CCC CGG 3'	(FRAG. NO: 1672)	(SEQ. ID NO:1687)				
	5'-CGG GTC GGG GCC CCC C-3'	(FRAG. NO: 1673)	(SEQ. ID NO:1688)				
25	5'- CGC GCC CGC G-3'	(FRAG. NO: 1674)	(SEQ. ID NO:1689)				
	5'-GGC GCC GTG CCG CGT CTT GGT GGC GGC GG-3'	(FRAG 972)	(SEQ. ID NO: 982)				
	5'-GTT CGC GCC CGC 3CG GGG CCC CTC CGG TCC-3'	(FRAG 973)	(SEQ. ID NO: 983)				
	5'-GTT CGC GCC CGC 3CG GGG CCC CTC CGG TCC-3'	(FRAG 974)	(SEQ. ID NO: 984)				
	5'-CGG GTC GGG GCC CCC CGC GGC C-3'	(FRAG 975)	(SEQ. ID NO: 985)				
30	5'-GCC TCG GGG CTG GGG CGC TGG TGG CCG GG-3'	(FRAG 976)	(SEQ. ID NO: 986)				
	5'-CCG CGC CTC CGC CTG CCG CTT CTG-3'	(FRAG 977)	(SEQ. ID NO: 987)				
	5'-GCT GGG CCC CGG GCG CCC CCT-3'	(FRAG 978)	(SEQ. ID NO: 988)				
	5'-CCC CTC TTG CTC GGG TCC CCG TG-3'	(FRAG 979)	(SEQ. ID NO: 989)				
	5'-ACAGCGCGTCTGTGTCTCCAGCAGCATGGCGGGCCAGCTGGGCC-3'	(FRAG 980)	(SEQ. ID NO: 990)				
35	5'-BCBGC CGTCTGTGTCTCCBGBGBTGCCGGGCCBGTGGGCC-3'	(FRAG 981)	(SEQ. ID NO: 991)				

Human Adenosine A₃ Receptor Nucleic Acid and Antisense Oligonucleotide Fragments

	5'-ACA GAG CAG TGC TGT TGT TGG GCA TCT TGC CTT CCC AGG G BCB GBG CB TGC TGT TGT TGG GCB TCT						
	TGC CTT CCC BGG GCC CTT TTC TGG TGG GGT GCT GTT GGT GGG CTT TCT TCT GTT CCC BCB GBG CBG						
40	TGC TGT TGT TGG GCB TCT TGC CTT CCC BGG GCC CTT TTC TGG TGG GGT GCT GTT GGT GGG C TTT CTT						
	CTG TTC CC GAATTCCCAG ATGGCAGAG GTGGCTGGC TGGTGCACCT AAGTGTGTCT CCTGCCTTA						
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	TGTGAGCTGA GAAAGAGAGG TGGAGGCTAA GCAGGTGTGA TGCTTCTCAG AGGTGCTGAG TTTTGCCT						
	TCTGAGCAGG GAATCTTGC TTATCCCTT GACCAAGGAT CTTTGCTGCA AAGGCTGGGT ATCGGCTGTG						

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 45 ATGACTTGCC TACI GCTTAT CTTTACCCAC GCCTCCATCA TGCTCTGCT GGCCATCGCT GTGGACCGAT
 ACTTGCGGGT CAACCTTAC CTCAGGTAGC CTGGGGCGTG GGGTGGGCAG CAATTGAGGC AGCTGGAAA
 TGAGGCTACA AAGCCAGAGC -3' (FRAG. NO.:) (SEQ. ID NO:2437)
 5'-CGAATTCCGGG GGACATCTGT TTGGGAAACT AAGAGCAGCA GCACTTTCAG ATTCACTCCA TATAGAGCTG
 TCCTACAGCA TTCTGGAAAC TTGAGGATGT GCGGGTCATA AACGGGCTGG AAGTGAACCA CCTGTGATGA
 50 GCCCTTCTA AGGAGAAGGG TTTCCAAGAG ATCACCCAC CAGAAAAGGG TAGGAATGAG CAAGTTGGGAA
 ATTTTAGACT GTCACTGCAC ATGGACCTCT GGGAAAGACGT CTGGCGAGAG CTAGGCCAC TGGCCCTACA
 GACGGATCTT GCTGGCTCAC CTGTCCTGT GGAGGTTCCC CTGGGAAGGC AAGATGCCCA ACAACAGCAC
 TGCTGTCAGTCA TTGGCCAATG TTACCTACAT CACCATGGAA ATTTTCATTG GACTCTGCGC CATAGTGGGC
 AACGTGCTGG TCACTGCGT GGTCAAGCTG AACCCCAGCC TGCAAGGAC CACCTCTAT TTCAATTGTC
 55 CTCTAGCCCT GGCGTACATT GCTGTTGGGG TGCTGGTCAT GCCTTGGCC ATTGTTGTCA GCCTGGGCAT
 CACAATCCAC TTCTACAGCT GCCTTTTAT GACTTGCCTA CTGCTTATCT TTACCCACGC CTCCATCATG
 TCCTGCTGG CCATCGCTGT GGACCGATAC TTGCGGGTCA AGCTTACCGT CAGATACAAG AGGGTCACCA
 CTCACAGAAG AATATGGCTG GCCCTGGGC TTTGCTGGCT GGTGTACCTC CTGGTGGGAT TGACCCCCAT
 GTTTGGCTGG AACATGAAAC TGACCTCAGA GTACCACAGA AATGTCACCT TCCTTTCATG CCAATTGTT

	TCCGTATG	GGATGGACTA	CATGGTATAC	TTCAAGCTTC	TCACCTGGAT	TTTCATCCCC	CTGGTTGTCA
	TGTGCCCAT	CTATCTTGAC	ATCTTTACA	TCATTCGGAA	CAAACCTCAGT	CTGAACATTAT	CTAACTCCAA
	AGAGACAGGT	GCA'TTTATG	GACGGGAGTT	CAAGACGGCT	AAGTCCTGT	TTCTGGTTCT	TTTCTTGT
5	GCTCTGTAT	GGCTGCCTT	ATCTCTCATC	AACTGCATCA	TCTACTTTAA	TGGTGAGGTA	CCACAGCTTG
	TGCTGTACAT	GGGCATCCCTG	CTGTCCCAGT	CCAACCTCCAT	GATGAACCCCT	ATCGTCTATG	CCTATAAAAT
	AAAGAACGTT	AAGGAAACCT	ACCTTTGAT	CCTCAAAGCC	TGTGTGGTCT	GCCATCCCTC	TGATTCTTG
	GACACAAGCA	TTGAGAAGAA	TTCTGAGTAG	TTATCCATCA	GAGATGACTC	TGTCTCATTG	ACCTTCAGAT
10	TCCCCATCAA	CAAAACACTG	AGGGCCTGTA	TGCCCTGGCC	AAGGGATT	TACATCCTG	ATTACTTCCA
	CTGAGGTGGG	AGC ATCTCCA	GTGCTCCCCA	ATTATATCTC	CCCCACTCCA	CTACTCTT	CCTCCACTTC
	ATTTTCCTT	TGTCCTTCT	CTCTAATTCA	GTGTTTGGA	GGCCTGACTT	GGGGACAACG	TATTATTGAT
	ATTATTGTCT	GTTC'CCTTC	TTCCCAATAG	AAGAATAAGT	CATGGAGCCT	GAAGGGTGCC	TAGTTGACTT
	ACTGACAAAAA	GGC'CTAGTT	GGGCTGAACA	TGTGTGTGGT	GGTGAECTAT	TTCCATGCCA	TTGTGGAATT
	GAGCAGAGAA	CCTC CTCTCG	GAGGATGCC	AGGAGATGTT	GGGAACAGAA	GAAATAAACT	GAGTTAAGG
	GGGACTTAAA	CTGCTGAATT C	-3' (FRAG. NO.:) (SEQ. ID NO:2427)				
15	5'-TTCCCAG	ATGGGCAGAG	GTGGCTGGC	TGGTGAACCT	AAGTGTGTCT	CCTGCCCTTA	TTCTCTCTAG
	TGGGTTATT	TTTCATGTGG	TATCTTGCC	ACAGCATGCT	GTGTTTGGAC	ACAAACCCCT	TTCCCTGGTT
	TCTCTGACCC	AGCTGAGATG	GAUTGATTCC	AAAAGAACTC	ACCTATGTAC	TGGGGTAGGG	GAGGGAGGGT
	TTTTTGCAGT	ATTAACTAA	GGTCAAAAGA	GTGCTATATA	GTGAGAAAGG	CTTCTTTTTT	TTTTTTTTT
20	TTTTTGGCA	GAGT GCTGCC	TCCTAGAAAT	TTCTCTTGGT	AACTCCCTTC	TCTGAAGCAC	AGATAAAGAA
	AACAATTACA	GTACAAACAT	TTATGAGGG	CACATTGGAG	GCCGATGAAG	CTTTCAGT	TCCAGCAGTG
	CAGGGATGTG	GGCA GAACCTG	ACATTGGAA	ATACTAGAAAT	GATGAAATT	CAGTGGAGA	GGACTGCCCT
	TTTTAATGTC	TGGGGAGTCT	GCTCAGGGAG	AAATGACAAG	TCTGGCGGGG	ACAAGTATGG	GATTGGTAA
	GACTTGGATC	AACTGGGAT	ACAGGGTGGG	GGTCGGGAGT	GGAATCAATG	AATGATGCCA	GAGCAGATCA
25	ACTAACAAAGA	GGACCCCTGAT	GAGCCCAGG	CAGAGCGTC	TCCCTTATGC	CCCACTCTGA	AGTGTGTTGTT
	AGTAAACACC	AGAAACGCCAT	TGTTGTTACT	GCTGAATT	ATTTGGGCT	GTACATATT	AGATGCTTAA
	GGTAAAAATG	ATAAGCCCT	CAAGCCACTG	TGTTGGTTT	GGTCCAAGTG	TTCCCTCTT	CTGCCTCTT
	AACACGCCG	GTAAAATAA	TCCCTTTGGA	TGGTGTGAG	AAGCACCTGA	ACCAAGTGGG	TCCCCAAATA
	ACAATGGCGT	GCAAGTGTCT	GGTCCCAGA	AGTTGGTGC	TAGGTAAGCA	GCTTCAGGG	GAGGGGGCTG
30	ATTCCCAGAC	AGTCGCCCTG	TCCTGCCGGG	ATGGGGCTGA	GGCTTGGGGA	ATGTTGGCAG	GAGGATATGC
	CATTGATT	TGTTGCACAC	GTTCTTTC	CTTCTTCTG	TATGTCGGT	CATTCTGCTA	TTCTGTCGTT
	CCTCACATAG	GTTGGACATT	GGCCGGCTGC	CAGCATAAGT	GCCAGTGTGA	TTTGCTAGG	TGTGAGCTGA
	GAAAGAGAGG	TGGAGGCTAA	GCAGGGTGTGA	TGCTTCTCAG	AGGTGCTGAG	TTTTGCCCT	TCTGAGCAGG
	GAATCTTGC	TTATCCCTT	GACCAAGGAT	CTTGTCTGCA	AAGGCTGGGT	ATCGGCTGTG	CTCAGCAAAG
35	CGTCAACTCG	TGCAAGAACT	TAGCAGGAAT	AGTTCTGGCT	AAGGTTAGGA	GGCTGCCACC	AAAGTCTT
	TTTTGTTCT	CTGCTTCTCC	CGTTGCC	CTTATCATGA	GATCTTTTG	CTAACGCTGG	AGAAAGATTG
	CATAGTCAGT	GCTTCCAGCT	CTGCTCC	CTGATCCTGC	ACTGCTCT	GGTCCCTGAA	TGAATGAACT
	CTGATACCCA	ATCTGTCTC	GAGCTTCTC	TATGCCACTC	ATGGCTCTC	TTCTGCTCTT	TCCATCTTT
	TGCTGAGAGT	TCTGAGCTCT	GTACTTCTC	TTGGCCCATC	TCACCTCTG	AAACACCCCT	GAAGAGGGTT
40	GCTTATCTG	ATGGAACCTA	AAAAGCCAA	AAAGTCAGG	CAGAGGCC	GAGGACATCT	GTGAGGAA
	CTAACAGCAG	CAGCACTTC	AGATTCACTG	CATATAGAGC	TGTCTACAG	CATTCTGGAA	ACTTGAGGAT
	GTGCGGTGCA	TAAGGGGCT	GGAAAGTGA	CACCTGTGAT	GAGCCCTT	TAAGGAGAAG	GGTTTCCAAG
	AGATCACCCC	ACCAAGAAAAG	GGTAGGAATG	AGCAAGTTGG	GAATT	CTGTCACTGC	ACATGGACCT
	CTGGGAAGAC	GTC'GGCGAG	GCTAGGCC	ACTGCCCTA	CAGACGGATC	TTGCTGGCTC	ACCTGTCCCT
45	GTGGAGGTTC	CCTC GGAAG	GCAAGATGCC	CAACAAACAGC	ACTGCTCTG	CATTGGCCAA	TGTTACCTAC
	TCACCATGG	AAATTTCAT	TGGACTCTGC	GCCATAGTGG	GCAACGTG	GGTCATCTGC	GTGGTCAAGC
	TGAACCCAG	CCTGCAGACC	ACCACCTCT	ATTCTATTG	CTCTCTAGCC	TGGCTGACA	TTGCTGTTGG
	GGTGCTGGTC	ATGCCTTGG	CCATTGTTG	CAGCCTGGGC	TCACAATCC	ACTTCTACAG	CTGCCCTTTT
	ATGACTTGC	TACTGCTT	CTTACCCAC	CCTCCATCA	TGTCTTGT	GGCCATCGCT	GTGGACCGAT
	ACTTGGGGT	CAAGCTTAC	GTCAGGTAGC	CTGGCGCGT	GGGTGGGCAG	CAATTGAGGC	AGCTGGGAAA
50	TGAGGCTACA	AGCCAGAGC-3'	(FRAG. NO.:) (SEQ. ID NO:2426)				
	5'-GGCAATTG	TTAGTTATCC	GCGGCCACCA	AGACGCGGCA	CGGCGCTGG	ACCGGAGGGG	CCCCGCGCGG
	CGCGAACTT	TGGGCTCGGG	CGAGTGGGT	GTGCTCCGCC	CAGCCCGAGA	CGGGCGGGCG	CGCGGGCCAA
	TGGGTGCCGC	CTCTTGGCCG	CGGGGGGCC	CGACCCGTGG	GTCCCGGCCA	CCAGCGCCCC	AGCCCCGAGG
55	CTCAGAACG	GCACGCGGAG	GCGCGGTCCG	GGCGCTATGG	CCATGCCCG	CGGGCTCAC	CGGGCTGCC
	CTCGCCCGC	GCGCTTCG	TAGGGGCGC	CCGGGGCCCA	GCTGGCCCG	CCATGCTGCT	GGAGACACAG
	GACGCGCTGT	ACGTGGCGCT	GGAGCTGGTC	ATCGCCGCGC	TTTCGGTGGC	GGGCAACGTG	CTGGTGTGCG
	CCGCGGTGG	CACCGCGAAC	ACTCTGCAGA	CGCCCACCA	CTACTTCTG	GTGTCCTGG	CTGCGGCCGA
	CGTGGCCGTG	GGGCTCTTCG	CCATCCCCT	TGCCATCACC	ATCAGCCTGG	GCTTCTGCAC	TGACTTCTAC
	GGCTGCCCT	TCCTGCCCTG	CTTCGTGCTG	GTGCTCACGC	AGAGCTCCAT	CTTCAGCCTT	CTGGCCGTG

CAGTCGACAG ATACCTGGCC ATCTGTGTCC CGCTCAGGTA TAAAAGTTG GTCACGGGGA CCCGAGCAAG
 AGGGTCATT GCTCTCCTCT GGGTCCTTGC CTTTGGCATC GGATTGACTC CATTCTGGG GTGGAACAGT
 AAAGACAGTG CCAC'CAACAA CTGCACAGAA CCCTGGGATG GAACCACGAA TGAAAGCTGC TGCCCTGTGA
 5 AGTGTCTCTT TGAGAATGTG GTCCCCATGA GCTACATGGT ATATTTCATA TTCTTGGGT GTGTTCTGCC
 CCCACTGCTT ATAAIGCTGG TGATCTACAT TAAGATCTTC CTGGTGGCCT GCAGGCAGCT TCAGCGCACT
 GAGCTGATGG ACCA'CTCGAG GACCACCCCTC CAGCAGGAGA TCCATGCAGC CAAGTCACTG GCCATGATTG
 TGGGGATTT TGCCCTGTGC TGGTTACCTG TGCACTGCTGT TAACTGTGTC ACTCTTTCC AGCCAGCTCA
 GGGTAAAAAT AAGCCAAGT GGGCAATGAA TATGGCCATT CTTCTGTACAT ATGCCAATTC AGTTGTCAAT
 CCCATTGTCT ATGCCTTACCG GAACCGAGAC TTCCGCTACA CTTTCACAA AATTATCTCC AGGTATCTTC
 10 TCTGCCAAGC AGAIGTCAAG AGTGGGAATG GTCAAGGCTGG GGTACAGCCT GCTCTCGGTG TGGGCCTATG
 ATCTAGGCTC TCGCCTCTTC CAGGAGAAGA TACAAATCCA CAAGAAACAA AGAGGACACG GCTGGTTTC
 ATTGTGAAAG ATACCTACAC CTCACAAGGA AATGGACTGC CTCTCTTGAG CACTCCCTG GAGCTACAC
 GTATCTAGCT AATATGTATG TGTCACTAGT AGGCTCCAAG GATTGACAAA TATATTATG ATCTATTCAAG
 CTGCTTTAC TGTGTTGGATT ATGCCAACAG CTTGAATGGA TTCTAACAGA CTCTTTGTT TTTAAAAGTC
 15 TGCCTGTTT ATGGTTGGAAA ATTACTGAAA CTATTTACT GTGAAACAGT GTGAACATT ATAATGCAA
 TACTTTTAA CTTAGAGGCA ATGGAAAAAT AAAAGTTGAC TGTACTAAAATG-3'(FRAG. NO:) (SEQ. ID NO: 2425)

5'-GBG CB TGC-3' (FRAG. NO:1676) (SEQ. ID NO:1691)

5'-TTG TTG GGC-3' (FRAG. NO:1677) (SEQ. ID NO:1692)

5'-TGC CTT CCC BGG 3'-3' (FRAG. NO:1678) (SEQ. ID NO:1693)

20 5'-GTT GTT GGG CAT CTT GCC-3' (FRAG. NO:1679) (SEQ. ID NO:3)

5'-GTG GGC CTA GCT CTC GCC-3' (FRAG. NO:1680) (SEQ. ID NO:5)

5'-ACA GAG CA TGC TGT TGT TGG GCA TCT TGC CTT CCC AGG G-3' (FRAG 982) (SEQ. ID NO: 992)

5'-BCB GBG CB TGC TGT TGT TGG GCB TCT TGC CTT CCC BGG G-3' (FRAG 983) (SEQ. ID NO: 993)

5'-CCC TTT TCT GGT GGG GTG-3' (FRAG 984) (SEQ. ID NO: 994)

25 5'-GTG CTG TTG TTG GGC-3' (FRAG 985) (SEQ. ID NO: 995)

5'-TTT CTT CTG TTC CC-3' (FRAG 986) (SEQ. ID NO: 996)

5'-CCC TTT TCT GGT GGG GTG-3' (FRAG 987) (SEQ. ID NO: 997)

5'-GTG CTG TTG TTG GGC-3' (FRAG 988) (SEQ. ID NO: 998)

5'-TTT CTT CTG TTC CC-3' (FRAG 989) (SEQ. ID NO: 999)

30 Human IgE Receptor β Nucleic Acid and Antisense Oligonucleotide Fragments

5'-TTT CCC CTG GGT CTT CC CTC CTG CTC TTT TTT C ATT TGC TCT CCT ATT ACT TTC TGT GTC CAT TTT
 TTC ATT AAC CGA GCT GT BTT TGC TCT CCT BTT BCT TTC TGT GTC CBT TTT TTC BTT BBC CGB GCT GT-3'
 (FRAG. NO:1681) (SEQ. ID NO:1694)

5'-CCC CTG GG-3' (FRAG. NO:1682) (SEQ. ID NO:1695)

35 5'-GCTCTCCTCTBTT-3' (FRAG. NO:1683) (SEQ. ID NO:1696)

5'-CBTTBCCGBGCTG-3' (FRAG. NO:1684) (SEQ. ID NO:1697)

5'-TTT CCC CTG GGT CTT CC-3' (FRAG 990) (SEQ. ID NO: 1000)

5'-CTC CTG CTC TTT TTT C-3' (FRAG 991) (SEQ. ID NO: 1001)

ATTTGCTCTCCTATTACTTCTGTCCTCCATTTCATTAACCGAGCTGT (FRAG 992) (SEQ. ID NO: 1002)

40 BTTTGCTCTCCTCTBTTBCTTCTGTCCTCCBTTBCCGBGCTGT (FRAG 993) (SEQ. ID NO: 1003)

Human Fc-ε Receptor CD23 Antigen (IgE Receptor)

Nucleic Acid and Antisense Oligonucleotide Fragments

5'-GCC TGT GTC TGT CCT CCT GCT TCG TTC CTC CTG CTT GGT GCC CTT GCC G GTC CTG CTC CTC
 CGG GCT GTG G GTC GTG GCC CTG GCT CCG GCT GGT GGG CTC CCC TGG CCT TCG CTG GCT GGC GGC GTG
 45 C GGG TCT TGC TCT GGG CCT GGC TGT GGC CGT GGT TGG GGG TCT TC GCT GCC TCC GTT TGG GTG GC TCT
 CTG AAT ATT GAC C'CT CCT CCA TGG CGG TCC TGC TTG GAT TCT CCC GA TCT CTG BBT BTT GBC CTT CCT
 CCB TGG CGG TCC TC C TTG GBT TCT CCC GB-3'(FRAG 1685)(SEQ.ID NO:1698)

5'-GT CCT CCT-3' (FRAG 1686) (SEQ. ID NO: 1699)

5'-TGT GTC TGT CCT CC-3' (FRAG 1687) (SEQ. ID NO: 1700)

50 5'-GTG GCC CTG GC-3' (FRAG 1688) (SEQ. ID NO: 1701)

5'-CGT GGT TGG GG-3' (FRAG 1689) (SEQ. ID NO: 1702)

5'-TCT CTG BBT BTT GBC C-3' (FRAG1690) (SEQ. ID NO:1703)

5'-GCC TGT GTC TGT CCT CCT-3' (FRAG 994) (SEQ. ID NO: 1004)

5'-GCT TCG TTC CTC CGT TTC-3' (FRAG 995) (SEQ. ID NO:1005)

55 5'-CTG CTT GGT GCC CTT GCC G-3' (FRAG 996) (SEQ. ID NO: 1006)

5'-GTC CTG CTC CTC CGG GCT GTG G-3' (FRAG 997) (SEQ. ID NO: 1007)

5'-GTC GTG GCC CTG GCT CCG GCT GGT GGG CTC CCC TGG-3' (FRAG 998) (SEQ. ID NO: 1008)

5'-CCT TCG CTG GCT GGC GGC GTG C-3' (FRAG 999) (SEQ. ID NO: 1009)

5'-GGG TCT TGC TCT GGG CCT GGC TGT-3' (FRAG 1000) (SEQ. ID NO: 1010)
 5'-GGC CGT GGT TGG GGG TCT TC-3' (FRAG 1001) (SEQ. ID NO: 1011)
 5'-GCT GCC TCC GTT TGG GTG GC (FRAG 1002) (SEQ. ID NO: 1012)
 5'-TCT CTG AAT ATT GAC CTT CCT CCA TGG CGG TCC TGC TTG GAT TCT CCC GA (FRAG 1003) (SEQ.ID NO:1013)
 5'-TCT CTG BBT BTT GBC CTT CCT CCB TGG CGG TCC TGC TTG GBT TCT CCC GB (FRAG 1004) (SEQ.ID NO:1014)

Human IgE Receptor α Subunit Nucleic Acid and Antisense Oligonucleotide Fragments

5'- GCC TTT CCT GGT TCT CTT GTT TTT GGG GTT TGG CTT ACA GTA GAG TAG GGG ATT CCA TGG CAG
 10 GAG CCA TCT TCT TCA TGG ACT CC TTC AAG GAG ACC TTA GGT TTC TGA GGG ACT GCT AAC ACG CCA TCT
 GGA GC BCB GTB GEG TBG GGG BTT CCB TGG CBG GBG CCB TCT TCB TGG BCT CC TTC BBG GBG BCC
 TTG GGT TTC TGB GCG BCT GCT BBC BCG CCB TCT GGB GC GTT GTT TTT GGG GTT TGG CTT GCC TTT CCT
 GGT TCT CTT BCB GTB GBG TBG GGG BTT CCB TGG CBG GBG CCB TCT TCB TGG BCT CC TTC BBG GBG
 BCC TTG GGT TTC TGB GGG BCT GCT BBC BCG CCB TCT GGB GC-3' (FRAG. NO: 1691) (SEQ. ID NO:1704)
 5'- TGG BCT CC -3' (FRAG. NO: 1692) (SEQ. ID NO:1705)
 5'-CCB TCT GGB-3' (FRAG. NO: 1693) (SEQ. ID NO:1706)
 15 5'-CT GCT BBC BCG-3' (FRAG. NO: 1694) (SEQ. ID NO:1707)
 5'-GTT TTT GGG GTT TG-3' (FRAG. NO: 1695) (SEQ. ID NO:1708)
 5'-GCC TTT CCT GGT TCT CTT GTT TTT GGG GTT TGG CTT-3' (FRAG. NO:1005) (SEQ. ID NO:1015)
 5'-ACAGTAGAGTAGGGATTCCATGGCAGGAGCCATCTCTCATGGACTCC-3'(FRAG.NO:1006)(SEQ.ID NO:1016)
 20 5'-TTC AAG GAG ACC TTA GGT TTC TGA GGG ACT GCT AAC ACG CCA TCT GGA GC-3' (FRAG. NO:1007) (SEQ.
 ID NO:1017)
 5'-BCB GTB GBG TBG GGG BTT CCB TGG CBG GBG CCB TCT TCB TGG BCT CC TTC BBG GBG BCC TTG GGT
 TTC TGB GGG-3' (FRAG. NO:1008) (SEQ. ID NO:1018)
 5'-BCT GCT BBC BCG CCB TCT GGB GC-3' (FRAG. NO:1009) (SEQ. ID NO:1019)
 25 5'-GTT GTT TTT GGG GTT TGG CTT-3' (FRAG. NO:1010) (SEQ. ID NO:1020)
 5'-GCC TTT CCT GGT TCT CTT-3' (FRAG. NO:1011) (SEQ. ID NO:1021)
 5'-BCBGTBGBTBGGGGBTTCCBTGGCBGGBBCBTCTCTCBTGGBCCTCC-3'(FRAG.NO:1012) (SEQ.ID NO:1022)
 5'-TTC BBG GBG BCC TTG GGT TTC TGB GGG BCT GCT BBC BCG CCB TCT GGB GC-3' (FRAG.NO:1013) (SEQ.ID
 NO:1023)

Human IgE Receptor (Fc Epsilon R) Nucleic Acid and Antisense Oligonucleotide Fragments

30 5'-GCC TGT GTC TGT CCT CCT GCT TCG TTC CTC TCG TTC CTG CTT GGT GCC CTT GCC G GTC CTG CTC CTC
 CGG GCT GTG G GTC CTC GCC CTG GCT CCG GCT GGT GGG CTC CCC TGG CCT TCG CTG GCT GGC GGC GTG C
 CCC BGB BCG BGB CCC GGB CCG BCB GGC CGT GGT TGG GGG TCT TC GCT GCC TCC GTT TGG GTG GC GAT
 CTC TGA ATA TTGA CCT TCC ATG GCG GTC CTG CTT GGA GBT CTC TGB BTB TTGB CCT TCC BTG GCG GTC
 CTG CTT GGB-3' (FRAG: 1696) (SEQ. ID NO:1709)
 35 5'-TCG TTC CTC TCG-3' (FRAG: 1697) (SEQ. ID NO:3001)
 5'-BGB BCG BGB C-3' (FRAG: 1698) (SEQ. ID NO:1711)
 5'-TGB BTB TTGB-3' (FRAG: 1699) (SEQ. ID NO:1712)
 5'-GCC TGT GTC TGT CCT CCT-3' (FRAG. NO:1014) (SEQ. ID NO:1024)
 40 5'-GCT TCG TTC CTC CGT TTC-3' (FRAG. NO:1015)(SEQ. ID NO:1025)
 5'-CTG CTT GGT GCC CTT GCC G-3' (FRAG. NO:1016)(SEQ. ID NO:1026)
 5'-GTC CTC CTC CTC CGG GCT GTG G-3' (FRAG. NO:1017)(SEQ. ID NO:1027)
 5'-GTC CTC GCC CTG GCT CCG GCT GGT GGG CTC CCC TGG-3' (FRAG. NO:1018) (SEQ. ID NO:1028)
 45 5'-CCT TCG CTG GCT GGC GGC GTG C-3' (FRAG. NO:1019) (SEQ. ID NO:1029)
 5'-CCC BGB BCG BGB CCC GGB CCG BCB-3' (FRAG. NO:1020) (SEQ. ID NO:1030)
 5'-GGC CGT GGT TGG GGG TCT TC-3' (FRAG. NO:1021) (SEQ. ID NO:1031)
 5'-GCT GCC TCC GTT TGG GTG GC-3' (FRAG. NO:1022) (SEQ. ID NO:1032)
 5'-GBT CTC TGB BTB TGT CCT TCC BTG GCG GTC CTG CTT GGB-3' (FRAG. NO:1023) (SEQ. ID NO:1033)

Human High Affinity IgE Receptor Oligonucleotide Fragments

50 5'-AACAGAAAA CGGTTGGTAG CTCTGGTGAA TCCCCAAAAGA ATGGGGCAGT TGCTAGCCAT GCTCCTGAAT
 ATGTATAAAC AGTACATCAT ATGACTAAGA GTTGTACTTA GGGGTTAGAT TTTATGTGTT TGAACCCCAA
 ATTAGTTATT TAATAGTTGG CACCCCCAAA CAAGTTACTT AACCTCACTA AGGTTCAGTT TTCCCTGTTA
 TAAAATGTAG ATACTGATAG TATGTACTTT ATAGGATTAT TGTGAAAAAT AAATGAAATA TCAGATTTAT
 TTAGGATAAC ACCGGCATA TGTGGGTAT TCAGAATTAG TTGCTGCTGT TTATCTGC TCTCCCTTGC
 ATCCCACCTT TCTAAGTTGT AAACTAAATA GTTGTACACA GATTGACAGA TTAAGAAAGG CTTGTGATTG
 55 55 TGCTAGACCT ATGCCATATGC CTCTGTCTCA CCAGATTCCA GGTGTATATG TGGAGGTGGG ATAGGGAGTG
 GAGTAAGTGG GTAATATTA AATTGCCAG TTGGGCACCA TCCTGAATAT TATCTCTAAA GAAAGAAGCA
 AAACCAGGCA CAGCTGATGG GTTAACCCAG TATGATACAG AAAACATTC CTCTGCTTT TTGGTTTAA
 GCCTATATT GAAGCCTTAG ATCTCTCCAG CACAGTAAGC ACCAGGAGTC CATGAAGAAG ATG GATCTTCATG
 TGGAAATGACT GGTITCATTC AATAGACTTA ATTCAAGCAGT CTGTGGGAA GAGCAAGGTA TGATAGAATG
 60 60 GTTCCTCAAG TGCTCAGAT GTGAAGTGGG TTTAAATATA CTGTCCCTGT CTTCTCAGA GTTTTGGTAA

AGATAAAAATA GGACACTCAT TAAAGGCAA TCTTGCAA TGACAAGCCA CTATAGACAT TAATAGAGTT
 TTCATTCCA GTATATCAT TAATATCAGA TCCTGGAAGA AGGTTGAGCC TTGACCTAGA GCAAAAAAAC
 AGAAGAATTAA GTAAAGGAAT CCTGGAGAAA GCCCCTGCTG TGTATTAAA GGAGAAAGGG AGATCATGTT
 5 GGGAAATTAT AATATTTAAA GTAAACAAAAA GCTAGGAAGT AAAATAAAAT AAATTATATG GCCTAGATCC
 CCATAAGTAA TGGITTAACT TCTGCCTCC TGTGTTCTGA GCCAGATTAG GGCACAGTAG AGAAAGAGGA
 GTCTCTGAAA ATGTTTCAA TTTCGCTGGT CAGACAGCGG ATCATCAGTG AATCAGATGA AAATTGTTGG
 ATTTATGCAC TAACPGATCA GCAGGAAATT AAACAAGAAA AGCGTTGGTA GCTCTGGTGA ATCCAAAAG
 AATTGCGAG TTGCTAGCCA TGCTCCTGAA TATGTATAAA CAGTACATCA TATGACTAAG AGTTGACTT
 10 AGGGGTTAGA TTTIATGTGT TTGAACCCC AATTAGTTAT TTAATAGTTG GCACCCAAA ACAAGTTACT
 TAACCTCACT AAGTTTCACT TTTCTGTTT ATAAAATGTA GATAGTGATA GTATGTAATT TATAGGATTA
 TTGTGAAAAA TAAATGAAAT ATCAGATTAA TTTAGGATAA CACCTGGCAT ATGTTGGTA TTCAGTAATT
 AGTTGCTGCT GTTITATTCT GCTCTCCCT GCATCCCT GCATCTAAGT GTAAACTAAA TAGTTGTACA
 CAGATTGACA GATIAAGAAA GGCTTGTGAT TGTGCTAGAC CTATGCCCT CTCTCACCAAG ATTCCAGGTG
 TATATGTGGA GGTGGGATAG GGAGTGGAGT AAGTGGGTAAT ATATAAATT GCCCCAGTGG GCACCATCCT
 15 GAATATTATC TCTAAAGAAA GAAGCAAAAC CAGGCACAGC TGATGGGTT ACCAGATATG ATACAGAAA
 CATTCCCTC TGCTTTTGG TTTTAAGCCT ATATTGAAAG CCTTAGATCT CTCCAGCACA GTAAGCACC
 GGAGTCATG AAGAGATGG CTCCTGCCAT GGAATCCCT ACTCTACTGT GTGAGCCTT ACTGTTCTC
 GGTAAAGTAGA GATICAATTA CCCCTCCAG GGAGGCCAA ATGAATTGG GGAGCAGCTG GGGTAGGAAC
 CTTTACTGTG GGTGGTACT TTTTCTAGGA CATGTGAAA CTATTGGCA TTTCCCAGGG ACTCTGTAGT
 20 GGAGCCAAGC TAGAAAGCAG AGGCAAGTGG GCTGAGCAAC ACCTAAGGAG GAAGCCAGAC TGAAAGCTT
 GTTCTTGCA TTGCTCTGG CATCTTCCAG AGTGCAAATT CCTCTACCAAG TAAATGAGGG TAGAGGAGAG
 AAAGAAAGCTC TTCTTCCCC TGATTCTCAT TCTGAAAAG ACGGTTGGTC CTTAAAATTG CATGGATGTA
 GATCTTATCC CCACACCCAG ATTCTAGTCC TCTGGAGATA AAGAAGACTG CTGGACACTA ATGTATCCTC
 TCTGGACTTT TGCAGCTCCA GATGGCGTGT TAGCAGGTGA GTCTCTGTT CTGTTCCCT TGGTGTATCA
 25 ACATGCTGGA GCAATGCTTT CCTCTCACTA TTTTCTCGT CCCATCACTT CTGCTTCTA ATGAGCATGA
 ATCTGTTCT TGCCAGACT ACTTCCCTC TCCACCTTG CTTGCTTTTC TGATTCTTGC
 CATTCTCTCA AGTCATTCTC TCCTCTGTT TAGTCATAA CCATGCTGT TGACATATA
 TCTCTCTCT AGACACTTTG GCATGATCTC GCTCAATAAT TACATTATA TTATTATTGC
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NO.:)(SEQ. ID NO:250)

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DRAFT - NOT FOR DISTRIBUTION

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 10 TTCATTCA ATAAAAATAA TATAAAACCA TGTAACAGAA TGCTTCTGAG TAAAAAAA AAAA
 10 AAAAAAAA-3' (FRAG. NO.:) (SEQ. ID NO:2502)
 5'-TCTCAATATA ATAATATTCT TTATTCTCG ACAGCTCGGT TAATGAAAAA ATGGACACAG AAAGTAATAG
 GAGAGCAAAT CTTGCTCTCC CACAGGAGCC TTCCAGTGTG CCTGCATTTG AAGTCTTGGA AATATCTCCC
 CAGGAAGTAT CTTCAGGCAG ACTATTGAG TCGGCCTCAT CCCCCACCACT GCATACATGG CTGACAGTTT
 15 TGAAAAAAAGA GCAAGGAGTTC CTGGGGGTAA CACAAATCTC GACTGCTATG ATATGCCCTT GTTTTGGAAC
 AGTTGCTGC TCTC'ACTTG ATATTTCACA CATTGAGGGA GACATTTTT CATCATTAA AGCAGGTTAT
 CCATTCTGGG GAGCCATATT TTTTCTATT TCTGGAATGT TGTCAATTAT ATCTGAAAGG AGAAATGCAA
 CATATCTGGT GAGA'GGAAGC CTGGGAGCAA ACACTGCCAG CAGCATAGCT GGGGAAACGG GAATTACCAT
 CCTGATCATC AAC'C'TGAAGA AGAGCTTGC STATATCCAC ATCCACAGTT GCCAGAAATT TTTTGAGACC
 20 AAGTCTTAA TGGCTTCCTT TTCCACTGAA ATTGAGTGA TGATGCTGTT TCTCACATT CTGGGACTTG
 GTAGTGTGTT GTCA'CTCACAA ATCTGTGAG CTGGGGAAAGA ACTCAAAGGA ACAAAGGTTTC CAGAGGATCG
 TGTATGAA GAAT'AAACAA TATATTCAAGC TACTTACAGT GAGTTGGAAG ACCCAGGGGA AATGTCCT
 CCCATTGATT TATAAGAACAT ACGTGTCCAG AACACTCTGA TTACAGCAGA AGGATCCAGA AGGCCAAGGT
 CTTGTTAAGG GGCTA'CTGGA AAAATTCTA TTCTCTCCAC AGCCTGCTGG TTTT-3' (FRAG.NO.:) (SEQ.ID NO:2503)
 25 5'-AAGCTTTCA AA'GGTGAAT TGGATAACTT CTGGCATGAG AAATGGCTGA ATTGGGACAC AAGTGGGAC
 AATTCCAGAA GAA'GGGCACA TCTCTTCTT TTCTGCAGTT CTTTCTCACC TTCTCAACTC CTACTAAAAT
 GTCTCATTTC CAGC'CTCTGT AAATCCTGCT AGTCTCAGGC AAAATTATGC TCCAGGAGTC TCAAATTTC
 TTATTCATA TTAC TCTTTA TTTAGTAGAC TTCTCAATT TTCTATTTCAT CACAAGTAAA AGCCTGTTGA
 TCTTAATCAG CCA'A'GAAACT TATCTGCTG GCAAATGACT TATGTATAAA GAGAATCATC AATGTCATGA
 30 GGTAAACCCAT TTCA'ACTGCC TATTCAAGAGC ATGAGTAAAG AGGAATATCA CCAAGTCTCA ATATAATAAT
 ATTCTTATT CTTG'GACAGC TCGGTTAATG AAAAATGGA CACAGAAAGT AATAGGAGAG CAAATCTTC
 TCTCCCACAG GAGC'CTTCCA GGTAGGTACA AGGTATTATT TTTTCTTAC CTCAGTCACT TGTGGCAGGG
 GAAGTCATAG TCA'CGGTGCT TAGGAGATGA AACTTATTG ATTTAGGCAT GGATCCATCT AGTTTAATTAA
 ATATATTGGG TATGAGGAAG CTACTGCTG TACTTCCAT GTGGTTCTCT CTCCTGGAG AGGAACATT
 TTACTCAGCT TGCA'AACTGG AAATAGATT TCTCACATTA GAAGCTCATT TTCTGGTAT GAGACAGGAG
 35 AGTTCATACT GTG'ATGTAG ATCTCTGGCT TCTGGGTCTG ACATGTGCTG AGGGACACAT ATCCTTCACA
 CATGCTTTA TAA' TACTTG ATAAAGTAAC CTGCTTCTTG ATTGGTCTTT ATAATCCATA AGCTGTGGGA
 TGCTTCTCTG AAG' TGAAAAT TAGTAATAGA GTCCCCTCTA GCTATTCAAA GCCATTCTT CATTGTATTC
 TGTGCACATG AAG' TGGGGT TTGTTACTGA CAAAATATAT TCAGATACAT TTCTATGTTA AAAGGATTGT
 GAGATGCATA GGTAAATGTG TTTATTCTA GTTTTACTTG TCAACATAGA TGAATGAGAA AGAACTTGAA
 40 AGTAACACTG GAT' AAGAAT AGGAAAATTG GGCATGGATT TTGCTCCATT TTGCCCCATC TAATCACTTG
 GATAGTGTTC AGG' GTTCTT GGTCACTTAC TTGGATGCTC TGAGCTTAG TTTCTTGGTG ATTACAATGA
 AGATTTGAAT TAC'GGATGG CTTGAAAAA ATAAACAAAA CTCCCCTTTC TGTCTGTCGA GAATGTTGCA
 CAGGGAGTTA CAGA'ATGTT TCATGACTGA ATTGCTTTA AATTTCACAG TGTGCTGCA TTTGAAGTCT
 45 TGGAAATATC TCCC' CAGGAA GTATCTCAG GCAGACTATT GAAGTCGCC TCATCCCCAC CACTGCATAC
 ATGGCTGACA GTTITGAAAAA AAGAGCAGGA GTTCTGGGG GTGAGTGAGC CTCTCCAAAC TTTGACTAGA
 GTAAGGGTTG GGTCTAGAAA AGAATATTGA GTTGCATCAA CTGTTTCCC ACTTGGATTC ATGAGAGGTG
 TTAGGTCTT TAAAAAAACAT GGTAGATAAA GAGTTGACAC TAACTGGTC CTTTGGGAA GAGCCAGAAG
 CATTCTCTCA TAAAGACTTT AAATTGCTAG GACCGAGAATG GCCAACAGGA GTGAAGGATT CATAACTTA
 TCTTACTTA GATG TAAAGA ACAATTACTG ATGTTCAACAA TGACTACATA CATAAAAGGCG CATGGAGAAA
 50 AGTATTGGCC TTCC'ATGCA TAGGTAGTGC TTGTATCAAT TCTTATAGTG GCTAGGGTAT CCTGGAAAAT
 CTTACGTGTG GATC'ATTTCT CAGGACAGTC TAGGACACTA ACGCAGTTTC TCATGTTTGG CTTCTTATT
 TAAAAAAATGA TAC'ATCTCG GGAAAATTG TTGATTTC ATGAAATTCA TGTGTTTTC TATAGGTAAAC
 ACAAAATTCTG ACTGCTATGA TATGCTTTC TTTTGGAAACA GTTGTCTGCT CTGACTTGA TATTCACAC
 ATTGAGGGAG ACA' TTTTTC ATCATTTAA GCAGGTTATC CATTCTGGGG AGCCATATTT GTGAGTATAT
 55 ATCTATAATT GTTIC'TGAAA TAACACTGAA CATAGGTTT TCTCTTCTC AGATCTAAC AGTTGTTTAT
 TCCCAGTATT AAGA' TGATAT TTATAATTCT TAATTATAAA TATATGTGAG CATATATAAC ATAGATATGC
 TCATTAACAA CAAC'AAAAGA TTCTTTTAC AATTAACGGT GGGTTAAACA TTTAGCCCAC AGTTTATCC
 CATGAGAAAC CTGA'ATCTAA TACAAGTTAA ATGACTTGCC TAAGGGCCAC TTGACTAATA GTAATTGAAC
 CTAAACTTC AGA' TCCAAC TCCAGGAACA TACTTCTAGC ACTATTCACT AATAAAAGTTA TATGATAAAT
 60 ACATACAAC T TATCTGTCA ACTAAAATA ACAACAGAGG CTGGGATGG TGGCTCACAC CCGTAATCCC
 AGCACTTGG GAGC' CTGAGG CAGGTGGATC ACCTGAGGTC AGGAGTTGA GACCAGCCTG ACCAACATGG
 TGAAACCTCA TCTC'ACTAA ATATAAAAAA TTAGCTGAGT GTGATAGTGC ATACCTGAA

	TAAGAGGCTG	AGG CAGGAGG	CTT GTTGAA	CCT GGAAGGC	AGAGGTTGCA	GTGAGCTGAG	ATT GTGCCAT
	TGCACTCCAG	CCT CGGCAAT	AAAGTCCGAAC	TCT GTCTCAA	AATAATAATA	ATAATAATAG	AAAATAAAGT
5	TGTCTTCATG	AAAAT ATGAGG	AAAGAGATTG	CTGGGGTGAG	AAACATTAAG	ATCAATGGC	ATATGGTAC
	CTTCTATGCC	CTAGAAACTC	TTT TANGGT	TTT CTCCCTG	GTATCTCTT	TACNCATCGT	TCTATCTGGA
	AAAATAGGTG	GATGAGTGAG	ATAATAACGG	TATATACTTT	TTAAAGGTCT	AATTGACATA	TATAAATTGC
	AAGTATTTC	GATGTCATT	TGCTAACCTT	GACACACATA	GACACACATG	AAAACATCAC	CACATTAATA
	CAATGTATGT	ATCCATCAT	CCAAAAGCTT	CCCTGTGTAT	CTTGTAACT	CTTCTTCCT	CCCTCCACTC
10	CTTGTCCCTC	CGTICCCAAG	AAAACATTGA	TCTGCTTCCT	GTGAATATAA	ATTAACCTAC	ATTTTTAGA
	GCTTTATATA	AGTATGTTCT	CTTTACTGTT	TGTCCTCCCT	CGCTGCACAG	TTATTTGAG	ATTCTTCAG
	TTTTTTCTT	ATATCGATAC	TTCATTACA	AGAATATATT	TTAATTCTAG	ACTATGTCAC	ATTGACTTTG
	TCGTCTGCTA	AATCCTTAGT	GCTCAGATGA	CTTGTTCAGG	ACTCTCCTG	AACCTGTACC	TCTGTTANAT
15	TGAAACTTGT	CTCTACTGTC	TTTTTATTTC	AAACACAGCT	TATTAGGTGT	CTCTCAACCC	ATCAAACNCA
	CAATCTGAGT	CTT TAGGAGA	TTGCTTGTAA	TTTGTGCTAT	TGACTTATAT	NTATATNAAA	TNTGAAATG
	TTTGGTAAAAA	ATA'CATCAT	GTACANTTTC	ATAATTACGC	TATNTNCACA	TGATATATGT	CAGACTCTGG
20	AAATATGCAT	GCCACAGACA	CGT GTTTCTT	GCCTAAAGGG	GCTGATGGAA	GACNCACATA	CNAATAGACG
	ATTGCAGTAG	AATGAGAGTG	GTGGTCTAAN	CAGTACATGT	CCTGATGTTG	CTCGGACAGT	TACTACNCA
	AGAGTACCCC	CTGCATTGTC	AGGGTTAGCA	TCTCCTGGAA	GCCTCATGTA	AATGAAGAAT	TTCATGCTCC
	ATCCAGGACC	TAATGAATAA	GAATCTGCAT	TTAGCAAGA	CCCTCATATG	ATTCA TATAC	ACTTTTTT
25	TTTTTTTA	GATGGAGTCT	CACTCTTGT	GCC CAGGCTG	GAGTGCATG	GCATGATCTT	GGCTCACTGC
	AACCTCTGCC	TCCC'GGGTTTC	AAAGTATTCT	CCTGCTCTAG	CCTCCCTAGT	AGCTGGGACT	ACAGGTGCAT
	GCCACAGTGG	CTGCGCTAATT	TTTGTATTTC	TAGTAGAGAC	AGGGTTTCAC	CATT TTGGTC	AGGCTGGTCT
	TGAACTCATG	ACCTCCGGTG	ATTCCCCCGC	CTCGGCTTCC	CAAAGTGTG	GGATTACAGA	CATGAGCCAC
	CACACCCGCC	TTA TCGTAT	ACNCATTAA	TTCTGAGAAG	CACTCTATAG	AAAATAAGAA	TAAGAAAATA
30	TTGGGCTCAC	AGG'GACATT	AATAAGTAAC	TTTATCGAGT	ACCCCAATT	TTACCTATGT	TTGGAAGATG
	GGGTTAAAAG	GACACATTGA	AAACAAGAAC	TCATTGTGGC	TTTTTTTCC	TCCTTTTGAA	ACAGTTTCT
	ATTCTGGAA	TGTIGTCAT	TATATCTGAA	AGGAGAAATG	CAACATATCT	GGTGAGTTG	CCGTTCTGT
	CTTTGTCAT	CCTT AAAAG	ATAAGAAGAA	CAGAGTTTA	AGAGTCTAA	GGGAAACACA	TCTTTGTC
35	CTATATTACT	TGTC AATGTG	GATATATGAT	TTTGTTCAA	TCTATTTGT	GTCTTAAGGC	TTTTTGCAAC
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	CGTTCTCTA	AAAATGTGCC	TACACCGCA	TTGTCTTGT	AGGCATATT	ACATGATCAA	ATAAAATAAT
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	TGAGAAAGTA	ATA'ATGCTT	CATTAACAA	TGCGGACATT	TTCAAGGTTT	CCCTTTTAA	CCAAAATTG
40	GAAGCAATGT	GGAATTTACT	GGATGCATCC	AGCCCTGAAA	TGAAGATAGG	TTTATTGAAT	GTGCCAGCAA
	GTGCAGGCC	AGG'CTGAGT	GTCTTCTATT	ATTATCAGGT	GAGAGGAAGC	CTGGGAGCAA	ACACTGCCAG
	CAGCATAGCT	GGGGGAACGG	GAATTACCAT	CCTGATCATC	ACACCTGAAGA	AGAGCTTGGC	CTATATCCAC
45	ATCCACAGTT	GCCAGAAATT	TTTGAGACC	AAAGTCTTA	TGGCTTCTT	TTCCACTGT	TGTATTTT
	TTTGTGTGGG	AAGACTAAGA	TTCTGGGTCC	TAATGTAAGT	AAGAAGCCT	CTTCTCTGT	TCCATGAACA
	CCATCCTTTT	CTGTAACCTC	TATTACACAG	TATAGTGGTT	CTGTAAGTTC	ACACAGCCCA	GGGAGATGCT
	GGCTGCCAC	TCCC'CTCAAC	CCAGGCAAAT	TCCTCGGGGT	TAAAGTTATC	TACTGCAAGT	GACGATCTCT
50	GGGTTTTCT	GTGCGCTGT	TTGTGTGT	GTGTGTGT	GTGTGTGT	GTATGTGTCA	CTTTAAAAGG
	ACTGGTCAGA	TGGTAGGGAG	ATGAAAACAG	GAGATGCTAT	AAGAAAATAA	ACTTTGGGG	CGAATACCAA
	TGTGACTCTT	TTGTTTGTC	ATTTGTGTC	GTTCAATAGG	AAATTGTAAT	GATGATGCTG	TTTCTCACCA
	TTCTGGGACT	TGGTAGTGT	GTGTCACTCA	CAATCTGTGG	AGCTGGGAA	GAACTCAAAG	GAAACAAGGT
55	AGATAGAAGC	CCGATATAAA	ATCTTGAATG	ACAGGTTAAC	GAATTGGAGC	TTTATTCTT	AAAATATGGC
	CTGGGTTTT	TGAFAACATT	CTTCCAGAAA	ATAGTTCTC	CAAGTTTAT	TACTTTGGTT	TACAAATCTC
	ACATTTAAAT	CACATTTTAT	ACCATAAGTA	GCACACATT	CATAATATT	CTCTGAATGA	GGGTTGGGAT
	AATAGGACTG	ATATGTTAGA	AATGCCTAA	AGTGTGTGGA	GCATGAGAGA	TGGATGTACA	GAAGGCTTGT
	GAGGAAACCA	CCCAGGTATC	TGGCTTGT	TTCTGCCCA	GAACTAGCCG	CCTATTCTG	TTCTGT
60	ATTCTTTGT	TTCTTGACTT	TTCTTTCCA	ACTTGCTCTA	AAACCTCACT	TTTCTTTCT	TTCTGATTCA
	TGACTACCAA	ATG'TTTCAC	TTGCCTCACC	CGTCCATTAC	ACCTTGATA	AGAACCA	GACCTTGTC
	TCATGTA	GCCC ATGTC	GATGGAAGAA	ACATACTCTC	TCCATCTGT	CACTTTCTG	AGGCATTCAA
	GTCTAGCCAC	CTT TAAAAT	CACTCTCCTC	CAGGCTGGC	ACGGTGTAC	GCCTGTAATC	TCAGCACTT
	GTGAGGCTGA	GGAGGGCGGA	TCACCTGAAG	TCAGGAGTTC	AAAACCAAGCC	TGGCCAATG	GCAAAACCAA
	ATCTTCTCA	ATTA FAACCA	AATCTTAAAC	CAAATCTCA	CTAAAAAATA	CAACAAAACA	AAACAACAAAC
55	AACAAAAACA	GAAAGGAAA	CATTAGCCCA	GC GTGGTGGC	AGGTACCTGA	GGTCCAGAT	ACTTGGGAGG
	CTGAAGCAGG	AGAATCGCTT	GAGCCCAAGA	GATGGAGGTT	GCAGTGAGCC	GAGATCATGC	CACTGCACCA
	CAGCCAGGGT	GACAGAGCCA	TACTTCCAG	CACATTGGGA	GGCCAAAGCT	GAAGAATAAT	TTGAGGTGAG
	GATTGAGGA	CCAGCCTGGC	CAACATGGT	AAACTCCGTC	TGTACTAAA	ATATAAAACT	TAGTGGGCA
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60	GGAAAGTTGCA	GTGAGCCAAG	ATCGTGGCCA	CTGCACTCCA	GCCTGGGTGA	CATAGTGAGA	TTCTGTCTCA
	AAAAAAATAA	AAGAAATTAA	AAAAATCACT	CTCTTCCAAA	GATAGATAAA	TAAGACAGCA	GATATAACTAA
	GGAATAACCT	CACCAACTTG	TCATTGACTG	ACATGATTTC	TTTGGCCCA	CTTGGCCAGC	TAGTCTGGT

TGGTTTCTG GAAATGAAAG AAATAATCAG AGTTAACGAG CAGAGAGCGT GAGACCCAGA AAGACAAAAG
 TAGATGAGGT AAG'CTCTTG AGCGAGACTT CTAGGGATGG GAAATTGAGT GTGATTGATA TGAAATGATT
 TTTCCCTAT CAGC TTCCAG AGGATCGTGT TTATGAAGAA TTAAACATAT ATTCACTAC TTACAGTGAG
 TTGGAAGACC CAGGGAAAT GTCTCCCTCC ATTGATTAT AAGAATCACG TGTCCAGAAC ACTCTGATTC
 5 ACAGCCAAGG ATCCAGAAGG CCAAGGTTT GTTAAGGGGC TACTGGAAA ATTCTTATTC TCTCCACAGC
 CTGCTGGTT TACATTAGAT TTATTCCCT GATAAGAATA TTTTGTCT GCTGCTTCTG TCCACCTTAA
 TATGCTCCTT CTATTGTAG ATATGATAGA CTCCTATTT TCTTGTCTA TATTATGACC ACACACATCT
 CTGCTGAAA GTCACATGT AGTAAGCAAG ATTAACTGT TTGATTATAA CTGTCAAAT ACAGAAAAAA
 AGAAGGCTGG CTGAAAGTTG AGTAAACTT TGACAGTTG ATAATATTC GTTCTAGGG TTTTTTTT
 10 TTTAGCATT CTTAATAGTT ACAGTTGGC ATGATTGTA CCATCCACCC ATACCCACAC AGTCACAGTC
 ACACACACAT ATG'ATTACT TACACTAT ATAACCTCT ATGCAAATAT TTACCAACCA GTCAATAATA
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 15 TAAATAGGTT AAAACACAGGG AAATTATAAG TGCAAGAGATT AACATTTCAC AAATGTTAG TGAAACATTT
 GTGAAAAAAAG AAGACTAAAT TAAGACCTGA GCTGAAATAA AGTGACGTTG AAATGGAAT AATGGTTATA
 TCTAAACAT GTGAAAAAAAG AGTAACCTGT AGATTTGTT AACAAATTAA AGAATAAAAGT TAGACAAGCA
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 ATAAAAAGGG TCGGGCGCGG AGGTCACGC CTGTAATCCC AGCCCTTGG GAGGCCAGG TGGCAGATC
 20 ACGAAGTCAG TAG'TTGAGA CCAGCCTGGC CAACATAGTG AAACCCCGTC TCTACTAAA ATACAAAAAA
 TTGAACCTGG GGG'GTGGTG GCAGTCACCT GTAGTCCCAG CTACTTGGGA GGATGAGGCA GGAGAATCGC
 GAGACTCCAT CTCAAAAAAA AAAAAGGATA AAGTCTCATT TTTGGCTT ACCAGTCAC TCCAGCCTTG GTGACAATGG
 AGTACAATAA GACCTAAATT AAAAGGATA AAGTCTCATT TTTGGCTT AAAAGTCAGA AATCTGAAAA GTGGAGGAAG
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 25 TTATAAGAGA AATCATTATT AAATGAAGCA AGTTAACACT CTAAGGATAA ATCTAGCCT AGAAGATACA
 GCTAAGCTAA ACT'CACATG CCTATAATTG GAGGGAAAAA CTAAGGATAA ATCTAGCCT AGAAGATACA
 ATAATTAGTC ATAAACATGC ATTGTGAAAC TGTAGAGAGC AGGTAGCCCA AAATAGAGAA AGATTAGATA
 AAGAGAAAAT AAG'ATCCAT CAGAGACAGT ATCTCTAGGC TTGGGCAAGA GAAAAGTCCA CAGTGATAAG
 CAACTCCACC TAAC GCATGA ATATGCGCA GAGAAAACAG CAATAGTGA TGAATGCAA AGGTGCTGAG
 30 CAAATTCCAC ACAT'GAGTAT TGTGCATGAG TAAATGAATA AAACATTG AAAGACCTTT AGAGAAAGAG
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 GGACTGAAA AAA'TCAGTCT GAGAGTATA GTCACAAATT ATGAAATAAT TACATTTAT GTATTGAGGA
 TGCCAAGATT AAAAGGTGAC AGGTAGATGT TAATTCCCT AGATTGTAA AGTGTACCG ACAATCACAC
 35 AACAAATAAT TAA'GTGACTT GGTATGTTT ATTAATTGT AGGGCCTGAG GTTTCCATT CTCATTTC
 TAAAATACAA TTT'GTTCT CCAAATTGA CAGCAGAATA AAAACCTAC CTTTCACTG TGTATCATGC
 TAAGCTGCAT CTCT'ACTCTT GATCATCTGT AGGTATTAAT CACACTCTT CCATGGCATG GATGTTACA
 TACAGACTCT TAAC'CTGGT TTACCAAGAC GGATCCAATC TATATCTTA CAGTTGTATA
 GTATATGATA TCTCTTTTAT TTCACTCAAT TTATATTTT ATCATTGACT ACATATTCT TATACACAAC
 40 ACACAATTAA TGAATTTTT CTCAAGATCA TTCTGAGAGT TGCCCCACCC TACCTGCCTT TTATAGTACG
 CCCACCTCAG GCAGACACAG AGCACAATGC TGGGTTCTC TTCACACTAT CACTGCCCA AATIGCTTT
 CTAATTTCAT ACT'CAATGT CATCTCTCC ATGAAGACCA CTGAATGAAC ACCTTTCAT CCAGCCTTAA
 ITTCTTGCTC CATAACTACT CTATCCCAGC ATGCAGTATT GTATCATTAA TTATTAGTGT GCTTGTGACC
 TCCTTATGTA TTCTCAATT CCTGTATTG TGCAATAAT TGAATAATG TAACTGATT TCTTATCTGT
 45 GTTTGTGTTG GCATGCAAGA TTAGGTACT TATCAAGATA ATGGGAAATT AAGGCATCAA TAAAATGATG
 CCAAAGACCA AGA'GAGTTT CTGAAGCTCT CCTTTCATC AGCTCTTAT CAAACAGAAC ACTCTATAAA
 CAACCCATAG CCACAAAACA GGATGTAGGA ACAATCACCA GCACACTCTA TAAACAACCC ATAGCCAGAA
 AACAGAATGT AAGGACAATC ACCAGCCATC TTTTGTCAAT AATTGATGGA ATAGAGTTGA AAGGAACCTGG
 AGCATGAGTC ATA'TTGACC AGTCAGTCCT CACTCTTATT TACTTGCTAT GTAAACTTGA GAAAGCTTT
 50 TTCTCTTGT GAACCTCAGG TTTTACATCT GAAAATGAGA AATTGGAAAC AAAAGATTCC TAACTGGTCT
 TTCTGTTCCC ATATCTGT ATTTTCAAT ATTTAGGATT TTTGGAATC ACAATTACTT AGTTTGTGGT
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 AAGAAGTGT GCGNGTCGTG GTGGCTCACG CCTGTAATCC CAGCACTTA GGGAGGCCAA GGCGGGTGGA
 TCACGAGGTC AGGAGATCGA GACCATCTG GCTAACACGG TGAAACCCCG TCTCTACTAA AAAATACAAA
 55 AAATTAGCCA GCC'GTGGTGG CGGGCGCTG TAGCCCACG TACTCGGGAG GCTGAGGCAG GAGAATGGCA
 TGAACCAGGG AGGCGGAGCT TGCCGTGAGC CGAGATAGCG CCACTGCAGT CCCTCTGGG CAAAAGAGCA
 AGACTGCGTC TCAAAAAAA AAAAAGGAA AAGGAAAGAA GTGTGTGGAG TAGCAGGACA CCTGCAACAA
 TAATTTTTT CTAATCCCT CTGAAAATG CTAATCAAAG GGTTTTTTC CTAAAATTG TCTTAGAAT
 AAAATTCCC CTTGGGAGA CCGAGGCTGG CAGATCACGA GGTCAAGGAGA TAGAGACCAC GGTGAAACCC
 60 CGTCTCTACT AAAAATACTA AAAATTAGCC GGGNGTGGT GGTGGGTACA CCTGTAGTCC CAGCTACTTG
 GAGGCTGAGG CTGG'GAATC ACGTGAAC-3' (FRAG. NO:_)(SEQ. ID NO:2504)

Human Histidine Decarboxylase Nucleic Acid and Antisense Oligonucleotide Fragments

5'-TCT CCC TTG GGC TCT GGC TCC TTC TC TCT CTC TCC CTC TCT CGC CTC CGC CCT GGC TGC TGG GGT GGT GGT GC TTT TGT TCT TCC TTG CTG CC GCC CCG CTG CTT GTC T TC CTC G CTC TGT CCC TCT CTC TCT GTB CTC CTC BGG CTC CBT CTC CCT TGG GC-3' (FRAG. NO:1700) (SEQ. ID NO:1711)

5 5'-GGC TCT GGC (FRAG. NO:1701) (SEQ. ID NO: 1712)

5'-CCC TTG G (FRAG. NO:1702) (SEQ. ID NO: 1713)

5'- TT TGT TCT TCC (FRAG. NO:1703) (SEQ. ID NO: 1714)

5'- TCT CCC TTG GGC TCT GGC TCC TTC TC-3' (FRAG. NO:1024) (SEQ. ID NO: 1034)

5'- TCT CTC TCC CTC TCT CTC TGT -3' (FRAG. NO:1025) (SEQ. ID NO:1035)

10 5'- CGC CTC CGC CCTI GGC TGC TGG GGT GGT GC-3' (FRAG. NO:1026) (SEQ. ID NO:1036)

5'- TTT TGT TCT TCC TTG CTG CC-3' (FRAG. NO:1027) (SEQ. ID NO:1037)

5'- GCC CCG CTG CTI GTC T TC CTC G-3' (FRAG. NO:1028) (SEQ. ID NO:1038)

5'-CTC TGT CCC TCT CTC TCT GTB CTC CTC BGG CTC CBT CTC CCT TGG GC (FRAG.NO:1029)(SEQ.ID NO:1039)

Human Beta Tryptase Nucleic Acid and Antisense Oligonucleotide Fragments

15 5'-CTT GCT CCT GGG GGC CTC CTG GTC CCT CCG GGT GTT CCC GGC GGG CCT GGC CTG GGG CBG GGG CCG CGT BGG CGC GGC TCG CCB GGB CGG GCB GCG CCB GCB GCB GBT TCB GCB TCC TGG-3' (FRAG. NO:1704) (SEQ. ID NO: 1715)

5'- GCT CCT GGG GGC CT-3' (FRAG. NO:1705) (SEQ. ID NO: 1716)

5'-CGT BGG CGC-3' (FRAG. NO:1706) (SEQ. ID NO: 1717)

20 5'-T GGC CTG GGG-3' (FRAG. NO:1707) (SEQ. ID NO: 1718)

5'-CTT GCT CCT GGG GGC CTC CTG-3' (FRAG. NO:1030) (SEQ. ID NO:1040)

5'-GTC CCT CCG GGT GTT CCC GGC-3' (FRAG. NO:1031) (SEQ. ID NO:1041)

5'-GGG CCT GGC CTG GGG CBG GGG CCG CGT BGG CGC GGC TCG CCB GGB CGG GCB GCG CCB GCB GCB GCB GBT TCB GCB TCC TC G-3' (FRAG. NO:1032) (SEQ. ID NO:1042)

Human Tryptase-I Nucleic Acid and Antisense Oligonucleotide Fragments

25 5'-CTT GCT CCT GGG GGC CTC CTG GTC CCT CTG GCT G TT CCC GGC CCT GGB CTG GGG CBG GGG CCG CGT BGG CGC GGC TCG CCB GGB CGG GCB GCG CCB GCB GCB GGC TCB GCB TCC TGG CCB CGG BBT TCC-3' (FRAG. NO: 1708) (SEQ. ID NO:1719)

5'-CT CCT GGG GGC CTC CTG-3' (FRAG. NO:1709) (SEQ. ID NO:1720)

30 5'-B TCC TGG CCB CGG BBT TCC -3' (FRAG. NO:1710) (SEQ. ID NO:1721)

5'-GTC CCT C-3' (FRAG. NO:1711) (SEQ. ID NO:1722)

5'-CTT GCT CCT GGG GGC CTC CTG-3' (FRAG. NO:1033) (SEQ. ID NO:1043)

5'-GTC CCT CTG GCT G TT CCC GGC-3' (FRAG. NO:1034) (SEQ. ID NO:1044)

35 5'-CCT GGB CTG GGG CBG GGG CCG CGT BGG CGC GGC TCG CCB GGB CGG GCB GCG CCB GCB GCB GGC TCB GCB TCC TGG CCB CGG BBT TCC -3' (FRAG. NO:1035) (SEQ. ID NO:1045)

Human Prostaglandin D Synthase Nucleic Acid and Antisense Oligonucleotide Fragments

5'-GGT GTG CGG GGC CTG GTG CC CCT GGG CCT CGG GTG CTG CCT GT GCG CTG CCT TCT CCT GG GTC CTC GCC GGG GCC C TT GCT GCC CTG GCT GT GCC CTG GGG GTC TGG GTT CGG CTG T CCC CBG CBG GBC CBG TCC CBT CCB CEG CGT GTG BTG BGT BGC CBT TCT CCT GCB GCC GBG-3' (FRAG.NO:1712)(SEQ.ID NO:1723)

40 5'-T TCT CCT GCB GCC GBG -3' (FRAG. NO:1713) (SEQ. ID NO:1724)

5'-CTT GCT GCC CTG GCT GT-3' (FRAG. NO:1714) (SEQ. ID NO:1725)

5'- TCT TCT CCT GG-3' (FRAG. NO:1715) (SEQ. ID NO:1726)

5'-GGT GTG CGG GGC CTG GTG CC-3' (FRAG. NO:1036) (SEQ. ID NO:1046)

5'-CCT GGG CCT CGG GTG CTG CCT GT-3' (FRAG. NO:1037) (SEQ. ID NO:1047)

45 5'-GCG CTG CCT TCT TCT CCT GG-3' (FRAG. NO:1038) (SEQ. ID NO:1048)

5'-GTC CTC GCC GGG GCC CTT GCT GCC CTG GCT GT-3' (FRAG. NO:1039) (SEQ. ID NO:1049)

5'-GCC CTG GGG GTC TGG GTT CGG CTG T-3' (FRAG. NO:1040) (SEQ. ID NO:1050)

5'-CCC CBG CBG CBC TCC CBT CCB CBG CGT GTG BTG BGT BGC CBT TCT CCT GCB GCC GBG -3' (FRAG. NO:1041) (SEQ. ID NO:1051)

Human Cyclooxygenase-2 Nucleic Acid and Antisense Oligonucleotide Fragments

50 5'-GGG CGC GGG CGB GCB TCG C TTT GGG CTT TTC TCC TTT GGT T TGB GCG CCB GGB CGG CGC BCB GCB GCB GGG CGC GGG CGB GCB TCG CGG CGG GCB GGG-3' (FRAG. NO: 1716) (SEQ. ID NO:1729)

5'-G GCB GGG -3' (FRAG. NO: 1717) (SEQ. ID NO: 1730)

5'-TCC TTT GGT T-3' (FRAG. NO:1718) (SEQ. ID NO:1731)

55 5'- GGG CGC GGG CGB GCB TCG C-3' (FRAG. NO:1042) (SEQ. ID NO:1052)

5'- TTT GGG CTT TTC TCC TTT GGT T-3' (FRAG. NO:1043) (SEQ. ID NO:1053)

5'-TGB GCG CCB GGB CCG CGC BCB GCB GGG CGC GGG CGB GCB TCG CGG CGG GCB GGG -3' (FRAG. NO:1044) (SEQ. ID NO:1054)

Human Eosinophil Cationic Protein Nucleic Acid and Antisense Oligonucleotide Fragments

5'-CCT CCT TCC TGG TCT GTC TGC CBG BCB BBT TTG GGB BGT GBB CBG TTT TGG BBC CBT GTT TCC CBG TCT CTG BGC TGT GGC-3' (FRAG. NO: 1719) (SEQ. ID NO: 1732)
 5'-TTC TCC TTT GGT T-3' (FRAG. NO:1720) (SEQ. ID NO: 1733)
 5 5'-T TTC TCC TTT GGT T-3' (FRAG. NO:1721) (SEQ. ID NO:1734)
 5'- GGG CGC GGG CGB GCB TCG C-3' (FRAG. NO:1042) (SEQ. ID NO:1052)
 5'- TTT GGG CTT TTC TCC TTT GGT T-3' (FRAG. NO:1043) (SEQ. ID NO:1053)
 5'-TGB GCG CCB GGB CCG CGC BCB GCB GGG CGC GGG CGB GCB TCG CBG CGG CGG GCB GGG -3'
 (FRAG. NO:1044) (SEQ. ID NO:1054)

Human Eosinophil Derived Neurotoxin Nucleic Acid and Antisense Oligonucleotide Fragments

5'-GCC CTG CTG CTC TTT CTG CT TCC CTT GGT GGG TTG GGC C GCT GGT TGT TCT GGG GTT C TTG CTG CCC CTT CTG TCC C TGT ITG CTG GTG TCT GCG C 5'- CCC CBB CBG BBG BBG CBG BCB BBT TTG GGB BGT GBB CBG TTT TGG BBC CBT GIT TCC TGT-3' (FRAG. NO: 1722) (SEQ. ID NO: 1735)
 5'-TTC CTG T-3' (FRAG. NO:1723) (SEQ. ID NO: 1736)
 15 5'-CTC TTT CTG CT-3' (FRAG. NO: 1724) (SEQ. ID NO:1737)
 5'-CCC CTT CTG TCC C-3' (FRAG. NO:1725) (SEQ. ID NO: 1738)
 5'- GCC CTG CTG CTC TTT CTG CT-3' (FRAG. NO:1047) (SEQ. ID NO:1055)
 5'- TCC CTT GGT GGG TTG GGC C-3' (FRAG. NO:1048) (SEQ. ID NO:1056)
 5'- GCT GGT TGT TCT GGG GTT C-3' (FRAG. NO:1049) (SEQ. ID NO:1058)
 20 5'- TTG CTG CCC CTT CTG TCC C-3' (FRAG. NO:1050) (SEQ. ID NO:1057)
 5'- TGT TTG CTG GTG TCT GCG C -3' (FRAG. NO:1051) (SEQ. ID NO:1059)
 5'- CCC CBB CBG BBG BBG CBG BCB BBT TTG GGB BGT GBB CBG TTT TGG BBC CBT GTT TCC TGT-3' (FRAG. NO:1052) (SEQ. ID NO:1060)

Human Eosinophil Peroxidase Nucleic Acid and Antisense Oligonucleotide Fragments

25 5'-GCG CTC GGC CTG GTC CCG G GGG TCT CCT CTT GTT GC TTG CGC CTC CTG CTG GGG GT CC CTC TGT TCT TGT TTT GGG GGC GGG CCC GGC CGT TGT CTT G GTT TGG GGG TTT CCG TTG GGG TTC TCC TGG CCC GGG CCT TGC CC GGC CGT GGT CCC GGC TTC GTTCCT GTC TCC GTC TCG GCT CTT CTG GGG CCT TGC GCT GTC TTT GGT G 5'-GCB CCG TCC BGT GBT GGT GCG GTB CTT GTC GCT GCB GCG CTC GGC CTG GTC CCG GBG BGC CACCGCTCCCT GTCAGCCAAC AAATATCCAT TGAGCGACAC CTGTGTCCTCA GGTGCTGCTC TGGGCCCTGG
 30 GAGAAGTGCA TCAGTGGGCT TGGTAGTAGA GGGTAGGGAT GGAGTGAAGG GTAGGCAGGA AGAACATGTC
 CAGGCTGGTA GGAGGGTGGGG TGGGGGGTTT CAGTCTCAA ACTCCCCATGA AAACCCAGAGA GAAGTTTCAG
 AACTCCACCC AAGAGGCTGG GTTTCTAGGG CCCAGAGCTG CCCTCCCCCA CCCTAGAATG GGCTATAAAA
 GTCCCTTCCC AGCTACGTCC AGAGAAGAGC TGGAGGAAGT GAGAGGTCGG CTGGGGGTCC TCAAAGTGAG
 AGGGGAGCAG AGGATCCCTCC CGTGCAGGCT GTGGATGTCA CTCACCTCCC AGCTGGTGAAG GCCTCGTGC
 35 35 AGAGATGCAT CTGCTCCCAAG CCCTGGCAGG GGTCTCTGGCC ACACTCGTCC TCGCCCAGCC CTGTGAGGGC
 ACTGACCCAG GTAATAGTCC CCTAGACAGG CAAGGAGGAG GGAGGGAAA TGGAAAGGGGA AGCACATTGGG
 TCTTGGAGGG GGTCTTGTGG CTTGCTGAAC CCTGAGTCCC CATCTCTTGT AACAGCCTCC CCTGGGGCAG
 TGGAGACCTC GGTCTCTGCAG GACTGCATAG CAGAGGCCAA GTTGCTGGT GATGCTGCCT ACAATTGGAC
 CCAGAAAGAGG TGGAACTTGGG TCTGGGGGCT GCATGGGCCT GGGAGGATCA GT TAATACCTTG TGGGGTCAGG
 40 40 GAGCCCATGT CCCGTGCTGA TGTTATTTC CCACCAGGT CGGGCTGTCT CCAACCCAGAT TGTGCGCTTC
 CCCAATGAGA GACGACCTC CGACCGTGGC CGAGCCCTCA TGTTCATGCA GTGGGGCCAG TTCATTGACC
 ATGACCTGGA CTCTCCCCCG GAGTCCCCGG CCAGAGTGGC CTTCACTGCA GGCCTTGACT GTGAGAGGAC
 CTGCGCCCCAG CTGCCCCCT GCTTCTCCAT CAAGGTACCT ACCCTCAGCC AATCTCCCAT GCCCTTGTGT
 GGCCTCCCCC AAACGCAAGG TGCTGGGGT GGGGATCTGG AAGACTGGAG CACCATCCTT AAGGAGCTGC
 45 45 CTGTGGAGCT AGGGTATGAG ACAGAGACAC AAG CACTGTCTCC TCTTCCATCT CAGATCCAC CCAATGACCC
 CCGCATCAAG AACAGCGTG ACTGCATCCC TTTCTTCCGC TCGGCACCC CATGCCCTCA AAACAAGAAC
 AGAGTCCGCA ACCAGATCAA CGCGCTCACC TCCTTTGTGG ACGCCAGCAT GGTGATGGC AGTGAGGGTCT
 CCCTCTCGCT GCGCCTCCGC AACCGGACCA ACTACCTGGG GCTGCTGGCC ATCAACCCAGC GCTTCAAGA
 CAACGGCCGG GCGCTGCTGC CCTTCGACAA CCTGCACGAT GACCCCTGTC TCCTCACCAA CGCTCGGG
 50 50 CGCATCCCCCT GCTCTCTGGC AGGTCAAGACA GGGAGGAAGG TGGTGTCTTC CCAGGAAACA GCCATCCCC
 GGGTCCCAAC TGGGAAGCAA TGGTGGGATG TGGTGAAGGT ACATGGTTTG GGACCTCAGT ATTAGGCACA
 CCATAAGCAT GGATCTGTGC AC TGAAGAGATG GAGGTCCAGT GAGGGCCAGG AGTTGGGCC ACCCCGTCTC
 TCCCATCCCC AGCCCTGGGT CTACCTGGT AGAAAGACAT TTCTCTGGGA AAGGCTGCAG TAAATCTGAG
 CTTGGGGTTT TCAAGGTGAC ACCCGATCAA CGGAAACCCC CAAACTGGCA GCCATGCACA CCCCTTTAT
 55 55 GCGAGAGCAC AACCGGCTGG CCACCGAGCT GAGACGCCTG AATCCCCGGT GGAATGGAGA CAAACTGTAC
 AATGAGGCTC GGAAAGATCAT GGGGGCCATG GTCCAGGTA GGAGCTCTGC ATCCCAGCAT CCCCC CTTGTATCT
 CCACCCACCA ATAGTAAATT AATGTTGTCA CATTGACGT GATGACAATA AAGAATATGT CTGAGCCACC
 CTTGAAAAG GCAAGGGTAT GGGTGAAGTAG CCTCTGGGAA ATGTTCTCTCC TGTCTTCCCT TCCAGATCAT
 CACCTACCGA GACCTTCTGC CCCTGGTTCT GGGCAAGGCC CGGGCCAGGA GAACCCCTGGG GCACTACAGG
 60 60 GGGTACTGCT CCAATGTGGA CCCACGGGTG GCCAATGTCT TCACCCCTGGC CTTCCGCTTT GGCCACACAA

TGCTCCAGCC CTTCATGTTT CGCTTGGACA GTCAGTACCG GGCCTCCGA CCCAACTCGC ATGTCCCACT
 TAGCTCTGCC TTCTTGCCA GCTGGCGAT CGTGTATGAA GGTGACCAGG TTTCCAGGG GGCAAATGGG
 5 GGTGAGGGTG GGGAGCATGC CCTCCCCTAG GTGG TCCAGCTGCT TCATGTCTCT CCAGAACTCT GTTCCCTGAC
 AAACGTACT AACATACCCG ACTGGCTTGT CCAGCTCTGG GCTAGCTTGG CATCATGTGA TAACCCAAGT
 AGCTTCCCAG AGGCTGGTCC AATCTGTGCT GCTCACATT CCTGCCACCA GGGGGCATCG ACCCCATCCT
 10 CGGGGGCCTC ATGGCCACCC CTGCCAAGCT GAACCGTCAG GATGCCATGT TAGTGGATGA GCTCCGGGAC
 CGGCTGTTTC GGCAAGTGAG GAGGATTGGG CTGGACCTGG CAGCTCTAA CATGCAACGA AGCCGGGACC
 ACGGCCTTCC AGGAGGGGG GCTGTCCACC TCTTCTCCCA GCTTGTCTCG GGCCAGGCTG CTCAAGGGGT
 TCTGGGAAGA CCCGTGGTACC CGACTGCCCTG GTAGGTTCTG GTGGCAGAAA CGAGGTGTTT TCACCAAAAG
 15 ACAGCGCAAG GCCCTGAGCA GAATTTCCTT GTCTCGAATT ATATGTGACA ATACCGTAT CACCACGGTT
 TCAAGGGACA TCTCAGAGC CAACATCTAC CCTCGGGGCT TTGTGAAC TG CAGCGTATC CCCAGGTTGA
 ACCTATCAGC CTGGCGAGGG ACATGAGGCT TCTGAGGTA AGGGGAGGCC ACCTCCAGCA CCCTGGGCTG
 GTTAAGCCTC ACACTCTTCC CTGGATGGAT GGCTGAGTCC TCTTAGGTC TCAAGCAGAG AAAACAGAAC
 TTGTCACTAG GTACTCTTC CAAGTGGCTT CCAAAATGTGC TAGTTCTGG GCTGACAGTC AATTCCAGGC
 20 CCTAGGACTT TGGGGGGAAA TAGGAGCAT CCAACTA GAATTCCGTG GCCAGGACCC CTGCCAGGGC
 ACTGACCCAG CCTCCCTG GGCAGTGGAG ACCTCGGTCC TGCGAGACTG CATAGCAGAG GCCAAGTTGC
 TGGTGGATGC TGCCATACAAT TGGACCCAGA AGAGCATCAA GCAGCGGCTT CGCACGCGTT CAGCCAGCCC
 CATGGACCTC CTGTCTTACT TCAAAACAAACC GGTAGCAGCC ACCAGGACAG TTGTCGGGC CGCAGATTAT
 ATGCATGTGG CTTGGGGCT GCTTGAAGAG AAGTTACAAAC CCCAGCGTC CGGACCCCTTC ATTGTCACTG
 25 ATGTGCTAAC AGAACACACAG CTGCGGTGC TGTCCCAAGGC CAGTGGCTG GCTCTGGG ACCAGGCGGA
 GCGCTGCAGC GACAAGTACC GCAACATCAC TGGACGGTGC ACAACAAGA GGAGACCCCTT GCTAGGGGCC
 TCCAACCAGG CTCGGCTCG CTGGCTGCC GCGAGATATG AGGATGGGCT GTGCTCCCCC TTGGCTGGA
 CCCCCAGCAG GAGCGCAAT GGCTTCCCTC TCCCCTTGTG CCGGGCTGTC TCCAACCAGA TTGTGCGCTT
 CCCCAATGAG AGAACGTACCT CCGACCGTGG CCGAGCCCTC ATGTTATGC AGTGGGGCCA GTTCATTGAC
 30 CATGACCTGG ACTCTCTCCC GGAGTCCCCG GCCAGAGTGG CTTCACTGC AGGGCTTGCAG TGTGAGAGGA
 CCTGCGCCCA GTCGCCCTCC TGCTTCCCA TCAAGATCCC ACCCAATGAC CCCCCCATCA AGAACCAAGCG
 TGAUTGCATC CCTCTTCTCC GCTCGGCACC CTCATGCC CAAAACAAGA ACAGAGTCG CAACCAAGATC
 AACCGCCTCA CCTCTTTGTG GGACGCCAGC ATGGTGTATG GCAAGTGGT CTCCTCTCG CTGCGGCTCC
 GCAACCGGAC CAACTACCTG GGGCTGCTGG CCATCAACCA GCGTTCAA GACAACGGCC GGGCCCTGCT
 35 30 GCCCTTCGAC AACATGACG ATGACCCCTG TCTCTCACC AACCCTCG CGCGCATCCC CTGCTTCCTG
 GCAGGTGACA CCCGATCAAC GGAAACCCCC AACTGGCAG CCATGCACAC CCTCTTATG CGAGAGCACA
 ACCGGCTGGC CACCGAGCTG AGACGCCAGA ATCCCCGGTG GAATGGAGAC AAACATGTACA ATGAGGCTCG
 GAAGATCATG GGGGCCATGG TCCAGATCAT CACCTACCGA GACTTCTGC CCCTGGTTCT GGGCAAGGCC
 CGGGCCAGGA GAACTCTGGG GCACTACAGG GGGTACTGCT CCAATGGAA CCCACGGGTG GCCAATGTCT
 40 35 TCACCCCTGGC CTTCGGCTTT GGCCACACAA TGCTCCAGCC TTTCATGTTG CGCTTGGACA GTCAGTACCG
 GGCCTCCGCA CCCACTCGC ATGCCCCACT TAGCTCTGCC TTCTTGCCTA GCTGGCGGAT CGTGTATGAA
 GGGGGCATCG ACCCCATCCT CGGGGGCCTC ATGCCACCC CTGCCAACCT GAACCGTCAG GATGCCATGT
 TAGTGGATGA GTCGGGGAC CCGCTGTTG GGCAAGTGGAG GAGGATTGGG CTGGACCTGG CAGCTCTCAA
 CATGCAACGA AGCCGGGACC ACGGCCCTCC AGGGTACAAT GCTTGGAGGC GCTTCTGTGG GCTCTCCAG
 45 40 CCCCGGAATT TGGCACAGCT TAGCGGGGTG CTGAAAAAAC AGGACTTGGC AAGGAAGTTC CTGAATTGTT
 ATGGAACACC TGACAACATT GACATCTGGA TTGGGGCCAT CGCTGAGGCT CTTTGCCGG GGGCTCGAGT
 GGGGCTCTT CTGCTTGTC TGTTCGAGAA CCAGTTCAGA AGAGCCGAGA CGGAGACAGG TTCTGGTGGC
 AGAACGAGGT GTTTCACCA AAGACAGCGC AAGGCCCTGA GCAGAATTTC CTTGCTCTGA ATTATATGTG
 50 45 ACAATACCGG TATCACACG GTTCAAGGG ACATCTTCAG AGCCAACATC TACCCCTCGGG GCTTGTGAA
 CTGCAGCCGT ATCC'CCAGGT TGAACCTATC AGCCTGGCGA GGGACATGAG GCTTCTGCAG GAGTCTATCC
 CAAGTCTCCA ACTITGGAG ACAAGGGGAA GGGGAGGAGC ATGAGGCTGC CTTGCTCTCCC TGGAGCAAGT
 GCAGGCTCGT GACCGCTCTG CTGGCTACAG CTCAGAGCTG GGTCCCCAG CCAGGAGTGA AGGCTGGGG
 CTCCTATCAG CAATGGACCT TCCGCTTGG GAGCCTCTTA GGTATTAGGC TATGAATCAG CGCCACGTGC
 AAAGGCTTGG GAGCAAGCC ATGTGGTCTT GCACCCCAGG CAAGAAAAGT CAGCTGGAGG GTTACAGCA
 55 50 CTTTCTACTG TTTCCAGCC CTCCCTCCCC TCCCTCACCA TGACTAAGAG ACCACTCGGT CCTAGCCTCC
 AGACACCCCA CAAACTCCT CTGAGCCTGA GGCCAGGCG CATGCTCTGC TTCTACCAAT AAAGCACTGC
 CGGAATTC-3' (FRAG. NO: 1726) (SEQ. ID NO: 3008)
 5'-CACCGCTCCT GTCAAGCCAAC AAATATCCAT TGAGCGACAC CTGTGTCCCA GGTGCTGCTC TGGGCCCTGG
 GAGAAGTGCA TCAGTGGGCT TGGTAGTGA GGGTAGGGAT GGAGTGAAGG GTAGGCAGGA AGAATGTCCC
 CAGGCTGGTA GGAGGGTGGG TGGGGGTTT CAGTCTCAA ACTCCCCATGA AAACCAAGAGA GAAGTTTCAG
 60 55 AACTCCACCC AAGAGGCTGG GTTCTAGGG CCCAGAGCTG CCCTCCCCCA CCCTAGAATG GGCTATAAAA
 GTCCCTTCCC AGCTACGTCC AGAGAAGAGC TGGAGGAAGT GAGAGGTCGG CTGGGGGTCC TCAAAGTGAG
 AGGGGAGCAG AGGATCCTCC CGTGCAGGCT GTGGATGTCA CTCACCTCCC AGCTGGTGAAG GCTCGCTGC
 AGAGATGCAT CTGCTCCAG CCCTGGCAGG GGTCTGGCC ACACTCGCC TCGCCAGGCC CTGTGAGGGC
 ACTGACCCAG GTATAGTCC CCTAGACAGG CAAGGAGGAG GGAGGGAAA TGGAAAGGGGA AGCACTTGGG
 TCTTGGAGGG GGTCTTGTGG CTTGCTGAAC CCTGAGTCCC CATCTCTTG AACAGCCTCC CCTGGGGCAG
 TGGAGACCTC GGTCTGCGA GACTGCATAG CAGAGGCCAA GTTGTCTGGT GATGCTGCCT ACAATTGGAC

CCAGAAGAGG TGGACTTGGG TCTGGGGCT GCATGGGCCT GGGAGGATCA GT-3' (FRAG. NO:_) (SEQ. ID NO:2483)
 5'-TAATACCTTG TGGGGTCAGG GAGCCATGT CCCGTGCTGA TGTTATTCTC CCACCAGGTC CGGGCTGTCT
 CCAACCAGAT TGTGCGCTTC CCCAATGAGA GACTGACCTC CGACCGTGGC CGAGCCCTCA TGTTCATGCA
 5 GTGGGGCCAG TTCATTGACC ATGACCTGGA CTTCTCCCCG GAGTCCCCGG CCAGAGTGGC CTTCACTGCA
 GGCCTTGAAT GTGAGGAGC CTGCGCCAG CTGCCCTCCCT GCTTCCCCT CAAGGTACCT ACCCTCAGGC
 AATCTCCAT GCCCTTGTGT GGCCCTCCCC AAAGGCAAGG TGCTGGGGGT GGGGATCTGG AAGACTGGAG
 CACCATCCTT AAGGAGCTGC CTGTGGAGCT AGGGTATGAG ACAGAGACAC AAG-3' (FRAG. NO:_) (SEQ. ID NO:2484)

10 5'-CACTGTCTCC TCCTCCATCT CAGATCCCAC CCAATGACCC CCGCATCAAG AACCAAGCGTG ACTGCATCCC
 TTTCTCCGC TCGGCACCC CATGCCCTAA AAACAAGAAC AGAGTCGCA ACCAGATCAA CGCGCTCAC
 TCCCTTGAG ACGCCAGCAT GGTGTATGGC AGTGGAGTCT CCTCTCGCT GCGGCTCCGC AACCAGGACCA
 ACTACCTGGG GCTGCTGGCC ATCAACCAGC GCTTCAAGA CAACGGCCGG GCCCTGCTGC CCTTCGACAA
 15 CCTGACGAT GACCCCTGTG TCCTCACCAA CGCTCGGGCG CGCATCCCC CCTCTCTGGC AGGTCAAGACA
 GGGAGGAAGG TGGTGTCTTC CCAGGAAACA GCCATCCCTG GGGTCCAAC TGGGAAGCAA TGGTGGGATG
 TGGTGAAGGT ACATGGTTTG GGACCTCAGT ATTAGGCACA CCATAAGCAT GGATCTGTGC AC-3'
 (FRAG. NO:_) (SEQ. ID NO:2485)

5'-TGAAGAGATG GAGGTCCAGT GAGGGCCAGG AGTTGGCCC ACCCGTCTC TCCATCCCC AGCCCTGGGT
 20 CTACCCCTGGT AGAAAGACAT TTCTCTGGG AAGGCTGCAG TAAATCTGAG CTTGGGGTTT TCAAGGTGAC
 ACCCGATCAA CGGAACCCC CAAACTGGCA GCCATGCACA CCCTCTTAT GCGAGAGCAC AACCAGGCTGG
 CCACCGAGCT GAGACGCCGT AATCCCCGGT GGAATGGAGA CAAACTGTAC AATGAGGCTC GGAAGATCAT
 GGGGGCCATG GTCCAGGTAA GGAGCTCTGC ATCCCAGCAT CCCCC-3' (FRAG. NO:_) (SEQ. ID NO:2486)

25 5'-CTTGTATCT CCACCCACCA ATAGTAAATT AATGGTGTCA CATTGACGT GATGACAATA AAGAATATGT
 CTGAGCCACC CTTGAAAAG GCAAGGGTAT GGGTGAGTAG CCTCTGGGG AATGGTCTCC TGTCTCCCT
 TCCAGATCAT CACCTACCGA GACTTTCTGC CCCTGGTTCT GGGCAAGGCC CGGGCCAGGA GAACCCCTGGG
 GCACTACAGG GGGTACTGCT CCAATGTGGA CCCACGGGTG GCCAATGTCT TCACCCCTGGC CTTCCGCTTT
 30 GCCCACACAA TGCACAGCC CTTCATGTTG CGCTTGGACA GTCAGTACCG GGCCTCCGCA CCCAACTCGC
 ATGTCCCACT TAGCTCTGCC TTCTTGGCA GCTGGCGGAT CGTGTATGAA GGTGACCAAGG TTTTCCAGGG
 GCAAATGGG GGTGGGGT GGGAGCATGC CCTCCCCTAG GTGG-3' (FRAG. NO:_) (SEQ. ID NO:2487)

35 5'-TCCAGCTGCT TCATGTCTCT CCAGAACTCT GTTCCCTGAC AAACGTTACT AACATACCCG ACTGGCTTGT
 CCAGCTCTGG GCTAGCTTGG CATCATGTGA TAACCCAAGT AGCTTCCAG AGGCTGGTCC AATCTGTGCT
 GCTCACATT CCTCCACCA GGGGGCATCG ACCCCATCCT CGGGGCCCTC ATGGCCACCC CTGCCAAGCT
 GAACCGTCAG GATGCCATGT TAGTGGATGA GCTCCGGGAC CGGTGTTTC GGCAAGTGAG GAGGATTGGG
 40 CTGGACCTGG CAGCTCTCAA CATGCAACGA AGCCGGGACC ACGGCCTTCC AGGTGAGGGG GCTGTCCACC
 TCTTCTCCA GCTTCTCG GGCCAGGCTG CTCAAGGGGT TCTGGGAAGA CCCTGGTACC-3' (FRAG. NO:_) (SEQ. ID NO:2488)

5'-CGACTGCCGTG TAGGTTCTG GTGGCAGAAA CGAGGTGTT TCACCAAAAG ACAGCGCAAG GCCCTGAGCA
 45 GAATTTCTT GTCTCGAATT ATATGTGACA ATACCGGTAT CACCACGGTT TCAAGGGACA TCTTCAGAGC
 CAACATCTAC CCTCGGGCT TTGTGAACTG CAGCGTATC CCCAGGTTGA ACCTATCAGC CTGGCGAGGG
 ACATGAGGCT TCTGCAAGGTA AGGGGAGGCC ACCTCCAGCA CCCTGGGCTG GTTAAGCCTC ACATCCTTC
 50 CTGGATGGAT GGCAGAGTCC TCTTAGGTCT CTAAGCAGAG AAAACAGAAC TTGTCACTAG GTACTCTTC
 CAAGTGGCTT CCCAATGTGC TAGTTCTGG GCTGACAGTC AATTCCAGGC CCTAGGACTT TGGGGGAAA
 TTAGGAGCAT CCAACTA-3' (FRAG. NO:_) (SEQ. ID NO:2489)

5'-GAATTCCTG GCCAGGACCC CTGCCAGGGC ACTGACCCAG CCTCCCTGG GGCAGTGGAG ACCTCGGTCC
 45 TCGAGACTG CATAGCAGAG GCCAAGTTGC TGGTGGATGC TGCTACAAT TGGACCCAGA AGAGCATCAA
 GCAGCGGCTT CGCAGCGGTT CAGCCAGCCC CATGGACCTC CTGCTCTACT TCAAACAAACC GGTAGCAGCC
 ACCAGGACAG TTGTCGGGC CGCAGATTAT ATGCATGTGG CTTTGGGCT GCTTGAAGAG AAGTTACAAC
 CCCAGCGGTC CGGACCCCTTC ATTGTCACTG ATGTGCTAAC AGAACCCACAG CTGCGCTGC TGTCCCAGGC
 50 CAGTGGCTGT GCTCTCCGG ACCAGGCCGA GCGCTGCAGC GACAAGTACC GCACCATCAC TGGACGGTGC
 AACAAACAAGA GGAAGACCTT GCTAGGGCC TCCAACCAGG CTCTGGCTCG CTGGCTGCC GCCGAGTATG
 AGGATGGGCT GTCAGCTCCC TTGGCTGGA CCCCCAGCAG GAGGCGCAAT GGCTTCTTC TCCCTCTTGT
 CCGGGCTGTC TCCAACCAGA TTGTGCGCTT CCCAATGAG AGACTGACCT CCGACCGTGG CCGAGCCCTC
 ATGTTCATGC AGTCAGGGCCA GTTCATTGAC CATGACCTGG ACTTCTCCCC GGAGTCCCCG GCCAGAGTGG
 CCTTCACTGC AGGGCTTGAC TGTGAGAGGA CCTGCGCCCA GCTGCCCTCC TGCTTCCA TCAAGATCCC
 55 ACCCAATGAC CCCCGCATCA AGAACCGAGCG TGACTGCATC CCTTCTTCC GCTCGCACC CTCATGCC
 CAAAACAAGA ACAAGTCCG CAACCAAGATC AACCGCTCA CCTCCTTGT GGACGCCAGC ATGGTGTATG
 GCAGTGAGGT CTCCTCTCG CTGCGGCTCC GCAACCGGAC CAAACTACCTG GGGCTGCTGG CCATCAACCA
 GCGCTTCAA GACAACGGCC GGGCCCTGCT GCCCTCGAC AACCTGCACG ATGACCCCTG TCTCCTCACC
 AACCGCTCGG CGCGCATCCC CTGCTTCTG GCAGGTGACA ACCGGCTGGC CACCGAGCTG AGACGCCCTGA
 60 CCATGCACAC CCTCTTTATG CGAGAGCACA ACCGGCTGGC CACCGAGCTG AGACGCCCTGA ATCCCCGGTG
 GAATGGAGAC AAACTGTACA ATGAGGCTCG GAAGATCATG GGGCCATGG TCCAGATCAT CACCTACCGA
 GACTTTCTGC CCCIGGTTCT GGGCAAGGCC CGGGCCAGGA GAACCTGGG GCACTACAGG GGGTACTGCT

CCAATGTGGA CCCACGGGTG GCCAATGTCT TCACCCCTGGC CTTCCGCTT GGCCACACAA TGCTCCAGCC
 CTTCATGTTG CGCTTGGACA GTCAGTACCG GGCTCTCGCA CCCAACACTCG ATGTCCCACCT TAGCTCTGCC
 TTCTTGCCA GCTGGCGGAT CGTGTATGAA GGGGGCATCG ACCCCATCCT CGGGGGCCTC ATGGCCACCC
 CTGCCAAGCT GAACCGTCAG GATGCCATGT TAGTGGATGA GCTCCGGGAC CGGCTGTTTC GGCAAGTGAG
 5 GAGGATTGGG CTGGACCTGG CAGCTCTCAA CATGCAACGA AGCCGGGACC ACGGCCTTCC AGGGTACAAT
 GCTTGGAGGC GCT'CTGTGG GCTCTCCCG CCCCGGAATT TGGCACAGCT TAGCCGGGTG CTGAAAAACC
 AGGACTTGGC AAGGAAGTTC CTGAATTGT ATGAAACACC TGACAACATT GACATCTGGA TTGGGGCCAT
 CGCTGAGCCT CTTITGCCGG GGGCTCGAGT GGGGCCTCTT CTGGCTTGTG TGTCGAGAA CCAGTTCAGA
 10 AGAGCCGAGA CGGAGACAGG TTCTGGTGGC AGAACGAGGT GTTTTCACCA AAGACAGCGC AAGGGCCCTGA
 GCAGAATTTC CTTCCTCTCGA ATTATATGTG ACAATACCGG TATCACCACG GTTCAAGGG ACATCTTCAG
 AGCCAACATC TACCCCTCGGG GCTTTGTGAA CTGCAGCCGT ATCCCCAGGT TGAACCTATC AGCCTGGCGA
 GGGACATGAG GCT'CTGCAG GAGTCTATCC CAAGTCTCCA ACTTTTGGAG ACAAGGGGAA GGGGAGGACC
 ATGAGGCTGC CTTCCTCTCC TGGAGCAAGT GCAGGCTCGT GACGCTTCTG CTGGCTACAG CTCAGAGCTG
 15 GGTTCCCCAG CCAAGAGTGA AGGCTGGGG CTCCATCAG CAATGGACCT TCCGCCTTGG GAGCCTCTTA
 GGTATTAGGC TATC AATCAG CGCCACGTGC AAAGGCTTGG GAGCCAAGCC ATGTTGGTCTT GCACCCCCAGG
 CAAGAAAAGT CAGCTGGAGG GTTTACAGCA CTTTCTACTG TTTCCAGCC CTCCCTCCCC TCCCTCACCA
 TGACTAAGAG ACCACTCGGT CCTAGCCTCC AGACACCCCCA CAATACTCCT CTGAGCCTGA GGCCAGGCAG
 CATGCTCTGC TTCTACCAAT AAAGCACTGC CGGAATTCT-3' (FRAG. NO: __) (SEQ. ID no: 2490)
 5'-TC GGC CTG GTC C'CG G-3' (FRAG. NO: 1727) (SEQ. ID NO:1740)
 20 5'-TGG GGG TTT CCC TTG-3' (FRAG. NO: 1728) (SEQ. ID NO: 1741)
 5'-TG GTC CCG GBG F GC -3' (FRAG. NO: 1729) (SEQ. ID NO: 1742)
 5'-GCG CTC CGC CTG GTC CCG G-3' (FRAG. NO:1053) (SEQ. ID NO:1061)
 5'-GGG TCT CCT CTT TTT GTT GC-3' (FRAG. NO:1054) (SEQ. ID NO:1062)
 5'- TTG CGC CTC CTG GGG GT CC-3' (FRAG. NO:1055) (SEQ. ID NO:1063)
 25 5'-CTC TGT TCT TGT 'TTT GGG GGC-3' (FRAG. NO:1056) (SEQ. ID NO:1064)
 5'-GGG CCC GGC CGT TGT CTT G-3' (FRAG. NO:1057) (SEQ. ID NO:1065)
 5'-GTT TGG GGG TTT CCG TTG-3' (FRAG. NO:1058) (SEQ. ID NO:1066)
 5'-GGG TTC TCC TGG CCC GGG CCT TGC CC-3' (FRAG. NO:1059)(SEQ. ID NO:1067)
 5'-GGC CGT GGT CCC GGC TTC GTT GC-3' (FRAG. NO:1060) (SEQ. ID NO:1068)
 30 5'-CCT GTC TCC GTC PCG GCT CTT CTG-3' (FRAG. NO:1061) (SEQ. ID NO:1069)
 5'-GGG CCT TGC GCT GTC TTT GGT G-3' (FRAG. NO:1062) (SEQ. ID NO:1070)
 5'-GCB CCG TCC BGT GBT GGT GCG GTB CTT GTC GCT GCB GCG CTC GGC CTG GTC CCG GBG BGC -3' (FRAG.
 NO:1063) (SEQ. ID NO:1071)

Human Intercellular Adhesion Molecule-1 (ICAM-1)

Nucleic Acid and Antisense Oligonucleotide Fragments
 35 5'-GCG CGG GCC GGG GGC TGC TGG G GGT TGG CCC GGG GTG CCC C GCC GCT GGG TGC CCT CGT CCT CTG
 CGG TC GTG TCT CCT GGC TCT GGT TCC CC GCT GGC CCC GTT GTC CTC TGG GGT GGC CTT C GCT CCC GGG
 TCT GGT TCT TGT GT TGG GGG TCC CTT TTT GGG CCT GTT GT GGC GTG GCT TGT GTG TTC GGT TTC TGC CCT
 GTC CTC CGG CGT CCC CGG BGC CTC CCC GGG GCB GGB TGB CTT TTG BGG GGG BCB CBG BTG TCT GGG CBT
 40 TGC CBG GTC CTG GGB BCB GBG CCC CGB GCB GGB CCB GGB GTG CGG GCB GCG CCG CGG GCC GGG GGC TGC TGG
 GBG CCB TBG CGB GGC TGB G-3' (FRAG. NO: 1730) (SEQ. ID NO: 1743)
 5'-GGG GGC TGC TGG G-3' (FRAG. NO: 1731) (SEQ. ID NO:1744)
 5'-T GTC CTC CGG CCT CCC-3' (FRAG. NO:1732) (SEQ. ID NO:1745)
 5'-G CCB TBG CGB GC C TGB G-3' (FRAG. NO: 1733) (SEQ. ID NO: 1746)
 45 5'-CTC TGG GGT GGC CTT C-3' (FRAG. NO:1734) (SEQ. ID NO:1747)
 5'-GCG CGG GCC GGG GGC TGC TGG G-3' (FRAG. NO:1064) (SEQ. ID NO:1072)
 5'-GGT TGG CCC GGG GTG CCC C-3' (FRAG. NO:1065) (SEQ. ID NO:1073)
 5'-GCC GCT GGG TGC CCT CGT CCT CTG CGG TC-3' (FRAG. NO:1066) (SEQ. ID NO:1074)
 5'-GTG TCT CCT GGC TCT GGT TCC CC-3' (FRAG. NO:1067) (SEQ. ID NO:1075)
 50 5'-GCT GCG CCC GTT GTC CTC TGG GGT GGC CTT C-3' (FRAG. NO:1068) (SEQ. ID NO:1076)
 5'-GCT CCC GGG TCT GGT TCT TGT GT-3' (FRAG. NO:1069) (SEQ. ID NO:1077)
 5'-TGG GGG TCC CTT TTT GGG CCT GTT GT-3' (FRAG. NO:1070) (SEQ. ID NO:1078)
 5'-GGC GTG GCT TGT GTG TTC GGT TTC-3' (FRAG. NO:1071) (SEQ. ID NO:1079)
 5'-TGC CCT GTC CTC CGG CGT CCC-3' (FRAG. NO:1072) (SEQ. ID NO:1080)
 55 5'- CGG BGC CTC CCC GGG GCB GGB TGB CTT TTG BGG GGG BCB CBG BTG TCT GGG CBT TGC CBG GTC CTG
 GGB BCB GBG CCC CGB GCB GGB CCB GGB GTG CGG GCB GCG CCG GCC GGG GGC TGC TGG GBG CCB TBG CGB
 GGC TGB G-3' (FRAG. NO:1073) (SEQ. ID NO:1081)

Human Vascular Cell Adhesion Molecule 1 (VCAM-1)

Nucleic Acid and Oligonucleotide Fragments
 60 5'-CCT CTT TTC TGT TTT TCC C CTC TGC CTT TGT TTG GGT TCG CTT CCT TTC TGC TTC TTC C C CTG TGT CTC

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CTG TCT CCG CTT TIT TCT TC GTC TTT GTT TTC TCT TCC TTG CTG BGC BBG BTB TCT BGB TTC TGG GGT
GGT CTC GBT TTT BBG GCT TGB GBB GCT GCB BBC BTT BTC CBB BGT BTB TTT GBG GCT CCB BGG BTC BCG
BCC BTC TTC CCB GC C BTT TTG BGT TGC TGT CGT-3' (FRAG.NO:1735) (SEQ.ID NO:1748)

5' -C TGT CGT-3' (FRAG. NO:1736) (SEQ. ID NO:1749)

5 5'-TGC TTC TTC C-3' (FRAG. NO:1737) (SEQ. ID NO:1750)

HSVCAM1AS1: 5'-CCT CTT TTC TGT TTT TCC C-3' (FRAG. NO:1074) (SEQ. ID NO:1082)

HSVCAM1AS2: 5'-CTC TGC CTT TGT TTG GGT TCG-3' (FRAG. NO:1075) (SEQ. ID NO:1083)

HSVCAM1AS3: 5'-CTT CCT TTC TGC TTC C-3' (FRAG. NO:1076) (SEQ. ID NO:1084)

HSVCAM1AS4: 5'-CTG TGT CTC CTG TCT CCG CTT TTT TCT TC-3' (FRAG. NO:1077) (SEQ. ID NO:1085)

10 HSVCAM1AS5: 5'-GTC TTT GTT TTC TCT TCC TTG-3' (FRAG. NO:1078) (SEQ. ID NO:1086)

CTG BGC BBG BTB TCT BGB TTC TGG GGT GGT CTC GBT TTT BBBB GCT TGB GBB GCT GCB BBC BTT BTC CBB
BGT BTB TTT GBG GCT CCB BGG BTC BCG BCC BTC TTC CCB GGC BTT TTG BGT TGC TGT CGT(FRAG.
NO:1079)(SEQ. ID NO:1087)

Human Endothelial Leukocyte Adhesion Molecule(ELAM-1)

Nucleic Acid and Antisense Oligonucleotide Fragments

15 5'-BBG TGB GBG CTG BGB GBB BCT GTG BBG CBB TCB TGB CTT CBB GBG TTC TTT TCB CCC GTT CTT GGC TTC
TTC TGT C CGT TGG CTT CTC GTC CC TGT GGG CTT CTC GTC CC CCC TTC GGG GGC TGG TGG GGC
CGT CCT TGC CTG CTG G GTT CTT GGC TTC TTC TGT CCG T TGG CTT CTC GTC CC TGT GGG CTT CTC
GTT GTC CC CCC TTC GGG GGC TGG TGG GGC CGT CCT TGC CTG CTG G CCTGAGACAG AGGCAGCAGT

20 GATAACCACCA TGAGAGATCC TGTGTTGAA CAACTGCTTC CCAAAACCGGA AAGTATTCA AGCCTAAACC
TTTGGGTGAA AAGAACTCTT GAAGTCATGA TTGCTTCACA GTTTCTCTCA GCTCTCACTT TGGTGCTTCT
CATTAAGAG AGTGGAGCCT GGTCTTACAA CACCTCCACG GAAGCTATGA CTTATGATGA GGCCAGTGCT
TATTGTCAGC AAACGTACAC ACACCTGGTT GCAATTCAA ACAAAAGAAGA GATTGAGTAC CTAAACTCCA
TATTGAGCTA TTCACCAAGT TATTACTGGA TTGGAATCAG AAAAGTCAAC AATGTGTGGG TCTGGTAGG

25 AACCCAGAAA CCTCTGACAG AAGAACCCAA GAACTGGGCT CCAGGTGAAC CCAACAATAG GCAAAAGAT
GAGGACTGCG TGGAGATCTA CATCAAGAGA GAAAAAGATG TGGGCATGTG GAATGATGAG AGGTGCAGCA
AGAAGAAGCT TGCCTATGC TACACAGCTG CCTGTACCAA TACATCCTGC AGTGGCCACG GTGAATGTGT
AGAGACCAC TAAATTACA CTTGCAAGTG TGACCCCTGGC TTCAGTGGAC TCAAGTGTGA GCAAATTGTG
AACTGTACAG CCCTGGAATC CCCTGAGCAT GGAAGCCTGG TTTGCAGTCA CCCACTGGGA AACCTCAGCT

30 ACAATTCTTC CTGCTCTATC AGCTGTGATA GGGGTTACCT GCCAAGCAGC ATGGAGACCA TGCAGTGTAT
GTCCTCTGGA GAAATGGAGTG CTCCATTCTC AGCCTGCAAT GTGGTTGAGT GTGATGCTGT GACAAATCCA
GCCAATGGGT TCGTGGAAATG TTTCCAAAAC CCTGGAAGCT TCCCATGGAA CACAACCTGT ACATTGACT
GTGAAGAAGG ATTGAACTA ATGGGAGCCC AGAGCCTTCAGA GTGTACCTCA TCTGGGAATT GGGACAACGA

35 GAAGCCAACG TGTAAAGCTG TGACATGCG AGGCCGTCCGC CAGCCTCAGA ATGGCTCTGT GAGGTGCAGC
CATTCCCCCTG CTGCAGAGTT CACCTTCAA TCATCCTGCA ACTTCACCTG TGAGGAAGGC TTCATGTTGC
AGGGACCAGC CCAGGTTGAA TGCACCACTC AAGGGCAGTG GACACAGCAA ATCCCAGTT GTGAAGCTTT
CCAGTGCACA GCC'TGTCCA ACCCCGAGCG AGGCTACATG AATTGTCTTC CTAGTGTCTC TGGCAGTTTC
CGTTATGGGT CCACCTGTGA GTTCTCTGT GAGCAGGGTT TTGTGTTGAA GGGATCCAAA AGGCTCCAAT

40 GTGGCCCCAC AGGGGAGTGG GACAACAGAGA AGCCCACATG TGAAGCTGTG AGATGCGATG CTGTCCACCA
GCCCCCGAAG GGT TGGTGA GGTGTGCTCA TTCCCCTATT GGAGAATTCA CCTACAAGTC CTCTTGTGCC
TTCAGCTGTG AGGAGGGATT TGAATTATAT GGATCAACTC AACTTGAGTG CACATCTCAG GGACAATGGA
CAGAAGAGGT TCCCTCCTGC CAAGTGGTAA AATGTTCAAG CCTGGCAGTT CCAGGAAAGA TCAACATGAG
CTGCAGTGGG GAGCCCGTGT TTGGCACTGT GTGCAAGTTC GCCTGTCCTG AAGGATGGAC GCTCAATGGC

45 TCTGCAGCTC GGACATGTGG AGCCACAGGA CACTGGTCTG GCCTGCTACC TACCTGTGAA GCTCCCACGT
AGTCCAACAT TCCCTTGGTA GCTGGACTTT CTGCTGCTGG ACTCTCCCTC CTGACATTAG CACCATTCT
CCTCTGGCTT CGGAATATGCT TACGGAAAGC AAAGAAATTG GTTCTGCCA GCAGCTGCCA AAGCCTTGAA
TCAGACGGAA GCTACCAAAA GCCTTCTTAC ATCCCTTAAG TTCAAAAGAA TCAGAAACAG GTGCATCTGG
GGAACTAGAG GGA'TACACTG AAGTTAACAG AGACAGATAA CTCTCCTCG GTCTCTGGCC CTTCTTGCT
ACTATGCCAG ATGCCTTTAT GGCTGAAACC GCAACACCCA TCACCACTTC AATAGATCAA AGTCCAGCAG

50 GCAAGGACGG CCTCAACTG AAAAGACTCA GTGTTCCCTT TCCTACTCTC AGGATCAAGA AAGTGTGTC
TAATGAAGGG AAAGGATATT TTCTTCCAAG CAAAGGTGAA GAGACCAAGA CTCTGAAATC TCAGAAATTCC
TTTTCTAACT CTCCCTTGCT CGCTGTAAAA TCTTGGCACA GAAACACAAT ATTGTGTTGGC TTTCTTCTT
TTGCCCTCA CAGIGTTCG ACAGCTGATT ACACAGTTGC TGTCTAAAGA ATGAAATAATA ATTATCCAGA
GTTTAGAGGA AAAAATGAC TAAAAATATT ATAACCTAAA AAAATGACAG ATGTTGAATG CCCACAGGCA

55 AATGCATGGA GGG'TGTTAA TGGTGCAAT CCTACTGAAT GCTCTGTCG AGGGTTACTA TGCACAATT
AATCACTTC ATCCCTATGG GATTCACTGC TTCTTAAAGA GTTCTTAAGG ATTGTGATAT TTTACTTGC
ATTGAATATA TTAAATCTT CCATACTCT TCATTCATA CAAGTGTGGT AGGGACTTAA AAAACTTGT
AATGCTGTCA ACTATGATAT GGTAAAAGTT ACTTATTCTA GATTACCCCC TCATGTGTTA TTAACAAATT
ATGTTACATC TGTITAAAT TTATTCAAA AAGGGAAACT ATTGTCCCT AGCAAGGCAT GATGTTAAC
60 AGAATAAAGT TCTGAGTGGT TTTACTACAG TTGTTTTTG AAAACATGGT AGAATTGGAG AGTAAAAACT
GAATGGAAGG TTTGTATATT GTCAGATATT TTTTCAGAAA TATGTGGTTT CCACGATGAA AAACCTCCAT

	GAGGCCAAC	GTTTGAACT	AATAAAAGCA	TAATGCAA	CACACAAAGG	TATAATTAA	TGAATGCTT
	TGTTGGAAA	GAA'ACAGAA	AGATGGATGT	GCTTGCATT	CCTACAAAGA	TGTTGTCAG	ATGTGATATG
5	TAAACATAAT	TCTIGTATAT	TATGGAAGAT	TTAAATTCA	CAATAGAAAC	TCACCATGTA	AAAGAGTCAT
	CTGGTAGATT	TTTAACGAAT	GAAGATGTCT	AATAGTTATT	CCCTATTGT	TTTCTCTGT	ATGTTAGGGT
	GCTCTGGAAG	AGAGGAATGC	CTGTGTGAGC	AAGCATTAT	GTTCATTAT	AAGCAGATT	AACAATTCCA
	AAGGAATCTC	CACTTTCAG	TTGATCACTG	GCAATGAAAA	ATTCTCAGTC	AGTAATTGCC	AAAGCTGCTC
	TAGCCTTGAG	GAG'GTGAGA	ATCAAAACTC	TCCTACACTT	CCATTAACCT	AGCATGTGTT	GAAAAAAA
	GTTTCAGAGA	AGTIC'TGGCT	GAACACTGGC	AACGACAAG	CCAACAGTC	AAACAGAGAT	GTGATAAGGA
10	TCAGAACAGC	AGAGGTTCTT	TTAAAGGGGC	AGAAAAACTC	TGGGAATAA	GAGAGAACAA	CTACTGTGAT
	CAGGCTATGT	ATGGAATACA	GTGTTATTT	CTTGAATT	GTTCAGTGT	TGTAATATT	TATGTAAC
	GCATTAGAAA	TTAGCTGTG	GAAATACCG	TGTGGTTGT	GTTCAGTT	TATTGAGAAT	TTTAAATTAT
	AACTAAAAT	ATTTATAAT	TTTAAAGTA	TATTTTATT	TAAGCTTATG	TCAGACCTAT	TTGACATAAC
	ACTATAAAGG	TTGACAATAA	ATGTGCTTAT	GTTC GATCAAAT	TTTACCTATT	ATGCATTGTA	TATATAAATA
	AGTATATAAA	TGCAACACAA	GACACAGCAA	TGATGGTGA	CAGTCTCAT	ACAATATAT	GGATGAATCT
15	CATAAAATGC	TGAGTTAAAG	AAATCAGACC	AAAGAACATA	TACTGAAAGA	TTCTCTCAT	ATACAAAGTT
	CAAAAATAGG	TGGACCAATT	CATGGTGGT	TTAGAAATCA	GAAGAGAGGC	TACCTTGTG	GGGAGGGGAC
	AGTTTAATGC	CCAC AAGCGG	TAATAAAGGA	ATCCCTCTGGG	GAGTGGTAAT	GATCTGGATG	CTGGCTACAG
	GATGTGTTGG	TTGTAAAAT	GCATTTTTT	ATATCTAGCT	TTTCCATGT	GTATATTATA	CTTCAAAGAA
	GTTCAAGTAA	TAATTCTCA	TGTCACTGTA	GAGTAGCTA	GTTCAGCCC	GCAACCTCT	GGCTTAATCT
20	TGTTTACCT	TAAGCCATCA	GTCATTACA	AGTAGGAAAA	TTCACAGGG	AAGTTAGAGT	ATAAAATCCA
	GAATGAAGGT	TTACTGGGT	AGAGTCTCTC	CATTTCAA	AGCCCGTTA	TTTCTTGATT	CCAGTTCTTA
	AGAAGTCTCA	GCA' TGTGTC	TTTTCATGT	ATCTTACAAG	AAGACAGCAT	GTGCTCTAA	CACCTGATAC
	ATTGTATCTA	CCAC CACTTG	GTAAACAGAA	AAGAACCCAA	TTTTCTTGT	AGGAGAAATT	TGGTGCCTAT
	TTCCTACCAG	GCAC CAATAA	GTGGGACCAA	TAGGTGGGAT	TAAGATACA	GTAGAAAGTA	TTTAAAAC
25	GCCAGGGGGC	AATAGTCTGA	AAATAAGTAA	ATTGGTGTCA	TAGAATGGAA	GTTCACAGGCT	TCTTCTTTT
	TTCCCACAAG	ATC' GCTCCT	TGAGCCCTA	GAGACTTTT	TGTCTGTAC	TGTTTCTTCA	TTCTCATCT
	GCAGAGCCAG	CCCT'GAGAAG	TGCA GACCAA	AGCCAGGGAA	GGCTCTGAA	AGATGTACAA	ATGGAAGTC
	CCTTAATAAC	CTCTGACTGC	TGCGCATAAT	ACATTCTACT	CAAAGAGGG	GTAAACAAAT	GGAACAGAA
	ACAGAGGCCA	GAAATAATGC	TGAACACTGA	CAACCATCTG	ATCTTGCAC	AAATCCACAA	AAACAAGCAA
30	TGGAGAAAGG	ACTCCTATT	CCATAATGGT	GCTGGGATAA	CTGCTAGCT	ATATACAGAA	GATTGAACCT
	GGGCCCTTC	CTTACATCAT	ATACAAAAAA	TAACTCAAGA	TGGAGTAAAG	ACTTAAATCT	AAAACCAAAC
	ACTATAAAA	CCCT'GGAAGA	TAGCCTGGG	AATACCATT	TGGACATAGG	ACCTGGCAAA	GACTTCATGA
	CAAGACACCA	AAAGCAATAG	CAACAAAAC	CAAATTGACT	AATGAAACTA	ATGAAACTCT	TTAGTTGTAC
	AACAGATAGT	TTATCTGTAC	AACAAAATAA	ACTATCAACA	GAGTAAACAA	CCTACAGAAAT	GGAAAATT
35	TTGCAAACT	ATGCATCTGA	CAAAGGCTA	ATATCCAGAA	TCTATAAGGA	ATTTAAACAA	ATTTACAAGC
	AAAAAAATGA	CCTCATTAAA	AAAGTGGGCAA	AGGACATGAA	CAGATGCTT	TCAAAATAAG	ACATTCACAC
	ATCCAACAAAC	CATA TGAAA	GATGTTAAC	ATCACTAATC	ATTAGAGGAA	TACAAATCAA	AAGCATAATA
	AGATACCATC	TAATACCAGT	AGGAATGACT	ACTATTAAAA	AGTCAGACAA	TAACAGATGC	TGGTGAAGGT
	TGTGGAGAAA	AGGGAATGTT	TATGCACTGC	TAGTGGGAT	GTAAACTAGT	TCAGCCATTG	TGGAAGAGAG
40	TGTGGTGATT	CCTCAAGAA	TGTAAAACCG	AACTGCCTT	CAATCCAGCA	ATCCCATTAT	TGGATATACA
	CCAAAAGGAA	TAG'AAATTGT	TTTACCGTA	AGGCGCATGC	ATGCATATGT	TCATTACAGC	ACTATTTACG
	ATAGCAAAGA	CATGGAATCG	TCTAAATGCC	CATCAGTGGT	AGACTAGCTA	AAAAAAA	AATGTGGTAC
	ATATACATCA	CAGA'ATAGTA	TGCAGCCATA	AAAATGAACA	AGATCATCAT	GTCCTTGCA	GCAACATGGA
	TGTAGTTGGA	GGCC'ATTATC	CTAAGCAAAT	TAATGCAGGA	ACAGAAAGCC	AAATACCACA	TGTTCTCATT
45	TATAAGTGAC	AGCT'AAATAT	TGAGTACACA	TGGACACAAA	GAAGGGAAAC	ATAGACATGG	GACCTACTTG
	AGAATAGAGG	GTGGGAGGGAG	GGTGAGGATC	AAAAAGTACC	CATAGGACAC	TGTGCTTATT	ACCTGGGTGA
	TGAAATAATT	TGCAACACAA	ACCCCTGTGA	CACACAATT	ACCTATATAG	AAAACCTGTG	CATGTACCCC
	TGAACCTAAA	AGT'AAATGGT	GGGGGGGTGG	GGTTAAGCTA	CTTGTGTTA	TAATCTGAG	CATTCTATT
	AAAATAAAAT	ATT'ACCTCA	TTAGAGTAAT	TAACATTAT	TAAGCAAAGA	GCCAAGTACC	TTACACACAT
50	GATGTTTAAT	CTCA CAATGA	TCTTAATCT	CATAACAACC	GTCCATTGTA	TGTACATATG	TGGAAATTGA
	GCCTTGAGA	GAT'AAATGC	ATGGGGCATG	CCATTGACT	AGAAACTGG	AGCATCAGGA	TTTAAACTCA
	GTTCTGAATG	GTTTGTAGG	CTTGTGTTT	TCCACATTAT	AGCATGGCCT	GCCATGAAGA	ACAGGTCTT
	TCTGGTGT	GTCTGTGTT	GTTCAGTGA	AGCAAATATT	TATTTAAATA	TTCAAGATAT	GCTGTTAAAT
	TTTTACTCAA	AAA'TTGAGT	ACAGTATGGA	TCTTCTGAAG	CCAAATAACT	CTTATTCAAT	GCTTAGTTGA
55	GAAATTAT	GGAGTAGTTC	TCAATTTTA	TGTAGTTCA	CTGCAAAGGT	AAGTCTTATG	GAAAGATTCA
	CTGTAATT	TTTCCTCAT	TTGGACATCA	GCTTTTCTT	TTCCTCAGAC	CCGCTGAAAG	ATAATTTTA
	AAATAAAAAC	CTTGTGTTTA	TATCAAGTGG	GGACATT	TCCAAATGAA	AACCGTGTAT	TCATTCTTATA
	TGATAAAAATC	AATGTTATTA	TTTTAAAAT	TTGATTAA	AAATCATTAA	AAATAAATT	TCAGATATT
	CCTGAAATT	TACCATCCAG	AGATAATAGT	GCTTAAAGAT	TTGATATATA	GACACACACA	CATATATACA
60	TATATATCAT	CCTTAACATTC	TTTGATAAA	TGTATATAA	GTTCATTA	AAAACCTAGGA	GATTAATGCC
	CTTTGAATGA	AAA'AAATAC	AATGTGTATG	CTTTAACATC	TTGCCTTAC	TTTATAACAT	TTATCACAGC
	AGTCATGAGA	TAA'GATTTA	CATGGTCATT	GTAGTAAGC	TAATAGCTAA	GTGCATGAAC	TCTGGAGCTA

	GCCTCCCTGG	ATTITAATCC	CAGATCTGTC	ACTGACCAGC	TGAGCAATAC	TAGGTAATT	GCTCTTGTTC
	CTTAGTTCT	TCATCTGTAA	AATAGAGATA	AAAATAATAT	CCACCTCAT	GGATTGGTGT	GAGCATTAAA
	TGAGCATACG	TATCTAGGCC	ACTTAACAAC	AATGCCCTCA	CATACTGAAC	ACAAATATAC	GAGCTGTTGT
	CTTATTGGC	TCATGTTTT	CCTACCACCA	AGCCGCATGC	ATGCAAGGAC	CATGTTGGTT	TTGTTCCACA
5	TTGCATCCC	AACCTGGTAT	ACAGTGTGCA	TTCAATAGTT	GTTGACTATT	ATTACTAGTG	GCATTTAAC
	AATATCTGTT	AAA1GAGTGA	AGAAATACCC	ATTACTGCA	AGTGTGCTA	ATATTGATGG	CATAATGGGG
	GAAACTCAA	CTCTGGAGTC	AAACAGGTT	TAAAACCTTA	TTCCCTCATC	CTCAGTTATT	GACGTTTTT
	TTTGGCAGG	TGTCGTGTG	GGACAACCTA	TTGAACCTTT	CTGAATTTC	AGCTCGCAT	ATATAAAATA
	GAGATAGTGA	TTCAATTCTG	CAATGTATGG	ATTTGAGACA	ATTGTGTAAG	TTTATCAATA	AATAGTAGCT
10	ATTTTGAT	AAGTATTACA	TATAATATCC	AGGGCACTGC	TTTGCAATA	CCAAAAGGGG	CACCAATTCTAT
	GCAGAATACA	ACA'AAATGG	TGTCCCTGG	GCAGTGCAGT	ATAGGAACCC	TGAGGGGACC	TACAGTATAC
	TTTATAGITC	ATACATTACA	AATTATCCT	TTATCAGAGT	CTCTCAAGGT	TGGATGTATT	TGAGGTCCAT
	AAGAGCAATT	TAGGATTAAAC	AGTAGCTGCA	GAAACCATCT	GCAGTGTAT	TCTCATTTA	AATCCGCAGGG
	AAAGAAAGACA	GCTATAAACT	TGGGACCTGG	GTTAAGCAT	TTTAAATGCC	AAGTCACCA	TTTCTAAAAA
15	CACAACAAAT	ACCC'AGTGAG	AGAGGGAGAA	GGGAAGTAAA	TGCCTCTGAA	TAAGCAAGTT	AATGTCAGTA
	GTTGTACTGT	ATGCATATTG	ATGAACAATA	GAGGAACCAA	TGTCCAATCA	GATGAGCAGG	ATATTGGCA
	ATAACAAGTT	GCCCTTGAGG	AAAATGATT	TTCTTGGCAA	GTTCTTATC	AGCATTACAA	AGCTAAAAGC
	TACGCTTATC	ATCACTTATA	CTAGCATACC	CTGTTGTGCA	AATGCTGTCT	GTGTTGCA	CTGCTATTGT
	TGATGCTTGG	TGCA-TGAATC	AGGACTCCAG	CCCACAAAGT	TTCCCAGAAC	TTTCTTATGG	CCATCATCTT
20	TAAGTGTCTG	GTGAACAGTC	ATAGTTGGT	ACACAAAAGG	GTCAACCTGG	GGGATGGCTA	GGGTTTGACT
	CAGTCGTTAC	ATTCAATAG	AGCAGGAAGG	GGAAATGGTG	GCTGTGTAACC	TCAGGGAATT	TTGCCAGTTG
	GTCCACCCCC	CTCTCTCTCT	CCTGCTCTGA	GGAAAGTGGCA	CAGCCTAGAA	CAGCACCCACA	GGTGAGAGAA
	ATGCAAACCC	TAACCAGAGA	AGCAGACTCT	TTGCCAGTAG	TAATAGTTCA	GGACCAACCAC	CAGCTTTAT
	TAAAATTTT	AATAACACTC	AAAGTATTGGC	AGAAAGAAAT	AATCTTGGGT	TAACATATAAC	TAGAATATTG
25	ACTCTCCTC	TGTGAAAGAA	TCAGCCAATC	ACATTTGTTT	ACATCAGTTC	CCCTGAAGAA	AAAAATACAA
	CTGATGTTGC	AGCAAGACAA	ATTAAAGCTA	GATGTAATAA	ACTTCCTTA	GCCTGAATG	CTAGGCTAAT
	TACATATTGG	AACTATTTT	TCAGGGAAAGA	ATTGTGTAAGG	GTTTCAGGG	AGAATTCTGA	AGAAAATATA
	GAGCTGAAAT	GATCTTGAG	CTCACTGAAA	CTGCAGGGTT	TAGATCCACA	CTGATACTCG	TTCTATTATC
	ACTGTAATGA	AGGCTGATGG	AATAAGTAAA	AATGTTTGT	ATTAGTATGT	TTTACACTT	ATTGCAAGG
30	CATAAAATAGG	TTAGGTTTTG	ATCTTAATT	AATTCTAAC	TGTATTGTC	ACAAGCTGTG	AGCAGTTTC
	AGGAGTTAGG	TATCTGGCCA	TGACTGATT	TTCAGGAGTT	AATCATCTGG	TAGAAGGGTC	ATACACAATA
	GGAAGATGTG	TGTGACAGGT	TGTGATCATT	ACTATAATCA	CACAGAGAGC	TGTAGAATT	TAGGCTGGCA
	GGGTGGCTCA	CGCTGTAAAT	CCCAGCACT	TGGGAGGCCA	AGGCAGGCCG	ATCAAGAGGT	CAGGAGATGG
	AGACCACCT	GGCTAACACG	GTGAAACCCC	GTCTGTACTA	AAAATACAAA	AAAAAAA	AGCCAGGGT
35	GGTGGTGGGC	GCCIGTAGTC	CCAGCTACTT	GGGGAGCTGA	GGCAGGAGAA	TGGCGTGAAC	CCGGGAGGTG
	GAGCTTGAG	TGACCCGAGA	TCGCATCACT	GCAATCCAAC	CTGGGCGACA	GAGGGAGACT	CAGTCTCAA
	AAAAAAAAAA	AAAAAAAGTC	ATGTTAGATC	CAGAGGGGTA	GCAACTGGG	CTGGGCTGTC	AGTCAACTCA
	GTCAACTCAG	TCAACTCTGC	TCCCCCACAG	GAGATGCCAG	TGATGCATT	TCATGGCCAA	CATTGTCAGT
	CAGCATCATT	GAATTACTCC	TGATTATAGA	GACACAGCTG	CAAACGATT	CCCATTAAAT	ATGATGTTTC
40	TTGCAATGTT	TGGAGGTAC	TCCTTTTAG	TAAGGGAAAT	CCCCTCTTCT	GGCTGCTGA	AAGTTTTTC
	TTTCCATT	AAAAATCGTG	AATTCTTT	TGCAATATTG	AGGTGGTTAT	ATGGTTCTC	TTCTCTAA
	TGTTAATATG	GTGATTTAAT	GGTTAGAAAT	TTCTTAATGT	AAATTCCACT	CATATTGCAG	AAATAAAACCT
	AAACTGAGCA	TGAAGCTATA	TTTTTATTT	GCTTCTATAT	TTGGTTGCTA	TACAGTATTA	TGTTTAAGAT
	TTGTTACAT	ATATTGTA	ATGGGATTGG	ACTATTTTC	CTTCTTGGCCG	ATTTTTATCT	GGTTTTAAA
45	TTAAGGATAT	TTTAGACTTA	TGAAATATT	GGCAAACAA	CCTTGGCAAG	TAATTTTTTG	GGGAATTGTT
	TTGGCTATT	TTGAGTATTA	CCCAATATAT	TTTAATTAAG	TTATTCTTAA	TGTTTCTTA	ATTAACAAAAA
	TTACCTACTC	TAGAGATATT	CTTATGTAC	TCCAGATTT	GTCTATTAT	ACCACTTTTC	TTTTTCCCTC
	GATGAGTGTG	ATAAGATGTT	ATCTATT	TTATCTTCTT	TGATCTTCTC	TTATCCTT	TTTCTATTAA
	CTTCTGAAGT	TTATTATTTT	CTTTTTCCA	CTTCCTTATG	GTTTATTCTT	TCAATTTC	TCTAACTTC
50	TAAGTGGGT	GTAAATT	TAGCTTGCTT	TGCTTTTTA	GGATAAGCAT	AAAAACTACA	AATTTCCCTT
	GTTATTCTT	TGCTGCCACCC	CAAATTGTT	ATATTCTAT	TGTCTAATT	CTATTCAATT	AGAATACCTT
	AAAGTTCTT	TTGGTTTTT	AAAAACTAAC	TTTTAAATT	GACAAATAAA	AATTGTGTAT	ATTATTGTTG
	CACAGCATAT	GGCTTGAAA	TATATGTACA	TTGTTGAATG	GCTAAATT	GCTTATTAAAT	GTATGCATTA
	TCTCACACAT	TTATCATT	TTGTGGTGAG	AGCTATGTGA	CTTTGAACT	TATGAGTTAT	TTAAATATT
55	TTAAATTATT	AAGCATATTG	GGATTAAAG	TAATTACCT	TTTATTATT	AACTTATAAC	AAGTAGAACAA
	GTAACTCTG	ATGATCTC	ATCATTGAAA	TTTATTGACA	TTTGCTTCAT	AGTCTATTAT	ATGGTCTACT
	TTGTTCATG	TTACATCTGT	AGTGAATTG	GCTAATAGTT	GAGTAAAGTA	CACATATGTC	TATGAAATCA
	AGTGTAAATCC	AGAGAAAAAG	AGAAATTAC	TGAATATATT	GTTCTAGGTG	CTATTATATG	TTGTCATGTT
	TAATCCTCAC	CACAATTGTA	TGAGGCAGCC	ATAATTAAATT	CCACTTACA	CATGAGGAGC	CTGAGGGTTA
60	AAAAAAAGC	TAGCTCTACT	ATTGTAAAG	AATGAAGCAA	AGATACAAAT	GAAGGCCAC	ATATCCTATA
	ACTAGATATT	TAACCATTT	AATTCAAGCT	TTAAAACCTGC	TAAATAAAAT	GTGCTCAAT	TTCTATATTG
	ACAGACATAC	CTTCCTAATG	AGCTGGGTT	CGAATTAGA	AACTTTGAT	GCTTCAGAGT	CCACACTGAA

	ATGTGGAGGC	ACA'TAGTGAG	TTGGTCCCCA	GCCTTCAGTC	CACCCACCTT	CTCTTACTA	AATCACCTT	
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	ACAGAGACAC	AGC/CATCCT	CAGGAAAACC	TGGAAAAGTC	CATACAAGTT	CTGGAAGCAA	GCTTGGGACG	
5	GTTTCAGTAG	TGTC-GTCTAT	AAGGGAGGCC	TCAGAAGACA	GGTTTCTTA	ATTCTGTGAA	CTTCTCCCAC	
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	GGTCTTCGTA	AATT'AATAAT	AATAATAACT	ATTACCATTA	TTATACCGAGT	AGCTGTCTT	TATTTAGTGC	
10	TTATTATTG	CCACTCACTG	TTCTAAATT	TTTACATGTA	TTATACAACT	GCCATATAAC	TGCCATATGA	
	GGGATGTACC	CTCA.TTGTCA	CCATTTTACC	GATGAGAAAA	CTGGCATAAA	ACGTTAAAGT	AACTTGTCCA	
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	CCTAAGTCAT	AGAGTCTTTA	AGAATCAGAG	CTAGAAGGAA	TCTTAGATGT	TATCTAGTC	GCCTCTCCC	
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15	GCTTTAACTT	TTCTCAGAAC	AAGAAATCCT	TTTGGTTTT	AATCTATATG	CACATCTGTA	TTTTCTCAA	
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25	TGAATACTTT	GTACACCTC	CTCCCAGCCA	ACCCCCCCCC	TCCCTGACCC	CAACTAGTCA	GAGACCAAAG	
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	CCCTTCCAGA	TGCIIGGATCC	CCAGGGATAG	GAACCTGCCC	CTTATGTGTC	CATAGCCCC	GGTAGTATGT	
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	GCTTCACCA	TTTCCTAGTTC	TTCTCTCT	ACTTCATTA	CCTTCTCT	TTTTTTTT	CTTCTCATGT	
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	CCCCCTGTCAT	CCTCCTCTTT	GCTCCATGAG	AAAGATCCAC	CTATGACCTC	TGGTCCCTCAG	ACCAACCAGC
	CCAAGGAACA	TCTCACCAAT	TTAAATTGG	GTAAGTGGCC	TCTTTTTACT	CTCTTCTCCA	GCCTCTCTCA
	CTATCCCTCA	ACA'CTTTCT	CCTTTCAATC	TTGCACCAC	GCTTCAATCT	CTCCCTTCCC	TTAATTTCAG
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	GAGTCTTCC	ATCTTCTT	TTCTACTGAC	CCATCTGACC	TCTCCCCCT	TCCCCAGACT	GCTCTCTTC
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	GCCCAACAAT	TTCTCTTAA	AGAGGTGGCT	GGAGCTAAAG	GCATAGTCAA	GGTTAATGCT	CCTTTTCTT
	TATCCAACCT	CTCCCATCTC	AGTTAGTATT	TAGGCTTTTT	TTCATCAAAT	ATGAATACCT	AGCCCCACTCC
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	GGCTGAGACA	TTT'AACCAA	ATTATTGCT	TCCCTGACTA	TTCTGGACT	ACAGCCACAT	CTCATTGCTG
	CCCTTCTTCC	CAACCCAAA	GTGGCAACTC	CTTGCCACT	TCCTCTCAT	TCCCCCTACC	TTAACCCACA
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	TTAGTAGTAA	AGGTAAATAT	TCATTAGAGA	TGAGAAGAGG	AGCAAGGAAA	TGCTTCTAGC	TGGAAATCTC
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65	TCAGATTTC	ATGIGCTTAC	CACTCAGAGA	TGGTGTAAA	ATGCAGACTC	TGATTCACTA	GGTCTGAGTG
	GAGCCTGAGA	TTC'GCACCC	CTAACAAAGCT	CTTGTAGTGT	GCTTATGCCA	CTGGCGCACA	GACCCCACTT
	GGAGAAATT	TTG'GGTGCA	TACGGTCTTT	GTCTCCAGAT	CTAATGAGTC	TGAAGGACAG	TGTAGATTGA

	TTTTTTAAAT	TTA1GTTTAT	TTTAATTAA	TTTAATTAA	TTTATTATT	TATTATT	TGAGATGGAG
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	TCCACCTGCC	ACGGCCTCCG	AAAGTGCAGG	GATTACAGGC	GTGAGCCACC	GAGCCAGCT	GTAGATTGAT
	TTTGAGCACT	GGAAAGTCAA	GAATTAGAA	GGCATGCTTA	AATGAAAAGT	GAAATTGGAG	AAAATTAAA
	CTCATGAAAT	AGTGTGGTT	ATAAAACTCGT	GATAAATTAT	ATCCTGGGAT	ATAATTAAAT	GAGATGGTAA
10	CACATTAGT	TTAFAAGAAAT	AAGTGACACT	TTTTTGTGT	GACACAAC	TCTTATTCTT	GGAAAGGACA
	AGGAGAGAAT	GAAATATGGT	ATGCTTCAC	AGCACCTTC	AAAGGGAGAA	CCAGATTCTG	AGGAGCTGGT
	CTCATGATGA	ACTCTCAGGG	TAAACCACAG	TTCAGCAGCT	GCAAAATGTG	TTGCCAAAAT	AGAGACAAAA
	AAATGTTTCT	GAAACAAAAA	TTTCACATAT	GCCCTCTCT	GAGGTTGGCA	TCATATCTTC	CTGTGTATCT
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15	GCAGAAGAGT	CAAATAAAC	CAGCAAGAAA	TGAAACCACA	AATGCCAAC	GAGTCATTCA	TTCACCATTC
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	CACCCCTCCT	CAGTGCCGTC	ACACAATGGT	TTCAAGTGTGA	AAAAAAAAC	CACGTTACTG	GAAAAGGAGG
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	GTGAACCATT	AAAATTAATA	TAGCAATTG	CTTAGCATGG	TAATTAGCT	TTTGTCTAATA	TCCTTCCAGC
	CAGTCTCTCC	TCCTGTGCC	CAAGGACATC	TTAAAAAAA	AAAATCTAGT	TGATCTGCTT	CCATCTAGTG
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	AATAAAAAGA	ACCTCCACTG	ATCGTACATC	CTCATCCAGT	TACCCCTGCC	CCACTTCTCC	TTCACAGCCA
	AACATTITAA	AAGAGATGAC	TGCTTGTCT	GTCTCTACTT	TCTCATCCTC	AGTAATGTC	AATGCTTGGC
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40	ATACTTACTG	GTTCCTTGG	CAATGTTGA	AACCGTCCC	CTTTCTTGT	TTCTTGGCA	TTCATTACCC
	CACACTCTT	CTCCCTCTCC	TTCTCCCTGC	CTGGCAACAT	CTTTCTATT	CTCTTCCCT	TAGGTGACTT
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	GCCTGGTGGC	AAGACCCAAT	ATGTCCATT	AAGTGTATAT	CCCTTCCCAA	TCTGCCATCT	CATCCTACCT
	GCAGATTCTT	CCCCITGAGGG	ACAGCTGCTA	ATACTGTAAA	ACTATGTGCC	ATTACAGCTC	ACAGCATCAT
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	GCTTAGATT	CACCCTGTAG	GACAAAATGG	TAGTAGAAA	TTAATGGGTG	GATTGTATG	TATGTGTGAT
	GTGTTTAAT	TGCCTTAAAT	TGATCAGTCT	CCCTGTTAGA	TGAATAATGT	ATTGAGGGG	AGCTAATTAA
10	AAATTGTGGA	ACTCATCTAA	TAAACTATTG	CAAGAATCTA	GAAGAAAGAT	AATGACGGCA	ATGGTAGTAG
	AGTTGACAAG	TGGAGACAA	ATTAGAAAAA	CACTAAGTTG	TTAAAATGG	TAGAATGTTA	CCCTGCATAA
	ATGTTGGGGG	AGTAAAGAGA	GTCTCATACC	AGGGTGCCCA	TGTAATGGT	GATTCCACAT	ACTGAGATAA
	GAAATACGAA	GAGAAAAGCT	GACTGGGAAC	AATTGGTTT	ATAGTCTTT	AAACATCCCA	AAGGACATCC
	TTAGCATATT	TGAC TTCAGA	GCTGGAGATA	GGCTTATCAG	TCCAAGATC	ACATAGATT	GTGAGTCGC
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	GTAGAAAGAA	TGAGAAAAGA	GTGATATGAG	AGAAACCAAG	ACAAAGAAAA	GTAAAATGTT	AAAAATGAGT
	GAAATAGGCA	TACCAATAAT	TAAGGATGAG	TAAGATAGGC	ATACCAATAA	CATAAGGGTT	AAAAAAATAGA
	GTTCAAAAT	GGGGTGAGGG	TAAGGTATA	GGAGGAGTC	ATGGCCCAGG	GATCAAGTGA	AATGAGTTAG
20	ATCTATAGAT	CTA'TTCAGT	TGGTTGACAT	TTAACATGTT	TTTGGTTTA	ATTCTTATT	GTTCACAAAC
	ATTGTTTTT	AAAAAAATTA	AATTGTCCA	TTCAATTCTAG	GTCACAAGC	AAGTGCCTCA	TATATACAGG
	CATTTGTGG	ATCCCAAAGA	TGCAATGATA	AATAGGACAC	TTACTGATCT	CAAGAAGTTT	TCAGTACCG
	AGGAGACGGA	CAAGTGAACA	GATGACTCA	ACATAAGTGG	GAGAAATGAG	GAAGAAATAT	GTGGAGCTAT
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25	ATGTGCAAAA	TGAGAGAGAA	GGCCACCAGC	AAAGTCAGT	TGCTACAGAG	CACATGTGTT	AAGTGTGGAG
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	GATAAAATGGC	ATAGTTCTT	CCAGACCTTA	GAGTTCTAAT	TAATCTAAC	AGCTCATTAG	ATCGTGAGCT
	TCTTGAGAGC	GGGAATCTAC	CATGCTAATT	CCTTATGGTA	ACCCCTGACAG	CTTTTATCCC	AAACACTGTGC
	TTCTTGTTG	ACTCAAAAG	ACTTGTGAG	AAAGTGAATCG	AAACCTCATG	CTGACTTATG	AAATCTTAC
30	GGAAAGGTA	CAAATTGTG	AAAGCAGAGC	TTTCTGATCA	AAACTTCCC	TTTCTCAGAG	TGGCTAGTAT
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	TAATATTCTG	TAACACTTAT	AGGAAACTTA	GTGGCATACC	TTGAAACTCT	TGAAATTACT	TGTTTTAAT
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	CTTTATAGAA	ATCA AAGATT	AAAAGTCCA	AATTGCTAA	AACGGTAGAG	TCCAATTAT	AAGAGACCAA
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	CAGAAATATT	CATA CACCAA	AGATAGTGC	ATTTTTATAT	AAAATTATAT	AAGGTTAGAC	CAAGAAGGAA
	GCACGCAGCA	CCAATCTC	TACTTCACAA	TGTAAAAC	GAGGTGATGT	GAGCCTAAGT	TTCCAACCTGG
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	TATGGACCCA	TCAAATATGA	GGGCTTGA	GATATCTAAT	TAACACACATA	ATTACACAAAT	GACTTCATAA

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	TCTTGCAAGT	GTAITGCTCA	AGTATCTCAT	TGCAATGCTT	TTTACTCTCA	CCTCATTGAA	CCTCCAGGCC
	ATTAACACATT	TCC TATTTC	TAACCATCAG	GTTTCTCTT	ACTTGTGTTG	TTGTTTATTT	GTTTCTTTT
	TTTTTTTTT	TTTGAGACAG	GGTCTCACTC	TGTTGCCAG	GCTGGAGTGC	AGTGGTATGA	TCTCGGCTCA
	CTGCAGCCTC	CATC CCCCTG	GTTCAAGTGA	TTCTCATGTC	TCAGCCTCCC	GAGTAGCTGG	GACTACAGGT
	GCATGCCACT	ACGUCTGGCT	AAGATTGTTG	ATTTTATTA	GAGAAGGGGT	TTTGCATGT	TGGCCAAGCT
20	GGTCTCGAAC	TCCIAACCTC	AGGTGATCCA	CCTGCCCTAG	CCTCCCAAAG	TGCTGAGATT	ATAGGCATGA
	GCCACTATGC	CCCACCTGGT	TTCTCCTTAT	TTATTTCAG	TCTATGCTGC	ACTATAAAAA	CTGCCTTGAC
	AAAAATTATA	ATAGTGAGAA	AATTATGACA	GTGAAAGAGA	TCTGAATAA	TCAACCCCCA	TCTTGCCTT
	ACCTTCCAGA	CTGC'CCTTAA	TAATTCTGA	GCTTGGGCCA	AGCTATCTT	GGCAGAAATT	TAGTTTATAG
	TTTAAATGAT	AATAGCCCTT	CTCCAAAACT	AAACTGCCTT	TGTAAAACTA	ATAAAAGACC	ACCAATGAAA
25	GGTAGGAGG	ATGAGAGGAG	CCTGAATTCT	GCTAAGGTGT	AGATGTAAC	AATTACCAAC	TGTTATTCCG
	GAGGTACCAA	GAT' TGCAAC	ATCGCCAATT	ACTCCTGCAG	ATAACAGCAC	TATCATAGAA	TCTGATTGGC
	CTTTTGAGAT	GTCITTCAG	ATTCTTACAT	TTCAACTGGT	GGCTCTACCT	GGACCCATCA	ACAAGTCCG
	TGGCTCCACC	CAGAAGCGAGA	CTTAAACATGC	ACAAGGACCA	TTTCCACAC	CGCTATGATT	GCATCCCAAC
	CAATCAGCAG	CAA'CATTCC	TCTGCCCTGCC	AAATTATCCT	TGAAAAATCT	TAGCCTTAGA	ATTGGGGGG
30	AGGCTGATTT	CAG'AATAAC	AAAACCCCGG	TCTCCCATTT	GGCTGGCTCT	GCATGAATT	AATTCTTCT
	CTATTGAGT	TCCCACCTTG	ATAAAATCACC	TTTATCTGGG	CAGCAAACAA	AAGGAACCCA	TTGGACAGTT
	ACACTGTTGG	CAGATATATC	TTGCTTCCAA	AATTTGGATT	TTGTTTAATG	AATTATTTCT	GTTTCTTGA
	TATTTACAAC	TGTC AATGTT	GTGTCTGAAT	TCTCTTATT	TCTTGTGAA	AAGAACTATA	TTGCTACAGC
	CAGTACATAC	AGAT'GGATAG	CTAATTACTC	AAACACGGGG	GATGTGACCA	TCACCGCACT	GTGCAAATGA
35	ATGTTACCCA	TTGICCACCTT	TTCCCAAACCT	ACATAGTGT	ATATGGTATA	TGACCCAATC	AACGGTGGCA
	AAGCTCCAGA	AATACCACAT	AGACATCAGG	GACACTTTAA	ACTAATCAGC	CTATAGTCCT	TTTCAGTAA
	TTTCCAAACCC	TGGITGTGCA	TCCAAATCAC	TTGGTAACAT	AAAAAAAACA	AAAAAAATATA	CACGCAACAT
	TCGCTCCCAA	TCCIACTGAA	TCAGAATATT	TTGGGTTGGT	TCAGGAACAT	TCAGGAGTTT	TTCAGGGTCC
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40	CAAAGATGTA	TTACCATGTA	AACACATTCC	TAGGACCCAG	GCCCTTGAA	TTAAAGGTT	TATCTAAGTA
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	CTCTCTGTGT	ATGT' GTGTGC	ACATTAGCAT	GTACGCTTGT	GTGGATTTTT	TTTTTTTTT	TTTTTTTTTC
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50	CTTGTGTGGA	TGT TTAAGC	TCCCAGGTGA	GTGAATACAA	AACTAGATCT	TTCCCTCTG	TAGCATCTGT
	ACTGTTACT	CTA' GCATCT	CAATTTTTT	TCTTTAGTA	TCTTTCCTTT	TTCTCTCTTA	TTACTTCCTC
	TTGTGCTATT	TTT AATTCATT	CTTTTTAAA	AAATTTTTTC	CCTTTTATT	CTATTGACCT	TTAGCCCTCA
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	CATGCATTGA	TTT AATTCATT	CAATAAATAT	TTGTTGGATG	TCCACTCTGT	ATCAGGAATG	TGCTAGGTTTC
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	GGGGTGTGGGG	GGTGTGGTAT	TTTTTATAGA	AATTGTCTCA	CACAATTATG	GAAGCTGAGA	AGTCCCAGTG
	CCTGCTGTCT	ACGAGCTGAG	AACCAGGAAA	GCCAGTGGAA	TACTTCAAAG	TCCAAAGGCC	CTGGAACCAA
	GAGTGCCAGT	GTTCGAAGGC	AGGAGAAGAT	GGGTGTCCC	GCTTAAAAG	ACAGTGAATT	CACTCTTTT
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	TTATAAAAATA	TTTTAAGTTA	TAATTTAAAAA	TTCTCAATAA	AACTCAAACA	CAAACCACAC	TGGTATTTC
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5	GTATTCCATA	CATA.GCCTGA	TCACAGTAGT	TGTTCTCTCT	TATTCCCAG	AGTTTTCTG	CCCCCTTAAA
	AGAACCTCTG	CTG' TCTGAT	CCTTATCACA	TCTCTGTTTT	GACTGTTGC	TTTGTGTTG	CCAGTGTCA
	GCCAGAACTT	CTC1GAAACT	TTTTTTCA	CACATGCTAA	TTAATGGAA	GTGAGGAGA	GTTTGATTC
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10	GAAAACGTGA	GAT' CCTTTG	GAATTGTTAA	ATCTGTTAT	AAATAAACAT	AAATGCTTGC	TCACACAGGC
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	TCGTTAAAAA	TCTA.CCAGAT	GACTCTTTA	CATGGTGAGT	TTCTATTG	AATTAAAAT	CTTCCATAAT
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15	TTCAAAACGT	TTGC CCTCAT	GGAAAGTTTT	CATCGTGGAA	ACCACATATT	TCTGAAAAAA	TATCTGACAA
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	GTTGAAGGCC	GTC' TTGCGCT	GCTGGACTT	GATCTATTGA	AGTGGTGTG	GGTGTGCGG	TTTCAGCCAT
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	GTGTATCCCT	CTACTTCCCC	AGATGCACCT	GTTTCTGTAA	ATATAAACAT	GCATGTCTAC	AGAACACTTA
30	ATATTCTGCA	TACIGATCAT	GACAACAAAA	TGTACCTTCT	AACACAGACA	CTCTCACTAG	GATAGACCAT
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	ATTAAAAAAA	AAA' AAGTAA	AAAGAAAAGA	TAAGAAAATAT	AGTACAGGCC	CCTATCTCAG	AGTTCTTAGC
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	AAATGAAATT	ACACAATAAA	GCTAGATCCG	TTTCTTCCC	CTCCTTCTAC	AAAAAATAAA	GCAACTTCC
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	TTTTGAACCTT	AAAC'GATGTA	AGAAGGCTT	TGGTAGCTTC	CATCTGATTC	AAGGCTTGG	CAGCTGCTGT
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	ATGGCATGCT	TTG1ATAAGA	ATGCAACTTA	CCTGGCAGGA	ACAAATTCT	TTGCTGCAA	AGAAAAGACA
50	AACAACCATT	AAT' CAGACT	AAATGACTTT	TAAGGATATA	TTAAATCCAG	ATACAATATG	ACTTAATTCA
	TCAAGTGTG	CAAACCTGAT	GCTTCAGGGC	CTCTGTAAATA	ATCAGAGCAC	AAGCATGGCT	CTGTGGCATC
	TAGGGTAAAA	TGC' AAAGTGC	ACAGCCATCC	AAAGGGCATA	GCAGCTTCT	AATGCCAGCA	AATAGCTACG
	GGGTCACTT	GCC' CAATTCA	GCTCCCAATT	TTTCATGAGA	AGTCAAAGT	CTTAATTAA	ATGTGAGATT
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	ATTTTTATT	CCTGAAACAC	TTCCCACACT	GAGTTGACT	ACTAACTCTT	TTCTTAATAC	TTCTGCTTAA
	TTATACTGCA	TTTATCCAG	ATTCTAATT	TTGTTAAAT	CAGTAAGCAA	GACCAGTACT	TATCAATGAG
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60	CGAAGCCAGA	GGAGAAATGG	TGCTAATGTC	AGGAGGGAGA	GTCCAGCAGC	AGAAAGTCCA	GCTACCAAGG
	GAATGTTGGA	CTCA GTGGGA	GCTAAGGAAG	TAAGAGACGA	AGAAAGGTCA	TGAGGAAGAA	TTGATGTTAA
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5	CTCTGTCTCC	TTTTCAGT	TGTCAGAATT	CTACCCCTTC	CATCAACATG	CAACTTCTGT	TTTTCTCTA
	TCCCCATACA	ACTAATATT	CACAACTTGT	CAACCTGGGC	GAACCTCTG	GTTGGATAT	AATGAATAGT
	TGATTACTGT	AACAAGATAG	CTCCCCCTTT	TCCTTTTAA	TCACCAAGACA	ACCACCATCA	ATCAATGCAT
	CACCTTCACA	GGTAGGTAGC	AGGCCAGACC	AGTGTCTGT	GGCTCCACAT	GTCCGAGCTG	CAGAGCCATT
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	GGATCCCTC	AAACACAAAAC	CCTGCTCACA	GGAGAACTCA	CAGCTGGACC	CATAACGGAA	ACTGCCAGAA
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	ACACACATAT	ATGCTGTGT	GTATATATGT	GTGTGTGTGT	ATATATATAC	ATATCCACAT	ATTCTTGCCC
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25	CACAATAGAG	AGCAGTTTT	GCATGCTGT	AATTGCCAA	GATGCCACAC	CACTGAAACT	ACCTCCCCACT
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	TGCCCCACATC	TTTCTCTCTC	TTGATGTAGA	TCTCCACGCA	GTCCTCATCT	TTTGCCTAT	TGTTGGGTTC
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	ACTTTCTGA	TTCCAATCCA	GTAATAACTT	GGTGAATAGC	TCAATATGGA	TTTACGGTAC	TCAATCTCTT
30	CTTTGTTTG	AATTGCAACC	AGGTGTGTGT	ACCTTGCTG	ACAATAAGCA	CTGGCCTCAT	CATAAGTCAT
	AGCTTCCGTG	GAGCTGTGTT	AAGACCAGGC	TCCACTCTCT	TTAATGAGAA	GCACTAGTGG	GAGAAAAAGA
	AAAGAAATGG	TAGAGTTTG	TACTGTGTG	GTAACTCT	GACAACGTG	CTTTTATTG	TCTTATTTT
	GGCAATGTT	GTGACATGGC	CCAGACTTT	CTCATCTTT	CAAAAGTAAG	AAGTACGTAT	GAAGAAACAG
35	CGACTTATTG	TTTATCTCTT	TTGTGACTGC	CACCCACTAG	GTACCTATC	CACACTCACT	CACAACATTA
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	AGAAGCACTG	TATGAGGTAC	TTTCCATGAA	CCATGCTATT	GAATCTCAC	AATGCATCTG	GGAAATAGGT
	CATTATGATC	CACACTTAC	ACTTAAGGAA	AGGGAGACAC	CAAGAGGTA	AGTAAATGAC	CCCAAGCCCA
	GGGAAGAAC	CATGCAGGT	AGAGGTCAAG	GATGCTGCCA	GATATCTGT	GCAGGACAGC	CCCAGACAAG
40	CAAGGATATT	TCACCTCTGAA	ATATCTATAG	TGCGAGAATG	AGAAATCTG	GTCTAATGGC	ACTGACTTAC
	CCAAAGTGAG	AGCAGAGAGA	AACTGTGAAG	CAATCATGAC	TTCAAGAGTT	CTTTTCACCC	AAAGGTTAG
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	TATTCAGAG	TTTAATCAAA	AAAATAAAC	AATTITAAGA	CTTTCATTAT	TTAGGTCAA	GAGAAAAGAC
	AGGTTTATG	TACAATACAA	TAAGAGCTTG	TACAGATGTG	TTTTTATTAA	GAAGGCCTTT	TGCAATATCTG
	TGTTTCATGG	CCCCAGGCTG	CCCTTATAAA	GCGTTCTGCA	CTTACCGTT	TGGGAAGCAG	TTGTTCAAAC
50	ACAGGATCTC	TCAGCTGGGT	ATCACTGCTG	CCTCTGTCTC	AGGTCAGTAT	AGGAGTTTG	ATGTGAAGTC
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	GGAGGATATT	GTCCACATCC	AGTAAAGAGG	AAATCCCCAA	TGGCATCCAA	AAACTTTCCC	GGGAATATCC
	ACGATGCTTA	AAAATACAAT	GATGTCAGAA	ACTCTGTCTC	TTGAAGCTAC	TTCACCTTIG	TCCATGCCCTT
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	TTCAGAAACA	GAAGGAAACC	AAGAATAGGT	TTGTCATCCA	TAGTCTACTA	CCTTCAATT	CTCATTCTATA
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	AAAATGGAA	ATAGATATT	ACATCTGGG	AAGTTTCTG	GTTTGTTCAG	TGAAAAAAAT	AAAAGGAGG
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	GGGAGTTCAA	GACCAGCCTG	ACCAACATGG	AGAAACGCCA	TCTCTACTAA	AAATACAAA	TTAGCTGGGC
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	GTGTAGTGGC	GCACTGCCTG	AATCCCAGCT	ACTGGGGAGC	CTGATGCAAG	AGAATCGCTT	GAACCCAGGA
	GGCAGAGGTT	GCAGTGAAGCT	GAAATCACAC	CATTGCACTC	CAGCCTGGGC	GACAGAGCAA	GACTCCATCT

	CAAAAAAAA	GAA ^t AAAAGA	AAAAGAAAAG	AAAAGAAAATT	TGTTTCAA	TGCAACAGAA	GGAGATGTAT
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	CATCTTACCC	TATCTAAATG	ATGGTAACAG	TAATGGGG	TCATTTAAT	TCATTTAAT	TGTAGGTTT
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	TGTCA	CCTGAACGAG	TAGTGGTAAA	AGCCTCGTT	TTCTCTTAC	TTGTTAGCAC	TGGTCTTCT
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	TGCTATT	AAAAAGCATG	TGCAAATGTA	TAGAGTAGCC	AAATCTTAA	AAACAATT	TCTTCGATAT
	CAATAAAGTA	CCT ^t ATAATT	ATATTGCTAA	TAGAAATTAG	TCGTAAACAT	CCCTAGATAA	CTAACTTTAT
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15	TA	AAAATAGC	CCC ^t GTGGTG	ATGAAGTT	ACATATATAT	GTCCTGGACC	CCCAATTATA
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	GAGCCCAC	CCT ^t ACCTGC	TACTCCAAAC	CATGATTCT	TTTGTGTTA	TGCCCCGAGA	TTCTTGTTC
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	CATTGCCAAC	CCA ^t CTTCG	TTTATTCT	TCCCCCTCTG	CTTGCTCTT	CCCCTCTAA	GATGGAAGTT
	CCCAAAACTC	TCT ^t TGGAAA	AAGCGCAGGT	CACAGATCT	ACAGTGTATT	GTGTTCTT	TACCTGGGAC
	AAAATAAACC	TCT ^t ATCTGT	TGAGATATGC	TTCA	TTTGGTTA	CAATATGTAC	ATGTATGTAT
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	AGAATATGAA	TAAT ^A AACTG	TCAATGATGT	CTCAAGCCTA	AAAAAACTA	TCCATCTGG	TGGGTGGGAA
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	AGTAAAACCC	ATGC ^T AAAGC	AGCAAGGCTC	TCTAGAGGCT	CTGGAGAGGA	TGAATTGAAT	TCTAGAAGAT
	GAAGTAGGGA	AGAC ^A GCTT	CCTTCTTGT	AAATGGATT	AAAGATTCAA	AGACCTTCGG	GAATCTCAA
	TTGTATAAAT	GGC ^A CCATAG	CTGTATGTT	CATGGAACAC	TACTTCCCAG	AGATGCCAG	TGAAAAAAGA
35	ATGCCACAGT	CAA ^A TAAGT	TGGAAACACT	CCATTATGTG	GCCACCTCT	TGAAGACTCT	AATGCACATT
	AGCATGTTAA	ACA ^A TCTG	GAAGTCTGC	AGAGCAGAAA	TTGCTTACA	TCTGCTAACG	CGGCAGTTTC
	CCAATATACT	TGAT ^T TATG	TAGTTTTTC	CTTACAACAC	CATTCTG	TATGCTTCA	ATGACATGAA
	ATAAAATATAT	ATGC ^A TGAGG	TTCTTCATTA	GGGCATACTT	TTAATAGAA	AATATTGAGA	ATAATCTAA
	TATAAAATGCA	CAGC ^A TTTAC	CTTTCTGCA	TAAACTATAT	ACAGGCATAC	CTTGGAGATA	CTATGGTTT
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	TTTGGTTTCC	CAATGTATAT	CAAAGTACA	TTTTACTAT	ACCATAGTCT	ATTATATATA	CAATAGCATT
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	AAACTTTCTT	CAT ^A TCAGCA	ATAAGGCTGT	TTCACTTTCT	TACTATTTT	TGTGATAGCA	CTTTCTT
	CCTCAAGAA	TTT ^T CTCTT	CTATT ^A CAA	TTTGTGAT	ACAAGAGGAC	TAGATTTAG	CTTATCTCAG
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	GCTGGTGGAA	GGTCTTGCG	CAGTGTGAT	GTCTGCTGAC	TGGGTGGCT	TGGCAATTTC	TTAAAGTAAG
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	TGCTGTTTTA	TCAACTAAGT	TTATGGAGTA	TTAGAAATCC	CTTGTGTC	TTTCAACAA	GTTCACACCA
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	CCACTAAAGT	TTT ^A TCCTG	GATTGCAACA	ATTCA ^A TTAC	ATCTTCAGGC	TCTACTTCTA	ATTCTAGTTC
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	TATTCTTAAT	GGC ^A CTAGA	ATGGTGAACG	TTTCAGAAAG	GT ^T TTGAGCT	GGCTTGGCC	GGATCCATCA
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	AGT ^A TTCTT	CCACCTTGGC	CTCCC ^A AAAC	ACTGGATTAC	AAGCTTGAGC	CACTGTGTC	AGCCCAAAT
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	GGTTACCAAGA	CATC AAAACA	ATACTCATCT	CCTCATACAT	CTCCTTCAGA	GCTCCTGGGT	GAGCAGGCC
60	ATTGTCAAAT	GAGC ^A GTAGT	ATCTTGAAAG	AAATTTTTT	TCTGAGCAGT	AGATCTCCAC	AGTGGACTTA
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50	GGTTTCCAT	TTGT TCAACA	AAAATAATGA	CACCCCTTTT	ATGGGATTTC	TGTGAGGACA	AATGATAACT
	AACATAGCCT	TGCA TAGTGT	CTGGCACAAA	ATAGCTACTC	AAAAAATAAT	AGAAACAAACA	TTTAAAAAAAT
	GTAGACTTTA	TTTTTITAGAG	TTTATGTAC	AAAGCAAAAT	TGAGCAGAAT	GTACAGAGAG	TTTCCGTATA
	GCACCTCTA	CCCC CAAGCA	CAGATAGCCT	CCCCCAGTAT	CAGCATCCCG	CACCAGAGTG	GTACATTAT
55	TATAACTGAT	GAATCTATAT	TGACGTGTCA	TTTCATCCA	AAATCCATAG	TTTATATTAG	GGATGCCTCT
	TGGTGTGTA	CCTTCTATGG	GTTTTGACAA	ATGTATAATG	ACATGTATT	ACCATTACAG	TATCATAAAG
	AATAGTTTCA	CTGT'CCTAAA	AATCTTTGAT	CTTCTTCCTA	TTCATCACTC	CCTCCCCATT	AATCCCTGAC
	AACTACTGCT	AATTTCCCTG	TCTCCATTGT	TTTGTCTTTT	CCTGAATGTC	ATATAGTTA	AATATACAGT
60	ATGTAGGATT	TTCAAACTGG	TTTATTTCAC	TTAGTAATAT	GCATTTGATG	TTCTTCCATA	TCTTTTCAA
	GCTTCATAGT	TCAATTATTA	TAGAATTGAA	TAATATTCCA	TTGTCTGGAT	GTACTACAGT	TTATGTATTC
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	CTATGTACAT	GTTC TTTTGT	GAATTGAACA	TTTCAGCTT	TTTAGCTCC	ATTCTTAGGA	GTGCAATTGC
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	TTTGCATTCT	CACCAAGCAAT	GAAGAGGTTC	CTGGTGTCTC	ACATACTCAC	CAGCATTG	TGCGTCAAT
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55	ATAGAGAAAG	GATATACGAG	GACAGTTCTG	TCCTTTATT	ATAGTCCATC	ATTTAATGAA	GGACTCTGTC
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	GGCACACATG	GTTGTGTATC	AGGCCCCCTG	TGGTCTGTCT	GAAGCATGGC	TTTTTTTT	TTTTTTTT
	TTTTTTGAG	ACGGAGTCTC	GCTCTGTGCG	CCAGGCTGGA	GTGCACTGGC	GCGATCTCGG	CTCACTGCAA
	GCTCCGCCTC	CCGC GTTCAC	GCCATTCTCC	TGCTCAGGCC	TCCCAGTAG	CTGGGACTAC	AGGCGCCCCG
60	CACCAGCCT	GGCT'AATTTT	TTGTATT	AGTAGAGGCG	GGGTTTCACT	GTGTTAGCCA	GGATGGTCTC
	GATCTCTGA	CCTTGTGATC	CGCCCGCCTC	TGCTCCTCAA	AGTGCTGGGA	TTACAGGCGT	GAGCCACCGC
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	ATTCTTCTC	AGTTAAGAGG	ACCTCTGTAG	TAGCACTTC	ATACCGTTAA	TTTTCATTT	TGTGCCAGC
	CCCTACTCTG	TGA AAAATGA	AATGAATCCT	GTTATCATT	CCCTCCCAGG	CCTTTCTCC	TTGTGGACAA
	TGTGTGGCTC	AAG/GAAAAT	TCAGTCAGTA	AATTGTTCA	GTGCACAAAC	TCTTATCAC	CTCTCACTGT
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	TAAATGTTT	TTGAATAAT	GCATACATGA	ATCCATTCC	TATATATAGT	ATGGTAGACA	GATCATTGAT
	ACCCAAGAT	GCCC AAATGC	TGATCCCCAG	AACTTGTGAA	TATGTTACAT	TTCATGTCAA	AAGGGACTTT
	GCTAATGTGA	TTAAGGATT	AGACCCTTGG	ATTGTAAGAT	TATCCCGAT	TAACCAAGGGC	CAATCTAACT
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	CAGGAACAAG	CATGCTCTAG	CTTATCTCAC	AAGGAACITG	ACAATTCT	TCAAAATCC	TAGTAGCTAA
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	ACCATCTTAC	TGG ^A TTCTAA	TATTTAATAG	TCTAGGTGTT	CCATTCTCA	CCAAATTAAT	GTATACATT
	AATACAATGT	CAA ^C CGAAAT	ATCTTAGGAA	TTGCTTACAA	ATTGTCAGAT	AATTACAAAG	TTTACCTGGG
50	AAATATAAGC	ATATATGAA	AGTGAATGG	ACCCCACAC	TCCCCC	ACAAAAAAGG	TCTGAAAGG
	ACAGAAATCA	AGG ^A GAGTCT	TGCCTGCCAG	ATACAAAATT	CTATTATAAA	GGTGTATTGA	TGAAAACAAT
	TTAATACTAG	TGTAGCAATA	GGCAGCAAAG	CAATGAAACA	GCATAAAAAG	ACCAGAACTA	TACCTAATTA
	TGATGAAGAT	TTA ^F GGTATG	ATAAACATGA	CATAATTCAA	ATCAGCAGAA	ATTGGCATAG	ATAGGGTTAA
	GACAAATAGC	TAAT ^C ATTAG	AGGGGAGGAA	GGAAAGGAGG	GAGGATAAAA	TTAGGTTCC	GCCTTCATCT
55	TACATTAAA	TAAT ^C CCAG	ATGTATTACA	TTTAAATT	TTTAA	GAAACCACAA	AATAACTGAA
	GAAAATATAA	GTT ^T TTATAT	AGTCTTTG	TGGGAATT	TTTTTTT	AGAGACAGGG	TCTTGCTCTG
	TCACCTAGCC	TAGA ^T GTCAA	TGGCATGATC	ATGGCTCACT	GCAGCCTGA	ACTCCTGGC	TCAAGTGTAC
	CTCCCAGCTC	AGCC ^C CCCCAG	GTAGCAGGAA	CTACAGGCAT	GCGACACCC	ATCCAAC	TTTTTATTT
	TTTGTAGAGA	CAGGGGTCTT	GCTTGTTC	CCAGGTTAT	CTCGA	TGCCTCAAG	CACCTCAGCC
60	TCCCAAGAG	CTGGGCTGAT	GGGACATT	TTAACATAGT	GCCACATTAC	CATAAAATGAA	AAGCTTGAA
	AATACTAATT	TTTAAACTA	ATATATATCA	GAAATT	TAAACAAAGT	AAAAAAGCAA	ACACAAAAAA
	TTTGTAGCAC	TTATGACAA	TATATGTATA	TATATGAA	CAAAAGAGC	CTTACAA	CAGTAAGAAA

	ACAATGAATA	CTCCCAATGG	AGTATTCAA	ACTAAA	ACTGC	TAAAAGCAAT	TCAAACAAA	AAACATAAAC
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	CATCTGATC	CAAG	ITAGCA	AACTGCAAA	GATAGGAAGC	ACTAATGAGT	GGAAATTG	GTAGAAGCAT
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	CTCTTCATAC	TAC	TATTATC	TCTTCCCCC	TCCTCATTT	TTA	TGAC	CTATTCTCT
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	ACAGCCCCCT	GTAACTGAT	GTATGTTACA	TGTGATGTAT	GTTACATAGT	TTTTTTCAT	GTTGATCACT
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	CTAAGAAGAG	TTGAAGGGC	AAGTGGGCT	AAAAACAGAT	TTTGTGAC	TTACCCACC	ATTCCCCCTA
	TCATGGGCT	GAATCTGCC	GGAGGAAGGA	GCATCTTAT	CTTGTA	TGAACACAC	AGTCTAGCAG
	CAGCACAGCC	AAGGCACTTG	GGGTTCATG	AGACTAAGTA	CATGCAATT	TATTGAAAG	GCTTAAAATA
	TATACAATG	ACCCCTGAAC	AACATGAATT	TGAATTGCAT	GGTCAGTTAT	ACGCAGATT	TCTTCCACCT
10	CTGCCACCCC	TGAGACAGTA	AGATCAATCA	ATCCCTTCC	TCCTACTCCT	CAGTCTACTC	AAAGATACTT
	GAAGTCTACT	TGAAAGATGAC	AAGCACAAAG	ACATTATGA	TGATCCACT	CCACCTAGTG	AATAGTAAAT
	ATGTTTCTC	TTCCCTCTAA	TTTTTAACA	CTTCTTCTC	TCTAGCTTAA	TTTATTGTTA	AGAATACAAT
	CTATAATACA	TATGACATAC	AAAATATGTC	TTAGTTGACT	GTTTATGTTA	TCTGTAAGGC	TTCAGGTCAA
	GAGTATGCTA	TTAGTGGTTA	AGTTTCGAG	GAGTCAAAAG	GTGTTATGTTG	ACTTCAACT	GCAGGGGGT
15	GGGCACCCCT	GCCCCATGT	TGTTCAAGGG	TCAACTTTAC	TGCCCAAGGC	AAGCCTTAC	ATCCACTTT
	TCCATCCCAT	CAGTAAATGG	AAAAAGATAG	CTACAGTATC	CCTCGCTCAA	ATCTTTTTT	TTGCAGATCA
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	AAATAGCATT	TTTGTAGAT	AACCTCCGT	ATAGATGATG	AAACTCTT	TAAGGGCTAT	CTGAATTAA
20	ATTCTTGA	AAGGCAGAAA	TTGGGATAGCT	AGTAGTCATA	AATGTA	GGCTCCCCC	AACCATCTGG
	GCTATATAGA	AGCTGCATCC	TTGGGACTGCA	GTAGAGGAGT	CTTACAAAGC	ACAGAGCAAC	TTCTCTCCTG
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	CACAAATGCCA	TCATAACCAT	GGTATAAAA	ATTCAAATG	TCCCAGCTGA	AGTGGAGGCA	AAGACTCAAG
	TTCATGGAGT	CAGAGTTCC	TTGCTATTCC	TCTTTTCAA	ATGACCA	AGTAAGCACC	TGAAGAAAAT
25	ACTATGGACG	GCATGAAAAA	GTGAAGATAG	GTTTAATCTT	CTCGAAAATC	TAATTCTCCA	GATGAAACGC
	TGACACTTAT	CCACCCACAA	GACCCCTATAG	CAGATGTGTC	ACTGGCCATC	ACATTGACA	CAGAGAAGTC
	ATAACTCAGT	CAGCACAGAG	ACATTCTCAT	GAGTTCTGTA	ACCATGGACA	GAACGTCGTC	TGTGGGACAT
	GAAAATGGA	ACTTAGAGGA	CAGGCACATC	TGAGAAATGG	GCAGTTAAA	GGCAGAACAT	AGCACATATG
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	CAAGTGCCTC	TCACGATTCT	CTTGTCCCAG	CCTCTCTAAT	AGCTCGGATT	ACTGGCATGC	ACCACCAACGC
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	CCTATTTACA	TAAGCCCCA	ACCTAATATT	TAGTGATATA	TATTAATGTG	AACAAGGAAC	TAACGAAGAC
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	ATTTTAAAGC	CACT GTACTC	CAGCCTGGGT	GACAGAGTGA	AACCCTTAAT	TCAAAAAAAA	AAAAAAAAAA
15	AAGAAAAGCT	GGA TATTGG	CAAATCAAG	TAACTAAGAG	AAAACATTA	ATTCACAGAA	TACATTATTA
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	GAACTAAGA	TAC TTTGGT	CCAAAATGAA	ACATTATTG	TAATTAATCT	CTTATTGAAA	TGGGTTCTA
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	TATTTCTTAG	AATT GTTCT	TGACCACCA	AAAAGATT	AACTGTTACA	TAGATGAAA	TGGATGTTGA
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 (SEQ. ID NO: 3009)

10 5'-GCCACCATGG AAACCCCTTG CCTCAGGGCA TCCTTTGGC TGGCACTGGT TGGATGTGTA ATCAAGTGATA
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30 5'-GATCAAATT TTIACCTATT ATGCATTGA TATATAAATA AGTATATAAA TGCACACACA GACACAGCAA
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	CGGACTGTCC	AACTTGCCCA	GCACCCACTC	CCAGAGCCCC	TGGAACTCTG	GCCCAAGGCT	CTCTGACTGA
	CTCCTTCCCA	GATCCTCTTG	GCTTAGTGGC	TGAAGACTGA	TGCTGCCTGA	TCGCCTCAGA	AGCCTCTGG
	ACCATCACAG	ATGCTTTGG	TAACCTTAC	AGTGGAGGGT	AAGTCGTCC	CCTCTTAAT	CAATGCAGAG
35	GCTACCAACT	CCACATTACC	TTCTCTTCAA	GGTCTCTGTT	CCCTCTGTCT	CATAATGTT	GTGGGTATTG
	ATGGCCAGGC	TTCTAAACCC	CTTAAAACTC	CCAAACTCTG	GTGCGCATTT	AAACAAACATT	CTTTTATAACA
	CTTCTTTTA	GTТА'CCCCA	CCTGCCAGT	TCCCTTATTA	GGCTGAGACA	TTTAACCAA	ATTATTGCT
	TCCCTGACTA	TTCCIGGACT	ACAGCCACAT	CTCATGCTG	CCCTCTTCC	CAACCCAAA	GTGGCAACTC
40	CTTTCGCACT	TCCTCTCATA	TCCCCCTAAC	TTAACCCACA	GGTATGGGAC	ACCTCTACTC	CCTCCCTGGC
	AACAAATCAC	ACCCCTCATTA	CTATCCCAT	AAAACCTAAT	CACCCCTAAC	TGGGTCAACG	CCAGTATCCC
	ATCCCACAAAC	AGGCTTTAAA	GGGATTAAAG	CCTGTTATCA	CTTGCTCTT	ACAACATGTC	CTTTTAAAGC
	CTGTAAACTC	TCCTTACAAT	TCCCCCATTT	TACCTGTCCA	AAAACTGGAC	ATGCCTTACA	GGTTAGTTCA
45	GGATCTGTG	CTTATCAACC	AAATTGTCTT	GCCTATCCAC	GCCATGGTGC	CAAACCCATA	TACTCTCTTA
	TCCTCAATAC	CTCCCTCCAA	AACCCCTCCA	TAACCCCTTAT	TCTGTTCTG	ATCTCAAAAC	ATGCTTTCTT
	TACTATTCT	TTGCACTCC	CATCCCAGCC	TCTCTTCACT	TTCACTTGG	CTGACCCCTGA	CACCCATCAG
	CCTCAGCAAC	TTACCTGGGC	TGTACTGGCG	CAAGGCTTCA	TGGACAGCCC	CCATTACCTC	AGTCAACCCA
50	AATTCTCT	TCATCTTATA	CCTATCCAGG	CATAGTTCTT	CATGAAAACA	CACGTGCTCT	CCCTGCTGAT
	CATGTCAGC	TAATCTCCCC	AAACCCAGGA	CTGCAAATT	GACTTACTC	ACATGCCCA	AATCAGGACA
	CTAAAGTACC	TCTTGGCTG	GGTAGACACT	TTCACTGGAT	AGGTAGATGC	CTTCCCACAA	GGGCCTAAGA
	AGGCCACCGT	GGTCATTTCT	TCCCTCTGT	CAGACATAAT	TCCTGGTTT	GGCCTTCCCA	CCTCTATAACA
55	GTCTGATAAT	GGAC AAGCCT	TTACTAGTC	AAGCACGCAA	GCAGTTCTC	AGGCTCTGG	TATTCTAGTA
	AACCTTCATA	CCCCTTACCG	TCCTCAATCC	TTAGGAAAGG	TAGAACTGAT	TAATGGTCTT	TTAAAACAC
	ACCTCACCAA	GCTCAGCCTC	CAACTTAAA	AGGACTGGAC	AGTACTTTA	CCACTTGGCA	TTCTCAGAAT
	TCGGGCCCTG	CCTCGAAATG	CTACAAGGT	CAGCCCATTT	AAGATTCTGT	ATGGACGCTC	CTTTTATAA
60	GGCCCCAGTC	TCATTCCAGA	CACCAAGCCA	ACTTGAAC	TGCCCTTAAA	ACTTGTCTC	CCTACAATCT
	TCTGTCTAGT	CATACTCTA	TTCACCATTC	TCAACTACT	GTAAATGCC	TGCCCCTTT	TACAGTGTG
	ATTTATACTT	TTCTCTCCAA	CCATCATAAC	TGATATCTCC	TGGTTTAC	TCAAACCGCC	ACCCCTTAAGT
	CTCTCTTAA	GTGGATAGAA	GATCTTCACT	GACAAGGTAC	ACTCCAATAC	TTTCAACCTA	ATAAAGCCCT
65	ATTCTTTACT	TTTATATTCA	CTCTTATTCT	TGTTCCCATT	CTTATGCCAC	TCTCTACCTC	TCCCCAGCTA
	TCTCCACCAC	ACTATCAATC	TCACTCACTC	TCTCTAGCC	ATTCTAACTC	CTTCTTTAAC	AAACAATTGC
	TGGCTTACA	ATTCTCTTT	CCTCCAAAAT	CACCGAGTCC	TCAATTACT	CACTGCTAAA	AAAGGGGACT
	CTGCATATT	TTAAATGAAG	AGTGTGTTT	TTACCTAAAT	CAATCTGGCC	TGGTATATGA	CAACATAAAA
	AAAACCTCAAG	GATA.GAGCCA	AAAACCTGC	CAACCAAGCA	AGTAATTATG	CTGAACCCCC	TTGGGCACTC
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	CCTTGTGTC	TCCAATTAGT	TTCTCAATT	ATACAAAACC	GTATCCAGGC	CATCACCAAT	CATTCTATAC
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	AGTAAAAATG	AAAAGGCAGA	AATGAAATCC	ACAGGCGAC	AGCCTGATGC	CACACCTGG	GCCTGGTGGT
	TAAGATCAC	CCCI GACCTA	ATCAGTTATG	TTATCTATAG	ATTACAGACA	TTGATGGAA	AAGCACTGTG
	AAAATCCCTG	TCTI GTTCTG	TTCCCTCTAA	TACCACTACA	CGCAGCCCC	AGTCATGTAC	CCCCTGCTTG
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	AAGCCCTTCC	TTCTTTAACT	CAGTGTCTGA	GGGGTTTTGT	CTGTGTCTG	TCCTGCTACA	GTTTCATCTA
	ACAACCCCAT	AATATCACCC	CTTACCAACAA	AATCTCCCTT	CAGCTTAATC	TCTCCCACCTC	TAGGTTCTCA
	CGCCACCCCT	AATCTGCTC	GAAGCAGCCC	TGAGAAACAT	CGCCCGTTAT	CTCTCCACAC	CACCCCCAAA

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5	AAGTAAAAAT	GGC ^t GGTTCC	TGCCCTAATC	GATGATATTG	CACCAATTGTG	ATTGTTCTCT	GCGCCACCTT
	GACTGAGGGG	TTA _t CCTTGT	GAAATTCCCT	CCCCTGGCTC	AGAAGCTCCC	CCACTGAGCA	CCTTGTGACC
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	ACAGCCCCAC	CCC _t CTCTCCC	TTTGCTGACT	CTATTTTGGG	ACTCAGCCCA	CCTGCACCCA	GGTGATTCAA
10	AAGCTTCATT	GCTCACACAA	AGCCTGTTG	GTGGTCTCTT	CACACCGACA	CGCGTATAA	TTATTATATT
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	TCCCTTGTCA	TAATGGTGG	GTAGGCTGTT	ATGGTGTG	CAGATTTCT	TTCCATAAAA	TGTCCATAAT
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	TGACAATTTC	ATGAACCTGG	TAECTCTGAGT	AAAGCATAGG	AGGAGTTATT	TCATAAAATG	TGGAGCACAA
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	AGTGTCCATT	TGGC TTCCCT	GGCCCTGATG	TGTTAGTGG	ATAAACATT	TTGTCAGGGT	TGCCATGTGT
	GTCTGTGAC	GTGTGACTG	TACACCTCCA	GGGGATGTAC	CCTAAACAC	ATGAATGTGA	TTGACACATC
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	GTGCACTGGT	GCTCTCATGG	CTTACTGCAG	CCTTGACCTC	CTGGGTTCAA	GTGATCCTCC	CACCTCAGTC
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25	AAAGTGTGGG	ATTAAGGTTG	ACAGCCAAGG	TGCGCTGGCC	ACAGATAGA	ACTATTAAT	GTTATCTTAA
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	ACTAGCTAA	CTGCGGTTA	TCTGTTCTC	GTTTCCCCA	CACTGATTCC	CACAGCAGTT	TTCAAGTTAT
	CGGTTGAGA	TCTTGTACAG	AAATGACTCC	AAGGAAAAAA	ATTTAAAAC	AACCCCTCTA	ATTTTTTAC
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30	GATTCTACAA	ACACTTATTA	AAAGATTAA	GAATTGCGAA	ATAAAATAGCT	TCCTTATTAA	GGTGAETTAC
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	CCTGTTCTCT	ATCCGTCACT	TCTGCCATCA	TCGCCAAGG	TAGGAAGAAA	GACAGGACAA	CCGGGGTCAA
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	GCTAATGAAG	TTCTGCTATA	TCAACAACTCC	CCACCCCCCT	CACACACTT	GTCTTCTGG	ATTGGTTAGA
	AAAATTACCT	AGGCCCAACT	ATTCTCAAAT	TAAATGAAA	GATAAGATCA	GAGTGGCACG	CAATTAGGGA
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	GCAACCTCCG	CCTCCGGGT	TCAAGTGATT	CTTCTGTCTC	AGCCTCCCGA	GTAGCTGGGA	TTACAGGTGC
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	CTTGAACCTGC	TGAGCTCATG	ATCCGCCCGC	CTCGCCCTCC	CAAAGTGTG	GGATTACAGG	CATGAGCCAC
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	AGAAAGAAGA	ATC\ATAGAC	ACAATAAAA	ATGTTAAAGG	GGATATTACC	ACTGATCCC	TAGAAATACA
	AACTACCATC	AGACATTAC	ATAAACATAC	TTACACAAAT	AAACTAGAAA	ATCTAGAAGA	AATGGATAAA
	TTCCCTGGACA	CATACACCC	CCCAAGACTA	AACCAGGAAG	AAGTCAATC	CCTGAATAGA	CTAATAACAA
15	GTTCTGAAAT	TAAGGCAGCA	ATTAATAGCC	TACCAACTAA	AAAAGGCCA	GGACCGATG	GATTACAGC
	CAAATTCTAC	CAGAGGTACA	AAGAGGTGCT	GGTACCATTC	CTTCTGAAAC	TATTCCAGAG	AATAGAAAAA
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	CAAAAAAAAGA	AAA\TTTCAGG	CCAATATCCC	TGATGAACAT	CATTGCGAAA	ATACTCAATA	AAATACGGCA
	AACTGAATCC	AGCAGCACAT	CAAAAAGCTT	ATCAACCACA	ATCAAGTTGG	CTTCATCCCT	GGAATGCAAG
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	GATTATCTCA	ATAGATGCAG	AAAAGGCTT	GGTAAATT	CAACACCCCT	TCATGCTAAA	AACTCTCAAT
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	TACTGAATGG	GCA\AAATCTG	AAAGCGTCC	CTTTAAAAC	TGGCACAAGA	CAAGTATGCC	TCTCTCACCA
	CTCCGTITCA	ACAT\GTATT	GGAAGTCTG	GCCAGGGCAA	TCAGGCAAGA	GAAAAGATA	AAGTGTATT
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25	GTCTCAGCCC	AAA\TCTCT	TAACATGATC	AGCAACTTCA	GCAAAGTCTC	AGGTTACAAA	ATCAATGTGA
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	CACGATTGCT	ACAAAGAGAA	AAAATACCT	AGGAATCCAA	CTTACAAGGA	ATGTGAAGGA	CCTATTCAAG
	GAGAAGTACA	AACC'ACTGCT	CAAGGAAATA	AGAGAGGACA	CAAATGAATG	GAAAACATT	CCATGCTCAT
	GGGTAGGAAG	AATCAATATC	ATGAAAATGA	CCATACTGCC	CAAGGTAAATT	TATAGATTCA	GTGCTATCCC
30	CATCAAGCTA	CTACTGACTT	TTTTCACAGA	ATTAGAAAAA	AACTACTTA	AATTTCATAT	GGAACCAAAA
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	AAACTATACT	ACAAGGCTAT	AGTAACCAAA	ACAGCATGGT	GCTGGTACAA	AAACAGATAT	ATGGACCAAC
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	GAAGACCTAA	AACC'ATAAAA	ATTCTAGGAG	AAAACCTAGG	CAATACCATT	CAGGACGTAG	GTATGGCAA
	AGACTTCATG	ACTAAACAC	CAAAGCAAC	AGCAACAAAA	GCCAAAATTG	ACAAATGGGA	TCTAATTAAA
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	ACCAACATGA	GATCCTACT	CATGCGAGT	AGAATGGCGA	TTATTAAAAA	GTCAGGAAAC	AACAGATGCT
	GGAGGAGATG	TGG\GAAATA	AGAATGTTT	TTACAGTGT	GGTGGAAAGT	TAAATTAGTT	CAATCATTGT
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	GATGAAGCTG	GAA\CCGTCA	TTCTCAGCAA	ACTAACACTG	GAACAGAAAA	CCAAACATTA	CCCATTCTCA
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	GCAGCAAACC	ACCA\TGGCAC	ATGTATACCT	ATGTAACAAA	CCTGCACGTT	CTGCTCATGT	ATCCCAGAAA
	TTAAAGTATA	ATT\AAAAAA	AGTTAAAAAA	AAGAAAGTTG	CTTCTAGTCAC	ATAACTAGTA	AGAGACATGG
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	CTCATTGCAC	TCAAGGAATC	CTAGGGTCTA	GTGCCCTTC	TCCCTCAGCC	TCCCAGTGTAG	CTAAGACTAC
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	AACCTCCAAA	CCCTTGAGAT	ACTCCAGAGA	TCACCGCTTT	GCTCTCTGT	GTCTAACCTC	ACTAACTTGG
	TGGTCAATT	CACACTCTG	ACTTTGAATA	CCATTAAAT	GCAGAACGAAT	TCTAAATTCT	GTACAACCAAG
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65	CTCTCATATT	TTAC\ATATCC	CAAACGTAAAC	TTCTGAATT	CTCCTCCAAT	CTGTAGGGCT	CTTCCCACAG
	CCTTCCATC	TCAG\GGGATT	ATAACTCCAT	CCTTCCAGTT	ACTCAGACCA	AAACTTTGG	AGTTAACTGA
	GACACCTCTC	TTTTTTTCA	CAAGTCATAT	CCAATGTGTC	AACAAATT	GGTAGTGGAA	ATATTGCAGG
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	TTACAGGAAG	CATGGTCCG	ATATCTGCTC	AGCTTCTGGT	AAGGCCCTAG	GAAGCTTACA	ATCATGGCAG
	AAGGTGAAAG	GGGAGCAGGC	ATATCACATA	GCAAAAGCAG	GAGCAAGAGA	GGGGATGTGGG	GAGGTGACAG
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	TGGTCAAAGG	ACCACATACC	AACCTTCCC	TAGCCTACGC	CTCCATTACA	GATGACCGCA	AGATTATT
	GCTCATGCT	GCCAACCAAG	GCTGCACTCA	CTGCAGTTGC	TATCAGTTA	TCATGGTTA	AAGGAATGTC
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	GCCCCACTGC	CTCCCTAGGA	CATCACTTCC	CCTGCAAGTC	TCTCAAGATG	ACAATATT	ATATATGTTT
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	GTTCTCCTT	ACTIGTTGT	TTGTTTATT	GTTTCTTTT	TTTTTTTTT	TTTGGAGACAG	GGTCTCACTC
	TGTTGCCCAG	GCTCAGTGC	AGTGGTATGA	TCTCGGCTCA	CTGCAGCCTC	CATCTCCCTG	GTTCAAGTGA
	TTCTCATGTC	TCAGCCTCCC	GAGTAGCTGG	GACTACAGGT	GCATGCCACT	ACGCCCTGGCT	AAGATTTGT
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	TTCAACTGGT	GGCTCTACCT	GGACCCATCA	ACAAGTCTG	TGGCTCCACC	CAGAAGCAGA	CTTAACATGC
	ACAAGGACCA	TTTICCACAC	CGCTATGATT	GCATCCCAAC	CAATCAGCAG	CAACCATTCC	TCTGCCTGCC
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	TTGGTAACAT	AAAAAAACA	AAAAAAATATA	CACGCAACAT	TCGCTCCAA	TCCTACTGAA	TCAGAAATT
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	GTACGCTTGT	GGTC ATT	TTTTTTTTT	TTTTTTTT	TGAGACAGAG	TCTCGCTCTG	TCGCGCAGGCT
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	GCCTCTTGAG	TAGCTGGAC	TATAAGCAGC	CACCACTATG	CCAGCTAAT	TTTTGTATT	TTAGTAGAGT
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	AAAGGGCATA	GCA' GCTTCC	AATGCCAGCA	AATAGCTACG	GGGTCACTT	GCCCAATTCA	GCTCCCAATT
	TTTCATGAGA	AGTC' CAAAGT	CTTAATTAA	ATGTGAGATT	TCCTATTG	AAACGTCAG	AACTTAAC
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	TTCCCTTATGA	GAGACTCTCA	AATTAAAGCC	TGTACTCCAA	ATAAAATCTCC	TTAGGAAGAA	TTTTATCCAT
	TTTCCTTAGA	GTGCTCATCA	TGGCAGTCC	ATTGCACAAT	TCCGGGAGGC	ATCATATAAT	TCAACATGAA
	TAGCACCCCC	TGGAGTTGTA	CAATATTAGG	CAGGACTAAC	ATTTTATT	CCTGAAACAC	TTCCCACACT
	GAGTTGACT	ACTAACTCTT	TTCTTAATAC	TTCTGCTTAA	TTATACTGCA	TTTTATCCAG	ATTCTAATTA
5	TTGTTTAAAT	CAGTAAGCAA	GACCATGACT	TATCAATGAG	AAAGAAATGT	ATTTTCAAAA	ACATTTTGA
	AGTACATTCA	TAAACTTCCCT	CACCTTCCG	TAAGCATTTC	CGAAGCCAGA	GGAGAAATGG	TGCTAATGTC
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10	TTCTGTACAT	TCATTACTAG	GAGCAGAAGA	GCTATCTAGT	TTAATACAAG	AAGCAGAGAT	GTGGCATTAC
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	CCAAGCTCGT	TCACAAATACC	ACACACACC	TTGTTAATA	AAACACTGCAC	TTGCTGCTC	TCTGCTCTC
	ACTCCCTCTT	GTITTCATT	TCCCCTTCT	CCTCTCTCT	CTCTGTCTCC	TTTTCCAGT	TGTCAGAATT
	CTACCCCTTC	CATCAACATG	CAACTCTGT	TTTTCTCTA	TCCCCATACA	ACTTAATATT	CACAACATTGT
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	TTCTTTTAA	TCACCAAGACA	ACCACCATCA	ATCAATGCAT	CACCTTCACA	GGTAGGTAGC	AGGCCAGACC
	AGTGTCTGT	GGCTCCACAT	GTCCGAGCTG	CAGAGCCATT	GAGCGTCCAT	CCTTCAGGAC	AGGCGAACTT
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	CAAACCCCTT	TGGGCAATC	TAGGTTTCA	AACTTTATGA	AGTATTTGAC	CTGTAACCTA	AAAAAGCTG
	CACTCAATT	TACCTTGGCA	GGAAAGGAAAC	TCTCTGTCC	ATTGTCCTG	AGATGTGCAC	TCAAGTTGAG
	TTGATCCATG	TAATCAAT	CCCTCCTCAC	AGCTGAAGGC	ACAAGAGGAC	TTGAGGTGA	ATTCTCCAAT
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	TGGGATTTC	TGTCCTCC	GCCCCTGAGT	GGTGCATTCA	ACCTGGCTG	GTCCCCTGCAA	CATGAAGCCT
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	TTTATTGTTT	TATGCTCTCC	CTTACAAATC	ACCAGAGCCT	CAGAAACACC	CATTCAAGC	ATAGAATAAA
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	GAATTCTTAC	ACATGGAAAG	TAATATGATA	AGAATTCTTA	CCAATAAAAA	AAAAGCAAGA	GAGAATAGCT
	GCTAAAGAAT	TAACACAAAT	ATGTATATAT	TAGTTATTCT	CTTTCTCCT	CTGATTCCAG	AGGACTTTGT
60	AATTCCACTA	ATTCTTCTTG	AGCTTCCAGG	ATGATCTGAG	ACTTGAATT	TTCATGTGCT	TTTGTCTTCC
	TATTGGCAG	CAT ^C TTATCT	TGAAGTTCC	GCTTTCTGCT	TGGGGACCTA	AAAACAAACT	AATGGGAATT
	TCTTCAAAAT	GAGC ^A AAACTC	TGGTGAATT	CCAAAGCGGA	AGAAACAAAGT	GAGGATCGGG	CTGGTTAATT
	AAGAGAACTT	TTCC ^T GAATG	AGGCCAGACT	GTTTGCCTGAC	TGTTGTTAAC	ATGAGGGAAG	AAATACCCCT
	GGATTTTAGA	AGA ^G CCCCCTT	GTTTGTITC	CTTGGCCATT	TGTGCTGCTT	GTTTGTAAAG	TCAGAAATT
65	CCTGAAGGAC	TATTATTAGC	TTTGTCTCA	CGTCAGAAAA	CTTCTGCTCT	GGCCACTTTT	AAACATATAA
	CTTGGATT	ACT ^T FATTAG	AAAATGTAAC	AATTACAGAC	AGCACTAAA	GGACACAAA	GGGCAAAGAA
	AATGGGTAAC	TTT ^T TTTCT	TCCCCAAATC	TAAAATAGGT	GATTTTGGAG	AAGTAGGAGA	AAAACCTGGA
	TTTCTAGAT	CTCT ^T AGAG	CTCAACAACT	GATATAGTTA	ATTATGTAAG	TCTTTGATAT	TTGGAAATGA

	TTGGATTAAC	CGGAATAACAA	TGAATATTAA	AATACAGTGA	TTTGGCCAGG	AGCAGTGGCT	CATGCCGTAA
	ATCCCAGCAT	TTGGGGAGGC	TGAGGCGGGT	GGATCACCTA	AGGCCGGAG	TTCCAGACCA	GCCTGGCCAA
	CATGGTAAA	CCCCATCTCT	ACTAAAATA	CAAATTAGC	CAGGCGTGGT	GGTGAAGAC	TGTAATCCA
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5	CGCCATTGCA	CTCCAGCCTG	GGCAACAAGA	GCGAAATTCC	ATCTCAATAA	ATAAATAAAT	AAATACAGTG
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	AGTCTCAGAT	TTCC'CGAGAG	CTTATTATT	TATACCAAGA	GTGCTTACT	ACCGCTCTG	CTAGCTGTGA
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	CTCAACTAGT	TTCTCTGCTC	TAGGTTTAC	ATTGCCAATA	TCAAGGTTGC	ATCCAGTTGG	GCTCTTCTTG
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	ATTATGACT	TTT TCTCA	CACCCAAGTA	GGGAGGAATC	AGTGGTCCCC	TAGAGGCCCA	GTGTAGAGGT
	GGCAGCACCA	ATCCCTAGGG	GAGAAGATCT	TGGTGTGAT	AATTCTGAG	CAGACAGTTA	GCTGAGAAATT
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65	GAAATCAAAA	TGG AGATCTT	GCAAGTTTG	TGAGAATGGG	TGAATGGTCC	AAATGAAGAG	ATAAGTTGTG
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	CACCCCTTT	ATGGGATTTC	TGTGAGGACA	AATGATAACT	AACATAGCCT	TGCATAGTGT	CTGGCACAAA
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	CCCCCAGTAT	CAGCATCCG	CACCAAGTGT	GTACATTCT	TATAACTGAT	GAATCTATAT	TGACGTGTCA
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	CATAAACAAA	TTGTGGTATA	TCCACAAATT	TTACGCAGCA	GTAAAAGGA	ATAAATGGTT	GAATAAGGAA
	TAACACACATA	ACAAGGATGA	ACCTTAAAC	CGTAAGGCTG	AATGGAAGAA	GTCAGACAAA	ACTAATACAT
	ACTGAATAAT	TCCP TTATA	TTGAAGTTCT	AGAAAATGAG	GACTAACCTA	TAGTAACAAA	AAGCAGAAAA
	ATTTCGCCCA	CTGGTGATGG	AGGGGCGCA	GGTATTGTA	AGTATCTGAG	AAAGGACAAC	TGGATAAAAG
45	GGGGCACAAG	AAAACTTTTG	AGGGTGAATTG	ATATGTTCAT	TATCTTG	CATGGTTCA	TAGGTGCATA
	CATATGTCAA	AACATCAAGT	TATACACTTT	AAAATGTC	AGTTTACTGT	ATATCTATT	TACTTCAGTA
	GAGAGGAAGG	AAGAACGTGG	GCAGGGTGGG	GGAGAGGAA	GGAAACGAGG	GAGGAAAGGC	CCTAATAGGA
	AGGAGTTTGG	AGTITAGATT	TTAAAATGAT	AAAGGATGTT	TGACACTCTA	GGCATATGAC	GAATATAGGA
	TTATGAGTCC	ACAA AAACCA	CCAGGAAGTC	ATGTATGTT	ATACTTTAA	GTGAAGGATC	AGTGGATTAT
50	CAACTCCCTA	ATGCTTTGCC	TCTCTATGAC	TGGCTGCTGT	CCTTCTCATC	CCAATACTCC	TTCCAAAGCC
	CCTTGCTTAA	ATGIAAGCT	TCTTCCCTCC	TTCAACACA	TCTCGCATTC	CGTACAAAAA	TAAGTTTCC
	TTAACACGAA	TGTACAGCAT	ATTATTGTA	CAATTTAAA	TTTTGGCCA	GGTGTGATGA	CTCATGCCCTG
	TAATCCACG	AAATGGGAG	GCGCAGATGT	GTGGATTACC	TGAGGTCA	AGTCAGAGAC	CAGCCTGGCC
	AACATGGTGA	AACTCTGTCT	CTACTAAAAA	TACAAAATT	AGCTAGTGT	AGTGTGGCAG	GTACCTGTAA
55	TCCCAGCTAC	TCAGGAAGCT	GAGGCAGGAG	AATCGTTGA	ACCTGGGAGG	TGGAGGTTGC	TGTGAGCAGA
	GATCAGACTA	TTGC ATTCTA	GGCTAGGAGA	CAGAGTGAGA	CTCGGTCCCC	AAAAAAAAC	ACATTITTT
	TTAATGTTTC	CTCC ITGCCT	GTAGGAAAAA	GGCTCTGACT	CCTTAGCTG	GGCATCAGAG	CTCTATCTAA
	ATGGACTTTA	ACCTGATTTT	GTGGCACTAA	TTCCATTGCA	GTACTTGTC	GCTCACTGGC	CTGTGCCTCT
	CTGCCACTAT	TTT TGGATA	ATGTCTCTC	TCCATCTGT	TTACTCAACT	ATATCCAACC	TCTAAGGCTG
	TGCTCCTACA	AAGCCTCCCC	TGGCTACTTC	AGCCCACAGA	GATATTAAAC	TGCTCTGCAG	TTCAGGACAT
60	TCTCTGACT	CTTAAATCA	CATTACTTA	TATATGATCT	TGTGATATT	TTTGTGACG	TGTTTACTTT
	AATTTCCTTC	CATAACCTAT	TCATTCAACA	AACTCAACAA	TTATTTTATA	AATGCCAAGT	TAGAAAAATA
	TTATTGATT	TATAFAGATT	ATAGATATGT	TTGAAATT	ATTTGGCAAT	CTGCAAGTAG	AAAAATAATT
	ATAATGTGGT	ATATCTGTGA	TAGAAGTATT	AGTCAGAGA	CCATGGGAA	CATAATCCAG	CCTGGAAGTT
	CAGGAGAGAT	ACGTGGAAGA	AAGGACGTCA	GAGCCTTTT	CCTACAGGCA	TGGAAGAAC	ATTAAGGAA
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	TGCAACCTCT	GTCT CCCGGG	TTCAAGTGT	TCTCTGCCT	CAGCTCCCA	AGTAGCTGGG	ATTACAGGTA
	CCTGCCACAC	ATGGATGATA	AATATGATCA	TATTTCTTG	TTCTTTCTCT	CCTCAGTTGT	CTTCCCTGAA
	GAAAGGAATG	CCTT TATAG	ATGACAAACT	CCCATTCTCA	AGAACAAAGGA	TTTTGACCA	ATTTAATTAA

	ATCAGATGTC	TGGCTTGAC	CTAGAAACAC	AGTCACGAAA	CTTGGTGATT	AGAGACCAAT	TCCCAAACAT
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5	TCAGTTGCA	TAGGAAACAC	CTTGTGATGC	CTAATCTTT	TATTTTATT	ACTCTATTAG	TCACTACAAC
	TATTTTCTGA	TTGCTATGGT	GATAGATGGT	TTAAAACAAG	CCTTCATTAA	GAATGTCAC	ACCATGGTCT
	CAGTCAAAA	CACCAACATT	TTTATTGGA	TTGACAATT	TGGGAATATC	CAATTCCAAG	AAGACAAGGA
	GACCTCTGAA	CTTICCTAAAT	GAAGACTCCA	ATCTCCTGA	TCTGATGGGA	AGCAGCTTGG	CAAGATTACC
	AACCACCACC	ACAGAGAGTG	GAECTCTAAC	TAAGACTTAA	AAGATAAGTA	GAAATTATCC	AGGTAAGAT
	GTGTACAGAG	AAGGAAGTAC	ATCCAGGGGA	AAAGAACAAAT	ACGTGAAAAA	GTACGGAAAT	GGTAAAAGT
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	GGACCAAAA	GAAGGCCAGT	GTGCCGTGAG	CATACTAACG	ACAGAGGAAA	ACACTGTTAT	ATGCTGAGAT
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	ATAATGTTAG	CTTAGACTAG	GATAGTGTGC	GTAGAAATAA	ATAAAGTGG	CACTCTACTT	TGGGGTAGA
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25	CTTGTGTTG	CAAATAATT	TTGAGAGGCT	TATTAGACAT	CCCAGTGGAG	ATTCAGGTG	AGTGGAGCCC
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	GCAGACAGAT	CAGCTGAGCT	CAGGAGTTG	AGACCAGCCT	GGGCAACATG	GGAAAACCCCT	GTCTCTACAA
	AATATGAAA	ATATTACCTG	GGCATGGTGG	CATATGACTG	TGGTCCAAGC	CACTGGGGG	GCTGAGATGG
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30	GGCAAATGCA	TAGIATTTAA	AGCCAGGGGA	GTAGATGAGA	TACTCAAAGT	AGGTGAAGAT	AAGGAGGCAA
	TGAAGGCCA	GGACTCTGGT	GTACATTGAG	ATGGTTATAA	GAGGAATAGA	AACTGGCAA	ATAAGTAACA
	CTGAGCACC	AATGAGGTGG	AGAGGAAAGC	CAGGAGATGA	AGCATCATAG	AAGGCAAGAG	AAGAAGGGTG
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35	TTTGGAAATA	TGATGAGCAC	TTTGTGAGGA	GTGTTGAGAC	AGAAGACCAA	TTAGAGTAGA	TTGAGGAGAT
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	GACACAGAGT	CTTAGCATGT	CTTGTCTTC	TATGGGAAAT	GTAAATAGTT	TGAGATCAGG	GATAGTATT
	TATTCTGCTT	TTTGATACCTC	TACATTACCT	AGCATAGAGC	TAGCTAATGT	GCACCTAAAGT	ATGTTCTCAA
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40	ATGGATGGAT	GGAAAGCTTC	TGATTTGCCA	AGAAGAGGAT	ACTGGTAGCA	GAAATAAAA	CAGCACTGGA
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	AGATAATTAA	TGTAATTGTT	CACTTAGGAT	TTTTAAATGT	GATCACTGAT	ATTGGACATG	TTCTCTAGTA
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	ACAGGGTGT	AGCTCTTCC	TTCCAACCTC	ATGGCTGTTG	TACCTTACCT	TCGACCCCCG	TGTTCTGAA
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	TTGAAATCCT	CCTITCCAT	TTTGTGTC	TTCCTTTCC	ATAGGCACCA	GAATATCAT	GGTGCCTGGA
	TCTCATCT	ACAGAAAAAA	AAAGTGAATT	GATAAAACTGA	TTTATATTGT	GTCCAAATGT	GATTGTATT
	TCAAAGATAA	CCTAAGGGGA	GAATGCTGTC	TGGCCCAACA	GCAGGCTCTC	GACTCATTT	CAGACACTGT
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	CATTATATG	TGCACTCATGC	TAGGGACTGG	AACCTAGTAA	GTGTAGCACA	TATTATTCA	TTAATCCTC
	ACAACAAACC	CATGAGGTG	GTTTTATGAT	CCCAATT	CAGAAGAAGA	AACTGATATT	CAGAACCAAGT
60	TAACTAACG	GTTCAAGGTC	ATGCAATTTC	TAAGATACAG	AACCAAGAGT	CAAAGACATG	ATTTTAAACC
	AAAGCTTTT	CTGCTACTCC	ACATTGCTC	CCTAGGTGAG	ATCTGAGGCA	TTCCCGAAA	AGAGAAGGGT
	CATAAAGCCA	AGGCGAACACA	AGCTTAGGAA	AAAAAAGGGA	AATGTCCTAA	ATAAACAGCT	TTCCCTATTAA
	CCAGAAACCA	CTACTTTAA	AAATATAATGG	AAAAAAATCCT	ATTCACTTAA	ACAATGTTAA	AAAAAAAAAA
	GATAGAAGAA	ACATAGGGAT	AAACTTAACA	CATTGTTAGG	ATATGTAAG	AAACTAAAAG	ATGTTAATAA
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65	TCTAGGTGTT	CCATTTCTCA	CCAAATTAAAT	GTATACATT	AATACAATGT	CAAACGAAAT	ATCTTAGGAA
	TTGCTTACAA	ATTGTCAGAT	AATTACAAAG	TTTACCTGGG	AAATATAAGC	ATATATGAAG	AGTGAATGGG
	ACCCCAACAC	TCCCCAAA	ACAAAAAAGG	TCTGAAAAGG	ACAGAAATCA	AGGAGAGTCT	TGCCTGCCAG
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5	GGAAAGGAGG	GAGGATAAAA	TTAGGTTCC	GCCTTCATCT	TACATTAAAA	TAATTCAG	ATGTATTACA
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10	CTACAGGCAT	GCGCACCCCC	ATCCAAC	TTTTTATT	TTTGTAGAGA	CAGGGTCTT	GCTTGTTC
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	ACTAAACTGC	TAFAAGCAAT	TCAAAACAAA	AAACATAAAC	TATGCATATA	TGTATGTGAA	AAAGTTAAC
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25	TAATTAATAT	AGATCAGAAC	ACTTAAAAA	TATTTATAGG	CCAGGCACGG	TGGCTCATGC	CTATAATCCC
	AGCACTTTGG	GAGGCCAAGG	CGGGTGGATC	ACCTGAAGTC	AGGAGTTGA	GACCACCTG	ACCAACATGG
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	GCCTATTGCA	ATATGCTTT	TAATGCTAA	AAAAATTGGG	GAAAATGCTT	TAAAAATATA	GATTAAGACT
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50	CTGTCCTAAC	CACTCAAACC	CTAGCTTTT	CTCTGAAC	CTAGAAATAT	TTTCTCTCA	TTGGCCATT
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55	CTGTCGCTA	GAATGGGGGG	AAAGTGGTGTG	ATCACAAC	ACTGCAAC	CTACCTCCC	GCTCAACAGT
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	ACATTA	ATTCCCCCAG	CAGGAGCCAA	CCAATT	CATCCTGATC	CAAGTTAGCA	AACTGCAAAA
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	CTCAATTCCA	TTCAATGTGAC	TGCTCC	CCTCCCTCT	CTCTTC	TACTATTATC	TCTTCCCCCC
	TCCCTCATTT	TTAATGTATG	ATCTTGTTC	CTATTCTCT	GAGAAAATAG	AAGCCATCAA	AAGAGAGTTT
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	TACTCTAACT	AGTACATAT	GATTCTGTC	CCCAGGTCCC	CTCCCTCAGT	TGTTTGAAC	ATAATCATTT
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5	ACCATGTTGT	CCAC GCTGGT	CTCAAAC	TGACCTCAAG	TGATCCGTC	GCCTCAGGCC	CTCAAAGTGC
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	TGGTCACTC	CAGC'AAAAC	TGACTAATCG	GGGGTCAGGG	ATACAAACCC	TGCA	GTTGTTTCT
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	AGGGTACATG	TGCAACACGT	GCAGATTG	TACACAGGA	TAATGTGCC	ATGTTGGTT	GCTGCACCCA
	TCAACTCGTC	ATTACATTA	GGTATTCTC	CTAATGCTAT	CCCTCCCCCA	GTCCCCCACC	CCCCGACAGG
30	CCCTGGTGTG	TGA'TGTC	CTTCTGTG	CCAAGTGT	TGTTTATGTG	ATAGATTACG	TTTATTGATT
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	GCTGGCGC	AGTGTGCGA	TCTTGGCTCA	CTGTAACCTC	TGCCACCTGG	GTTCAGCAA	TTCTCCTGCC
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	CCCAAAAGTGC	TGGGATTACA	GGCATGAGC	ACTGCGCCCA	GCCCACAGGT	TTTCAAAGA	CTAAACTAA
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	CTCTCAGCCA	AAGC AATACC	AAAGTAAACC	TGAAA	GTTTGGCCA	GGATTGGGGG	TAGGTGGGG
	AAGCCCAACA	TGA'CTCATTA	TTCTCTC	CCTTGGAT	TCAGGCACAA	CTGAATGTCA	GCATTGACAC
	TAAAACACAG	ATCITAAGAC	TGACAAGCC	GACTTTGT	AGCAGAGAGC	CAGGCCCTGG	AAGAAATCAA
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	GTAGCTGG	TTACAGATCC	ATGCCACTAT	GCCCAGCTAA	TTTTGTATT	TTTGTTAGAG	ACAGGGTTTC
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	GACTAAAAG	CCCCACTCCT	TCAAGTTATC	CCGCC	GGACTGAACC	AATGACACC	TTATATGTG
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	TCATCAGTCA	CTG'GCCAGC	TTCATATCTG	ACTGAGGTCA	TACAGTT	TGATTGTTAG	CTTTGCTACT
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	TGCCTCTAA	GCATCAGCT	CACCA	CCAGTCTC	TCCCCTATTA	GTCTGATTAA	AATCTGCTTA
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	TATGTTATT	AGGA AACTAG	TCATT	TAATAGAAC	AAATGCTGG	CCTTGGGGT	TGGCAATGGA
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	TTGAATGTA	TGTITACAGT	GATCCAGACC	TGGGGATGCT	TGCTTCCGA	CGTGTCTGG	GATCGCGCTT
	CTGAAAAAGC	TCACTCTACA	ACGCCTCTC	CGGACCTAA	TCGCGCACCA	GTGAGTCGAG	TCCTCCAGGG
	GCTAGAGAAG	CCCGACTTTC	TTTCCGGCT	TGAGGGACCC	GGGCTCACCA	AGAAACCAAGC	CGCCCTCCCTC
30	TCTATGGTT	TGGAGCCGGC	GGAGAGCGCG	CAAGGGTTGG	CGGGACTGCG	AGTTCCGGT	CTGGGCTTTG
	GCGGGTCTGG	TTTGAAGCTC	TCCTGTTGA	CGAAAGTATG	TCTCAGGAAG	GTGCGGTCCC	AGCTAGCGCG
	GTTCCCTGG	AAGP ATTAAG	TAGCTGGCA	GAGGAGCTAT	GCCGCCGGGA	ACTGCCGTCC	GTCCTGCC
	GACTCCTCAT	ATCTCTTCTT	GGTTGTCACT	TCTACCTAGA	GAAGGGTGTG	GGCAGGTCGC	GAACCTTCT
	CTTCTGTCCC	TTCA GACCCA	CCGCCAGGCT	GGGTTATATT	ACCGCGGCT	GAACCCCCCTC	TTTCTTTG
35	CAGTGAGTGG	GATC AAAAGT	GAGGGACTGG	AGGGGAAGCG	ACAACCGTGG	TAGATTAAG	TAAGGCTTTG
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	CTTCTTCAG	TTTTCTGTGA	CTCGTTGCTT	GCAATTAAAGT	GTAAATACTT	TTGCTAGTGG	ATAATGGGG
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	CTGAGCTTT	GTCT CCGTA	AAAAGGGTGG	TGAATATGAA	TAAGGGCTTT	CTTAGCGTTA	TAAGAATTAA
40	AGGGCATAGT	TCTCTGGTGT	GAAATCTTA	AAAGATGTT	AGTAAATAAA	AATGATTTTC	CTCCTTCCCC
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	TCGTCGGGT	GCACACATT	CTTGATTGGT	CTCATGCCIT	TGTGGTTGTA	AATGTGCTG	GAATCCTAGC
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45	CAAAAGAAA	AAA`TAACCT	TCACTTGAGA	GAATCTCAAT	ACTGCACAAA	TATTGTGCAG	CTAAAGCCT
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	AGTTTTGTG	TAGG TACAGA	ACTGCCGTCT	TCAAGGAGTT	TCAACTTGAA	AACAAATAGC	CACCCCTAAA
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	ACAAAAATTC	TTTGTTCAT	ATTGTATAA	GATCTGATAT	AGCTGCAATC	AATCTTGCA	TTTTCTTCA
	CCAACGCATT	GCGACCTTTA	GGGATACAAG	TATGTTGTG	CATGTATATG	TATGTATCAG	TCTTTAAAT
	TTGATATAGT	CATACTTTG	TTTTTATT	GAAAAGTTAG	AGTGTGAAT	TGGTATCCC	TTTATGAAAC
	ATTATATTCT	AAAAATTGT	AGTACGATTA	TTGGGAATTA	TAACTCATTT	TCCTGTAACA	CTGTTATACA
20	TAGTACCTT	TGCTTTCAGA	CTAGCCCTCA	ATTTTATT	ACTATAGTAG	TCCTAAATT	TAAGGATTAAT
	AGTACTCAGG	ACC'AACAGT	TATAATGTCAT	TTGTTTTT	TTTTTTGAG	ATGCGCTTC	ACTCTGTAC
	CCAAGCTGGA	GTGCACTGGT	ATGACCTTGG	CTCACTGCAG	CCTCTGCTC	ACGGGTTCAA	GGGATCGTC
	TGCTTACGCC	TCCTGAGTAG	CTGGGATTAT	AGGCCTCTGC	CACCAAGCCT	GGCTAATT	TTTATGAGAG
	ACGGGGTTTC	GCACTGTGG	CCAGGCTGGT	CTCGAACCTC	TGACCTCAGG	TGGTCCACCC	GCCTTGGCCT
25	CCCAAAGTGC	TGGGATTACA	GGTGTGAGCC	ACCGCGCCCC	GCCTATATGT	AATAATT	ATGGGACCAT
	GAATTGAATA	TTTCTCCTT	GAATAGCAAT	GACATAGCCC	CTTCTATTGT	ACATCTGCAA	GCTGATACAG
	GGAATTCCCTT	TGTACCTGCG	CTCTTCCCTG	CCAGTCAGCT	ATGGGGTGA	AAGTGTAGGG	GTTCATCCAA
	GTCCTAAACAC	TGGTAGCAAC	TCCTAGGGCA	GGGCTGATCT	GGAAGGACAG	ACCCCTAGGGG	AGGGTGGAAAC
	TTTAAAAAAGA	AGTICCTGAAG	GTAGTAAGAA	GGAAATGAGG	AGTAGTGT	GGAAGGGGCT	AACTTTTTC
30	TTCTTGCCTC	TCTCTTTAT	CTCACCTGCC	CCTCCCCCTG	TATCCCTTCT	TCCTTTTCTC	CTTCCCTTT
	TTGTCCTC	TTCATCTGT	CATCTTCT	GATCCTCTT	ACCTTGTCAA	AAGGAGAACT	TTGTTGGGT
	ATCCTATATC	AATCGCAGGA	AGGTTGTTT	CTTCTTAC	TTTATCCTAT	AGATTCATAT	TCTCAACACC
	AACTCCTCC	TTTTCAGTT	TCCTCTTGC	TTCTCTTGCAC	ACCACAGAGT	TTGCACTGAG	TACTTGGAGA
	GGAAAATTAA	ACAGAGATAC	TTGGACCAAG	AGTAAGATGA	AGAAAAGTCA	AAACAAGCTA	TAGTCTATAG
35	TGGCAAGAGA	GAGTATGGG	GCTGCTTAGC	CAGGGTGGCT	GTACATAAAG	TATATCTCA	TTTATATATAA
	ACTGTTATA	GATCGAAATC	AGAAAATT	AATTCTCTTA	ACTGTCAAAG	AAAATTCTCA	TTTTTCAAA
	TTTGGGACTG	ATAATGTA	CCAGTTCTGC	TTACTGTCCA	TTGCCCTGAAA	TGGAGCTTTG	AGGTGGACTG
	TATAATTCT	TCAATCTAA	CTCCAAATT	TGATCAGCGA	CGCCCTCTGC	TGTTCACTAT	TAATATTAT
	TTACCAATCA	AAGTAAAGTA	TTGAAGTTT	CCTGGCAGTT	TTCACTTTGT	GTTTAGTCC	ATTAGGCTG
40	CTATAACAAA	ATCCCTTAA	CTGGGTAAGG	GATTATAAT	ATTAGAAATT	TATCTCTCAC	AGTTCTGGAA
	GCTGGGAAGC	CCAATATCAA	GGCACCGATA	GATTGGTGT	CTAACAGGGG	TGTGCCGTCT	GCTTCAAA
	TGGCCCCCTG	TTGCTGCATC	CTCACTTAGT	GCAAGGGCA	AGACAGCTCC	CTTCAACCTC	TTTTATAAGG
	GCACTTATGT	CATCATGAG	GGCACAGGCC	TCATGACTTA	ATCACTTCCC	CAAAGCCCC	ACCTCTTAAT
	AGTATCACAT	TGGCTGTTAG	GTGTCTGGGA	GGACACCAAT	CTTCAGGCCA	TATCATCTCA	CTTGGAAAAAA
45	AGTCAAAATA	AAAACAGTAG	ATTTAATTAA	TATTACACTA	TTTATAGAAG	CATGTGATGT	ATCATCCCT
	GTATTAAATT	CCTGGGGTTG	CCGTAACAAG	TTACCACAA	CTAGGTGGCT	AAAACAATA	GAATTATT
	CTCTCACATT	TCTAAGGGCA	GAAGTTACA	GTGTGTCAT	AGGGCCATGT	TCTCTGGAAG	GCTTTAGGGG
	AGAATATATT	TCAATCTTT	CTCTTAGCTT	CTCGGTGTCA	CTGGCAATCC	TTAGCTTACT	TTGGCTTCT
	GTGTCTTAC	ATCATCTTT	TATAAGAAC	CCAGTGTAG	TGATTAAGGG	CATACCTTAC	TTAATATGA
50	CCTCATCTTA	ACTAATTATG	TCTCTAA	CCCTATTCTC	AAATAAGGCC	ACATTCTGAA	GTATTGGGAG
	TTAGAACTTA	AAGCTTTTG	GGAGGGACAC	AGTCAACCC	ATAACAACCC	CTAAATCTGA	TATTATTTCT
	CAATTAAAGTC	TTGAATTGG	TTTCAAAAG	AGAATATTCT	ATTAGAGTTT	TTAATGTATA	TTTTAACAT
	ATAGTTCTTT	AGCCCTTAA	TTTTTTT	TTTTTTTTT	TTTTTTTTT	TTTTGAGAC	GGAGTCTCGC
	TCTGTCCGCC	AGGCCTGACT	GCGGACTGCA	GTGGCGCAAT	CTCGGCTCAC	TGCAAGCTCC	GCTTCCCGGG
55	TTCACGCCAT	TCCCCCTGCC	CAGCCTCCCG	AGTAGCTGGG	ACTACAGGCC	CCTGCCACCG	CGCCCGGCTA
	ATTTTTTGT	ATTTCTAGTA	GAGACGGGGT	TTCACCTTGT	TAGCCAGGAT	GGTCTCGATC	TCCTGACCTC
	ATGATCCACC	CGCCCTGGCC	TCCCAAAGTG	CTGGGATTAC	AGGCGTGAGC	CACCGCGCCC	GGCCTGCC
	CAAITATTTA	GTTITCTAT	AAACAGGGAA	ATTATTGT	GTGGCCCTTA	GAACAAATT	AATTCTCACT
	CTAATTCTTA	CTTATGTTTA	TATAATGCTT	TTAGAAATT	GTATTATTCA	GAAAATAAAC	ATATACTATT
60	GTATCTGTG	CCTACACTTA	GATTTTATTG	CCTGCTATAT	TTAAATT	TTAGTATT	AATTGTTTA
	TTAAAGAAAG	AATCTGCGCTG	TAATCTCAGC	ACTTTGAGA	GGCCAAGGCA	GAAGGATTGC	TTGAGCCCCAG
	GAGTTTGGAGA	CCACACTGAG	CAACACAGGG	AGACCCCCAT	CTCTACAAA	AATAAAAAAA	TTCTCCAGGC
	CTCATGCGAC	ATACCTGTAG	TTCTAGTTAC	TTGGGAGACT	GGGGTGGGGAG	GATGCATTGA	GCCCAGGAGA
	TTGAGGCTGC	AGTCAGCCAT	GATCAGGCCA	CTGTA	GCTTGGACAA	CAGAGTGAGA	GCTTGTCTAG
	ATAGATAGAT	AGATAGATA	TCTAAATAGA	TAATAGACAG	ATTATCTAA	TAGATAATAG	ACAGATTATC
65	TAATAGATA	ATACACAGAT	TATCTAAATA	GATAATAGAC	AGATTATCTA	AATAGATAAT	AGACAGATTA
	TCTAAATAGA	TAATAGACAG	ATTATCTATC	TAATAGATA	ATAGATTATC	TAATAGATA	ATAGATAGAT
	AGATTAGATA	GATGATAGA	TAGATAGAGC	TTGGACAACA	GAGTGGAGAC	CTGTCAGAT	AGATAGAAAC
	AAAGAAGAA	AGAAAGAAATG	GTGCTCATAT	TTTAAAGCAT	TGAAAAATGG	TCTTCCTTGC	TTATATTACC

	CACACCTTCT	TTGTGGCAT	TAAGATGCAA	ACTTGTGTTT	AAACAGTGA	GTAATCAA	GATGGGACTG
5	TTAAGTTATT	TGTGTTATT	ACCTGCTTT	TGAAAATGTA	AAAATAAAC	TCTAGGTTA	ATTAGTAGTA
	TGCTATTAG	TAATGAAGTA	AAGCTAGAGG	CTTCGAACAA	ATCTTGTTA	ATTTCCTCTT	GAATGAGAGA
	GAAAATTAA	AGTAAGCAA	CAAATAAGTT	GTGTGTCACC	ACTCATTCA	TCATTTAAC	AGTATTCCA
10	GAGTACTTAT	TCTGTGCCAG	GAAATGTTGT	AGGTGCCCTC	AACAACCTAG	AGTCTAGCCT	GAGACACAAG
	TAAGTAGGTA	ATTATTATAG	AATGGTATGA	TCTTGGAGG	ACTGGGTATT	GGCTGGCTCA	TGGGAGTACA
	AGATAGGTAC	CCAGTGATGA	AGTCAGGAAA	GGTTCTTAT	GGTGATATGA	TGACGTCTAT	GCTGATTATA
	AGGTCACTGT	AGAATAAACT	TTGTGCTTT	AAATTTCAT	AGCACTGTAT	TAGAGAGTT	ATCTTCAAAA
15	TAATCGAAAA	GGCTGAGTGT	GGTGACCCAT	GGCTGTAATC	CCAGCACTTT	GGGAGGCCGA	GGTGGGCAGA
	TTGCTTGAGC	TAGGAGTCG	AGACCAGCT	GGCCAACATG	GTGAAACCCC	GTCTCTACTA	AAAATACAAA
	AATTAGCCAG	GAG'GATGGT	GCGCACCTGT	AATGCCAGCT	ACTTGGGAGG	CTGAGGCCAGG	AGGATCATT
	GAACCCAGGA	GGTGAGGTT	GAAGTAAGCC	GAGGTCTATGC	CACTGCAC	CAGCCTGGGC	AACAGAGTGA
20	GAECTCATCT	CAAAAAAAAA	AAAATGATC	AAAGAAAGGT	GAATTTTCAT	TCACCCATT	TCTGCTGAGG
	AAAATGGACT	ATTICAAT	ATTTTAATA	AGGGTCAAAA	TGAGGGATC-3'	(FRAG.NO:) (SEQ.ID NO:2480)	(FRAG.NO:) (SEQ.ID NO:2480)
25	5'-CCTGAGACAG	AG3CAGCAGT	GATACCCACC	TGAGAGATCC	TGTGTTGAA	CAACTGCTTC	CCAAAACGGA
	AAGTATTTC	AGCCTAAACC	TTGGGTGAA	AAGAACTCTT	GAAGTCATGA	TTGCTTCACA	GTTTCTCTCA
	GCTCTCACTT	TGGTGCTCT	CATTAAGAG	AGTGGAGCCT	GGTCTTACAA	CACCTCCACG	GAAGCTATGA
	CTTATGATGA	GGCCAGTGC	TATTGTCAGC	AAAGGTACAC	ACACCTGGTT	GCAATTCAA	ACAAAGAAGA
30	GATTGAGTAC	CTAAACTCCA	TATTGAGCTA	TTCACCAAGT	TATTACTGGA	TTGGAATCAG	AAAAGTCAAC
	AATGTGTGGG	TCTGGTAGG	AACCCAGAAA	CCTCTGACAG	AAGAAGCCAA	GAACCTGGCT	CCAGGTGAAC
	CCAACAATAG	GCAAAAGAT	GAGGACTGCG	TGGAGATCTA	CATCAAGAGA	GAAAAAGATG	TGGGCATGTG
	GAATGATGAG	AGG'GCAGCA	AGAAGAAGCT	TGCCCTATGC	TACACAGCTG	CCTGTACCAA	TACATCCTGC
35	AGTGGCCACG	GTGAATGTT	AGAGACCATC	AATAATTACA	CTTGCAAGTG	TGACCCCTGGC	TTCAGTGGAC
	TCAAGTGTGA	GCAATTGTG	AACTGTACAG	CCCTGGAATC	CCCTGAGCAT	GGAAGCCTGG	TTTGCAGTCA
40	CCCACGGGA	AACTTCAGCT	ACAATTCTC	CTGCTCTATC	AGCTGTGATA	GGGGTTACCT	GCCAAGCAGC
	ATGGAGACCA	TGCAATGTT	GTCCTCTGG	GAATGGAGTG	CTCCTATTCC	AGCCTGCAAT	GTGGTTGAGT
	GTGATGCTGT	GACAATATCC	GCCAATGGGT	TCGTGGAATG	TTTCCAAAAC	CCTGGAAGCT	TCCCATGGAA
45	CACAACCTGT	ACATTGACT	GTGAAGAAGG	ATTGAACTA	ATGGGAGCCC	AGAGCCTTCA	GTGTACCTCA
	TCTGGGAATT	GGGACAACGA	GAAGCCAACG	TGTAAGCTG	TGACATGCG	GGCCGTCGGC	CAGCCTCAGA
	ATGGCTCTGT	GAGCTGCAGC	CATTCCCCG	CTGGAGAGTT	CACCTTCAA	TCATCTGCA	ACTTACCTG
	TGAGGAAGGC	TTCAATGTTG	AGGGACCAGC	CCAGGTTGAA	TGCAACCAC	AAGGGCAGTG	GACACGAA
50	ATCCCAGTT	GTGAAGCTTT	CCAGTGACACA	GCCTGTCCA	ACCCCGAGCG	AGGCTACATG	AATTGTCTTC
	CTAGTGTCTC	TGGCAGTTTC	CGTTATGGG	CCAGCTGTGA	GTTCTCTGT	GAGCAGGGTT	TTGTGTTGAA
	GGGATCCAAA	AGGCTCCAAT	GTGGCCCCAC	AGGGGAGTGG	GACAACGAGA	AGCCCACATG	TGAAGCTGTG
55	AGATGCGATG	CTGTCCACCA	GCCCCCGAAG	GGTTTGGTGA	GGTGTGCTCA	TTCCCTTATT	GGAGAATTCA
	CCTACAAGTC	CTCTTGTGCC	TTCACTGTG	AGGAGGGATT	TGAATTATAT	GGATCAACTC	AACTTGAGTG
	CACATCTCAG	GGACAAATGGA	CAGAAGAGGT	TCCTTCCTGC	CAAGTGGAA	AATGTTCAAG	CCTGGCAGTT
	CCGGGAAAGA	TCAACATGAG	CTGCAGTGGG	GAGCCCGTGT	TTGGCACTGT	GTGCAAGTT	GCCTGTCCTG
60	AAGGATGGAC	GCTCAATGGC	TCTGCAGCTC	GGACATGTGG	AGCCACAGGA	CACTGGCTG	GCCTGCTACC
	TACCTGTGAA	GCTCCACTG	AGTCCAACAT	TCCCTTGGTA	GCTGGACTTT	CTGCTGCTGG	ACTCTCCCTC
	CTGACATTAG	CACCAATTCT	CCTCTGGCTT	CGGAAATGCT	TACGGAAAGC	AAAGAAATT	GTTCTGCTCCA
	GCAGCTGCCA	AAGCTTGTAA	TCAGACGAA	GCTACCAAA	GCCTTCTTAC	ATCCTTTAAG	TTCAAAAGAA
	TCAGAAACAG	GTGCAATCTGG	GGAACTAGAG	GGATACACTG	AAGTTAACAG	AGACAGATAA	CTCTCCTCGG
65	GTCTCTGGCC	CTTCITGCC	ACTATGCCAG	ATGCCATTAT	GGCTGAAACC	GCAACACCCA	TCACCACTTC
	AATAGATCAA	AGTCAGCAG	GCAAGGACGG	CCTTCAACTG	AAAAGACTCA	GTGTTCCCTT	TCCTACTCTC
	AGGATCAAGA	AAAGTGTGTC	TAATGAAGGG	AAAGGATATT	TTCTTCCAAG	CAAAGGTGAA	GAGACCAAGA
	CTCTGAAATC	TCAAAATTCC	TTTTCTAACT	CTCCCTTGCT	CGCTGTAAA	TCTTGGCACA	GAAACACAAT
70	ATTITGIGGC	TTTCITCTT	TTGCCCTTCA	CAGTGTTCG	ACAGCTGATT	ACACAGTTG	TGTCATAAGA
	ATGAATAATA	ATTATCCAGA	TTTTAGAGGA	AAAAAATGAC	TAAAAATATT	ATAACTTAA	AAAATGACAG
75	ATGTTGAATG	CCCACAGGCA	AATGCATGGA	GGGTTGTTAA	TGGTGC	CCTACTGAAT	GCTCTGTGCG
	AGGGTTACTA	TGCAAAATT	AATCACTTC	ATCCCTATGG	GATTCACTG	TTCTTAAAGA	GTTCTTAAGG
	ATTGTGATAT	TTTACTTGC	ATTGAATATA	TTATAATCTT	CCATACTCT	TCATTCAATA	CAAGTGTGGT
	AGGGACTTAA	AAAATTTGTA	AATGCTGTCA	ACTATGATAT	GGTAAAAGTT	ACTTATTCTA	GATTACCCCT
80	TCATTGTTA	TTAACAAATT	ATGTTACATC	TGTTTAAAT	TTATTTCAA	AAGGGAAACT	ATTGTCCCC
	AGCAAGGCAT	GATGTTAAC	AGAATAAAGT	TCTGAGTGT	TTTACTACAG	TTGTTTTTG	AAAACATGGT
	AGAATTGGAG	AGTAAAAC	GAATGGAAGG	TTTGTTATATT	GTCAAGATATT	TTTTCAGAAA	TATGTGGITT
	CCACGATGAA	AAACTTCCAT	GAGGCCAAC	GTTTGAACT	AATAAAAGCA	TAAATGCAA	CACACAAAGG
	TATAATTAA	TGAAIGTCTT	TGTTGGAAAA	GAATACAGAA	AGATGGATGT	GCTTGCATT	CCTACAAAGA
	TGTTGTCAG	ATGTGATAG	TAAACATAAT	TCTTGTATAT	TATGGAAGAT	TTTAAATTCA	CAATAGAAC
85	TCACCATGTA	AAACAGTCAT	CTGGTAGATT	TTAACGAAT	GAAGATGTCT	AATAGTTATT	CCCTATTGTT
	TTTCTCTGT	ATGTAGGGT	GCTCTGGAA	AGAGGAATGC	CTGTGTGAGC	AAGCATTTAT	GTTTATTAT
	AAGCAGATT	AAACATTCA	AAGGAATCTC	CAGTTTCAG	TTGATCACTG	GCAATGAAA	ATTCTCAGTC
90	AGTAATTGCC	AAACCTGCTC	TAGCCTTGAG	GAGTGTGAGA	ATCAAAACTC	TCCTACACTT	CCATTAACCT

AGCATGTGTT GAAAAAAAAGTTTCAGAGA AGTTCTGGCT GAACACTGGC AACGACAAAG CCAACAGTCA
 AAACAGAGAT GTGA TAAGGA TCAGAACAGC AGAGGTTCTT TTAAAGGGC AGAAAAACTC TGGGAAATAA
 GAGAGAACAA CTA CTGTGAT CAGGCTATGT ATGGAATACA GTGTTATTT CTTTGAAATT GTTTAAGTGT
 5 TGTAATATT TATG TAAACT GCATTAGAAA TTAGCTGTGT GAAATACCAG TGTGGTTGT GTTTGAGTT
 TATTGAGAAT TTAAATTAT AACTAAAAT ATTATATAAT TTTTAAAGTA TATATTATT TAAGCTTATG
 TCAGACCTAT TTGACATAAC ACTATAAAGG TTGACAATAA ATGTGCTTAT GTT-3' (FRAG.NO.:) (SEQ.ID NO:2479)

5'-CCT TGC CTG CTG C-3' (FRAG. NO: 1739) (SEQ. ID NO: 1752)

5'-GTT GTC CC-3' (FRAG. NO: 1740) (SEQ. ID NO:1753)

5'-GTT CTT GGC TTC 'TC TGT C-3' (FRAG. NO:1080) (SEQ. ID NO:1088)

10 5'-GGC TGG TGG-3' (FRAG. NO:1083) (SEQ. ID NO:1092)

5'-CGT TGG CTT CTC 'GTT GTC CC-3' (FRAG. NO:1081) (SEQ. ID NO:1089)

5'-TGT GGG CTT CTC 'GTT GTC CC-3' (FRAG. NO:1082) (SEQ. ID NO:1090)

5'-CCC TTC GGG GGC TGG TGG-3' (FRAG. NO:1083) (SEQ. ID NO:1091)

5'-GGC CGT CCT TGC CTG CTG G-3' (FRAG. NO:1084) (SEQ. ID NO:1093)

15 Human P Selectin Fragments

5'-TTT TCT CTT TCG CTT TCT TTT CGT CTC CTG TTC CTC CTT TT TTG CTG TTT TTT CTC CTT CTT CTC TCC
 TTT CTT TTC-3' (FRAG. NO: 1741) (SEQ. ID NO: 1754)

5'-TCC TTT CTT TTC-3' (FRAG. NO: 1742) (SEQ. ID NO: 1755)]

5'-CTC CTT TT-3' (FRAG. NO:1743) (SEQ. ID NO:1756)

20 5'-TTT TCT CTT TCG CTT TCT TTT CGT CTC CTG TTC CTC CTT TT-3'(FRAG.NO:1085)(SEQ. ID NO:1094)

5'-TTG CTG TTT TTT CTC CTT CTC TCC TTT CTT TTC-3' (FRAG. NO:1086) (SEQ. ID NO:1095)

Human Endothelial Monocyte Activating Factor

Nucleic Acid & Antisense Oligonucleotide Fragments

5'-TTT TCT CTT TCG CTT TCT TTT CGT CTC CTG TTC CTC CTT TT TTG CTG TTT TTT CTC CTT CTC TCC
 25 TTT CTT TTC-3' (FRAG. NO: 1744) (SEQ. ID NO: 1757)

5'-CC TTT CTT TTC (FRAG. NO: 1745) (SEQ. ID NO: 1758)

5'-CTG TTC CTC CTT 'T-3' (FRAG. NO:1746) (SEQ. ID NO:1759)

5'-TTT TCT CTT TCG CTT TCT TTT CGT CTC CTG TTC CTC CTT TT-3'(FRAG.NO:1087)(SEQ. ID NO:1096)

5'-TTG CTG TTT TTT CTC CTT CTC TCC TTT CTT TTC-3' (FRAG. NO:1088) (SEQ. ID NO:1097)

30 Human IL3* Nucle c Acid and Antisense Oligonucleotide Fragments

5'-CTC TGT CTT GTT CTG GTC CTT CGT GGG GCT CTG TGT CGC GTG G GTG CGG CCG TGG CC GGC GGB CCB
 GGB GTT GGB GCB GGB GCB CGG GCB GGC TCB TGT TTG GBT CGG CBG GBG GCB CTC (FRAG. NO:
 1747) (SEQ. ID NO: 1750)]

5'-G GBG GCB CTC-3' (FRAG. NO: 1748) (SEQ. ID NO: 1761)

35 5'-GT GGG GCT CTG-3 (FRAG. NO:1749) (SEQ. ID NO:1762)

HUMIL3AAS1: 5'-CTC 'GT CTT GTT CTG GTC CTT CGT GGG GCT CTG-3' (FRAG.NO:1089)(SEQ.ID NO:1098)

HUMIL3AAS2: 5'-TGT CGC GTG G GTG CGG CGG TGG CC-3' (FRAG. NO:1090) (SEQ. ID NO:1099)

GGC GGB CCB GGB G' T GGB GCB GGB GCB CGG GCB GGC GGC TCB TGT TTG GBT CGG CBG GBG GCB CTC
 (FRAG. NO:1091) (SEQ. ID NO:1100)

40 Human IL3 Receptor Nucleic Acid and Antisense Oligonucleotide Fragments

5'-TCT GGG GTG TCC TGG CCT TCG TGG TTC CTC CTT CGT TTG CCG TCC GCG GGG GCC CCC GGG CCT
 GGC TGC GCT CCT GGC CCG CCT CTT TCC CGG GCT CTT GCG CTG GGG GGT GCT CC CGT GTG TTT GCG CCC
 45 TC CTC CTG GTC GCG CTT GTC GTT TTG GGG CGC GCT TTG CCC GCC TCC CGG CGC CTG GCC CGG CC TTC
 CTG GGC TGC GTG CGC GTT CTG TTC CTC CTG GCT CTG GGG TGT CCT GGC CTT CGT GGT TCC TCT TCC
 TTC GTT TGC CGT CGG CGG GGG CCC CGG GGC CT GGC TGC GCT CCT GCC CGG CCT CTT TCC CGG GCT CTT
 GCG CTG GGG GGT GCT CCC GTG TGT TTG CGC CCT CCT GGT CGC GCT TGT CGT TTT GG GGC CGG CTT

TGC CCG CCT CCC GGC GCC TGG CCC GGC CTT CCT GGG CTG CGT GCG CGT TCT GTT CTT CCT GGC GCA
 GGA GAC AGG GCA C GG CGA TCA GGA GCA GCG TGA GCC AAA GGA GGA CCA TCG GGA ACG CAG CTC CGG
 AAC GCA GGA CAG AGG TGC C GC BGG BGB CBG GGC BGG GCG BTC BGG BGC BGC GTG BGC CBB BGG BGG

50 BCC BTC GGG BBC GCB GCT CGG GBB CGC BGG BCB GBG GTG CC-3' (FRAG. NO: 1750) (SEQ. ID NO: 1763)

GBG GTG CC-3' (FRAG. NO: 1751) (SEQ. ID NO: 1764)

5'- GCC CCG C-3' (FRAG. NO:1752) (SEQ. ID NO:1765)

5'-TCTGGGGTGTCTG (FRAG. NO:1092) (SEQ. ID NO:1101)

5'-GCCTTCGTGGTTCC (FRAG. NO:1093) (SEQ. ID NO:1102)

55 5'-TCTTCCTTCGTTGC (FRAG. NO:1094) (SEQ. ID NO:1103)

5'-CGTCCCGGGGGGGCCCCGGGCCT (FRAG. NO:1095) (SEQ. ID NO:1105)

5'-GGC TGC GCT CCT GCC CCG C (FRAG. NO:1096) (SEQ. ID NO:1104)

5'-CTCTTCCCCGGCⁱ CTT (FRAG. NO:1097) (SEQ. ID NO:1106)
5'-GCGCTGGGGGTG CTCC (FRAG. NO:1098) (SEQ. ID NO:1107)
5'-CGTGTGTTTGC^jCCCTCTGGTCGC (FRAG. NO:1099) (SEQ. ID NO:1108)
5'-GTTGTGCTTTGC (FRAG. NO:1100) (SEQ. ID NO:1109)
5 5'-GGCCGGCTTGCCC^kGCCTCCC (FRAG. NO:1101) (SEQ. ID NO:1110)
5'-GGCGCCTGGCCCG^lGCC (FRAG. NO:1102) (SEQ. ID NO:1111)
5'-TTCCTGGGCTGCG^mGC (FRAG. NO:1103) (SEQ. ID NO:1112)
5'-GTTCTGTTCTTCTT CCTGGC (FRAG. NO:1104) (SEQ. ID NO:1113)
10 5'-GCB GGB GBC BGG GCB GGG CGB TCB GGB GCB GCG TGB GCC BBB GGB GGB CCB TCG GGB BCG CBG CTC CGG BBC GCB GGB 5' CBG BGG TGC C (FRAG. NO:1105) (SEQ. ID NO:1114)

Human IL-4 Nucleic Acid and Antisense Oligonucleotide Fragments

5'-CTC TGG TTG GCT TCC TTC GCC GGC BCB TGC TBG CBG GBB GBB CBG BGG GGG BBG CBG TTG GGB GGT
GBG BCC CBT TBB TBG GTG TCG B-3' (FRAG. NO: 1753) (SEQ. ID NO: 1766)
5'-GCC GGC BCB-3' (FRAG. NO: 1754) (SEQ. ID NO: 1767)
5'-T TCC TTC-3' (FRAG. NO:1755) (SEQ. ID NO:1768)
5'-CTC TGG TTG GCT TCC TTC-3' (FRAG. NO:1106) (SEQ. ID NO:1115)
5'-GCCGGCCTGCTE GCBGGBBGBBCBGBGGGGGBGCBGTTGGGBGGTBGBCCCCTTBGBTGGTGTCGB-3' (FRAG.
NO:1107) (SEQ. ID NO:1116)

Human IL4 Receptor Nucleic Acid and Antisense Oligonucleotide Fragment

20	5'-TCT GCC CTG TCC GCC GGC TCT TCG GTG GCT CGG CCC CGC TCC TTG TCT TGC CGC GGG TTG GTT CCT GGG CCT GGT TCT TGC GGG CGT TTC GGT CTG CTG GCT GGT CTG GGC CCG CGG TGC GGC GGG TGG CTT GCT GTT CTG CCT GGG CTC TCC CCT CTC CTC CTT TTC TCC CTT CCT CTG TCT TGC CTC CTT CCT CTG GGT CCT CTT GGC CTG GGC GCT CTT CCC CTC GGG CGG CTG CGG GCG CTC GTG CTG CCT GGT CCG CTC CCT GGG GGT GCT CCT TCC CTT TCC CCG CTC GTG GGG TTT GCG GGG CTG GGC TGC CCT GGG GGG TCT GGG CCT TTT GGG
25	GTC GGC TGG CTG CTC GGG GCC TGG GCT TCC CTG TGC CCC TTT CCT CTG CTG GGT CCC CCT CCC GTT CCA AGC TGC ACC GCA CAG ACC GGC GCT ACA GGA CAG AGC CAG GCA AGC ACC CAT GGG GAT CCA GGC CCA GCT GTT CCB BGC TGC BCC GCB CBG BCC GGC GCT BCB GGB CBG BGC CBG GCB BCC CBT GGG GBT CCB GGC CCB GCT G -3'(FRAG. NO: 1756)(SEQ ID NO:1769)
30	5'-TCTGCGC-3' (FRA G. NO: 1757) (SEQ ID NO: 1770)
30	5'-CCT GCT CCT GGG G (FRAG. NO:1758) (SEQ. ID NO:1771)
	5'-TCTGCGCGCCCCCTC CTCC (FRAG. NO:1108) (SEQ. ID NO:1117)
	5'-CGCCCCGGCTCTCT (FRAG. NO:1109) (SEQ. ID NO:1118)
	5'-CGTGTGGGCTTCGG (FRAG. NO:1110) (SEQ. ID NO:1119)
35	5'-CCCCCGCGCCCTCCG) TGTCTC (FRAG. NO:1111) (SEQ. ID NO:1120)
	5'-TGCTCGCTGGGCT1G (FRAG. NO:1112) (SEQ. ID NO:1121)
	5'-GGTTTCCCTGGGGCCCTGGGTTTC (FRAG. NO:1113) (SEQ. ID NO:1122)
	5'-TCTGCCGGGTCGT1TTC (FRAG. NO:1114) (SEQ. ID NO:1123)
	5'-GGGTGCTGGCTGC (FRAG. NO:1115) (SEQ. ID NO:1124)
40	5'-CTTGGTGCTGGGGCTCC (FRAG. NO:1116) (SEQ. ID NO:1125)
	5'-GGCGGCTGCGGGC)GGGTTGGG (FRAG. NO:1117) (SEQ. ID NO:1126)
	5'-CTTGGCTGGTTCCTGGCCTCGGG (FRAG. NO:1118) (SEQ. ID NO:1127)
	5'-CCTCCTCCTCCCTCCCTGCTCCCTTTCTCTCT (FRAG. NO:1119) (SEQ. ID NO:1128)
	5'-TCCCTGCTGCTCTC (FRAG. NO:1120) (SEQ. ID NO:1129)
	5'-TGCCCTCCCTTCCCCTCTGG (FRAG. NO:1121) (SEQ. ID NO:1130)
45	5'-GGTGCCTCCCTGGC)CCCTGC (FRAG. NO:1122) (SEQ. ID NO:1131)
	5'-GGCTGCTCCCTGGC CC (FRAG. NO:1123) (SEQ. ID NO:1132)
	5'-CTCTGGGTGGGGC)GGC (FRAG. NO:1124) (SEQ. ID NO:1133)
	5'-GGGGCGTCTGTGTC (FRAG. NO:1125) (SEQ. ID NO:1134)
	5'-CTGGCCTGGGTGCC (FRAG. NO:1126) (SEQ. ID NO:1135)
50	5'-GCCTCTCCTGGGGC)GGTGGCTCCCTGTCC (FRAG. NO:1127) (SEQ. ID NO:1136)
	5'-CCTTTCCCCCGGCTCC (FRAG. NO:1128) (SEQ. ID NO:1137)
	5'-GTGGGGGCTTGGC (FRAG. NO:1129) (SEQ. ID NO:1138)
	5'-GGG GGT CTG TGG CCT GCT CCT GGG G (FRAG. NO:1130) (SEQ. ID NO:1139)
	5'-AGGGGTCTGGGGCCCTC (FRAG. NO:1131) (SEQ. ID NO:1140)
55	5'-TTTGGGGGCTGCTGC CTTG (FRAG. NO:1132) (SEQ. ID NO:1141)
	5'-GCCTGGCTGCCCTCC (FRAG. NO:1133) (SEQ. ID NO:1142)
	5'-GGGGCCTGCCGTGGGGC (FRAG. NO:1134) (SEQ. ID NO:1143)
	5'-TGCCTCTGTTGCTCCCTT (FRAG. NO:1135) (SEQ. ID NO:1144)
	5'-TGCCTGCTGCTGG (FRAG. NO:1136) (SEQ. ID NO:1145)
60	5'-GGTTCCCGCCCTCCCT (FRAG. NO:1137) (SEQ. ID NO:1146)

5'-GTT CCC AGA GCT TGC CAC CTG CAG CAG GAC CAG GCA GCT CAC AGG GAA CAG GAG CCC AGA GCA AAG
CCA CCC CAT TGG GAG ATG CCA AGG CAC CAG GCT G (FRAG. NO:1138) (SEQ. ID NO:1147)
5'-GTT CCC BGB GCT TGC CBC CTG CBG GBC GCB GCT CBC BGG GBB CBG GBG CCC BGB GCB BBG
CCB CCC CBT TGG GEG BTG CCB BGG CBC CBG GCT G-3' (FRAG. NO:1139) (SEQ. ID NO:1148)

5 Human IL5* Nucleic Acid and Antisense Oligonucleotide Fragments

5'-TCCCTGTTTC CCCCGTTTCG TTCTGCGTT GCCTTGGCG TTTTTGTT GTTTCTCTC TCCGTCTTC
TTCTCCCCCT GTGGGB3TTT CTGTGGGGBT GGCBTBCBCG TBGGCBGCTC CBBGBCGCTBG CBBBCTCBBB
TGCBGBGCB TCCTCTGGC TCTGBBBGCG TGGGAATTTC TGTGGGGBTG GCATACACGT AGGCAGCTCC
AAGAGCTAGC AAAC CAAAT GCAGAAGCATC CTCATGGCTC TGAAAACG-3' (FRAG. NO: 1759) (SEQ. ID NO:
10 1772)
5'-GCC CCG GG-3' (FRAG. NO: 1760) (SEQ. ID NO: 1773)
5'-G GGT TTC T-3' (FRAG. NO: 1761) (SEQ. ID NO: 1774)
5'-GTG GGG BTG GC-3' (FRAG. NO: 1762) (SEQ. ID NO:1775)
5'-CCB BGB GCT BGC-3' (FRAG. NO: 1763) (SEQ. ID NO: 1776)
15 5'-TCC CTG TTT CCC CCC TTT-3' (FRAG. NO:1140) (SEQ. ID NO:1149)
5'-CGT TCT GCG TTT GCC TTT GGC-3' (FRAG. NO:1141)(SEQ. ID NO:1150)
5'-GTT TTT TGT TTG TTT TCT-3' (FRAG. NO:1142)(SEQ. ID NO:1151)
5'-CTC TCC GTC TTT CTT CTC C-3' (FRAG. NO:1143) (SEQ. ID NO:1152)
20 5'-CCT CCT GCC TGT GTC CCT GCT CCC C-3' (FRAG. NO:1144) (SEQ. ID NO:1153)
5'-GAG GGT TTC TGG CTT CCT CTC T-3' (FRAG. NO:1145) (SEQ. ID NO:1154)
5'-TGT CTC TCT GTC CTT TTG TT-3' (FRAG. NO:1146) (SEQ. ID NO:1155)
5'-TGT TGT GCG GCC TGG TGC CCT GCC CCG GG-3' (FRAG. NO:1147) (SEQ. ID NO:1156)
25 5'-GTG GGA ATT TCT GTG GGG BTG GCA TAC ACG TAG GCA GCT CCA AGA GCT AGC AAA CTC AAA TGC AGA
AGC ATC CTC ATG GCT CTG AAA CG-3' (FRAG. NO: 1764) (SEQ. ID NO: 1777)
5'-GTG GGB BTT TCT GTG GGG BTG GCB TBC BCG TBG GCB GCT CCB BGB GCT BGC BBB CTC BBB TGC BGB BGC
BTC CTC BTG GCT CTG BBB CG-3' (FRAG. NO:1148) (SEQ. ID NO:1157)

Human IL-5 Receptor Nucleic Acid and Antisense Oligonucleotide Fragments

5'-CTCAGTGGCC CCCAAAGGA TGAGTAATACT ATGCGCCACG ATGATCATAT CCTTTTACT ATGAGGCCGT
30 GTCTGTCGTG TCTITCCTTT GCTCTTGGT TGCTTTGCT GTGCCCTGCC TCTCTGCCCG TGTCTGTCGT
GTCTTCCTT TGCCTTGGT GTGTCTTGC TGTGCCCTGC CTCTCTGCC CGTGTCTGTC GTGTCTTCC
TTTGCTCTTG GTGTGCTTT GCTGTGCCCT GCCTCTCTGC-3' (FRAG. NO: 1765) (SEQ. ID NO: 1778)
5'-CCG TGT C-3' (FRAG. NO: 1766) (SEQ. ID NO: 1779)
5'-GCCCTGCC-3' (FRAG. NO: 1767) (SEQ. ID NO: 1780)
5'-CCG TGT CTG TCG TGT CT-3' (FRAG. NO:1149) (SEQ. ID NO:1158)
35 5'-TCCCTTGCCTCTG-3' (FRAG. NO:1150) (SEQ. ID NO:1159)
5'-GTGTGTCTTGCTCT-3' (FRAG. NO:1151) (SEQ. ID NO:1160)
5'-GCCCTGCCCTCTC C-3' (FRAG. NO:1152) (SEQ. ID NO:1161)
5'-CT CBGTGGCCCCC BBBBGGBTG BGTBBTBCBT GCGCCBCGBT GBTCBTBTCC TTTTBCTBT GBGG (FRAG. NO:
1768) (SEQ. ID NO: 1781)

40 Human IL-6 Receptor Fragments

5'-GGGGGTGGCT TCTGCCGCG TCTCTGGGCC GTCCCGTCCC TCGGCCCCGC GCCGCGCTCG GCTCCTCTCC
CTCTGGCCCG GCTCGGGCG GGGCGGGCG GTGGGCGGGC GGCGCTGCC TGCGCGCGC GCTGGCCCCCT
GCTGGCCGTC GGCCTGCGC TGCTGGCTGC CCTGCTGGC GCGCCGGGGC CTGTCGCCCT CTGCGGGCGC
45 TGTCTCTGG CTTGCTTCC GGCTCTTCTG CTGGGGTGGG GCTGGGCGGC CGGGCGGTG CTGGGGCTCC
TCGGGGGGGG GGG CTCTTCC GGGCTGCTC CCTCGGGGGC GGGGGTTCT GGCCTGGGG GTCTTGCCTG
GCCTCCGGGC TCC GCTTGT CTGCTTCC TTCTCTGGTC GGTGTTGGCT CGGGGCTCCG TGGGTCCCTG
GCGCCGGTT GTG TTTGTC TTTTCCCCCTG GCGCTCCCTGT GCCCCTCTCC TCTCTTCCCT CTGCTTCTCG
CTCTCTTTC TGGA GCGCTC CCTGCTGCTC TTGGTTTGG GCTTTTTTC TCTCTCTCC TTTTCGTGCG
50 TGGGCCTCCG CACGCTCTT GCCACCTCT GCGCAGGGCA GCGCCTTGG GGCCAGCGCC GCTCCCGCG
CGGCCAGCAG GGCAGCCAGC AGCGCGCAGC CGACGGCCAG CATGCTTCC CTCGGCTAC CACTCCATGG
TCCCAGAG GCG GACAGGC GCBGCGCTC TTGCCBCCTC CTGCGCBGG CBGCGCTTGG GGGCCBGC
CGCTCCCGC GCGGCGCBGCB GGGCGGCCBG CBGCGCGCB CGBCGCCB GCBTGTCTCC TCCCTGGCTB
CCBCTCCBTG GTCCCGCBGB GGCGBGCBGG C-3' (FRAG. NO: 1769) (SEQ. ID NO: 1782)
5'-CCCGCGC-3' (FRAG. NO:1184) (SEQ. ID NO:1193)
55 5'-GGCCBGBGBGG-3' (FRAG. NO:1186) (SEQ. ID NO:1195)
5'-GCBGCBGCBGCG-3' (FRAG. NO: 1770) (SEQ. ID NO: 1783)
5'-C GCBGCGCBGCG-3' (FRAG. NO: 1771) (SEQ. ID NO: 1784)
5'-GGGGGTGGCTCTCCTGCC3' (FRAG. NO:1153) (SEQ. ID NO:1162)
5'-GCGTCTCTGGGCCGTCCC-3' (FRAG. NO:1154) (SEQ. ID NO:1163)

5'-GTCCTCGGCCCCCGCCGCGCTCGGCTCTCTCCC-3' (FRAG. NO:1155) (SEQ. ID NO:1164)
 5'-TCTGGCCCGGCTC-3' (FRAG. NO:1156) (SEQ. ID NO:1165)
 5'-GGGGCGGGCGGGCGGGTGGGC-3' (FRAG. NO:1157) (SEQ. ID NO:1166)
 5'-GGCGCTGCCCTGCC-3' (FRAG. NO:1158) (SEQ. ID NO:1167)
 5 5'-GCGCGCTGGCCC-3' (FRAG. NO:1159) (SEQ. ID NO:1168)
 5'-TGCTGGCCGTCGGCTGCGCGTCTGGCTGCCCT-3' (FRAG. NO:1160) (SEQ. ID NO:1169)
 5'-GCTGGCCGCGGGG-3' (FRAG. NO:1161) (SEQ. ID NO:1170)
 5'-GCCTGTCCGCTCTGCGGG-3' (FRAG. NO:1162) (SEQ. ID NO:1171)
 5'-CGCTGTCTCCTGGC-3' (FRAG. NO:1163) (SEQ. ID NO:1172)
 10 5'-TTGTCTTCCGGCTCT-3' (FRAG. NO:1164) (SEQ. ID NO:1173)
 5'-TCTGCTGGGTGGG-3' (FRAG. NO:1165) (SEQ. ID NO:1174)
 5'-GCTGGGCAGCGCG-3' (FRAG. NO:1166) (SEQ. ID NO:1175)
 5'-GCTGGGGCTCCTCGGGGG-3' (FRAG. NO:1167) (SEQ. ID NO:1176)
 5'-GGGGGCTCTCCGG-3' (FRAG. NO:1168) (SEQ. ID NO:1177)
 15 5'-GCTGTCTCCCTCCGG-3' (FRAG. NO:1169) (SEQ. ID NO:1178)
 5'-GCGGGGGTTCTGGGCC-3' (FRAG. NO:1170) (SEQ. ID NO:1179)
 5'-GTGGGGGTCTTGCCT-3' (FRAG. NO:1171) (SEQ. ID NO:1180)
 5'-TGGCCCTCCGGGCTCC-3' (FRAG. NO:1172) (SEQ. ID NO:1181)
 5'-TGCTTGTCTGCCTCCCTTC-3' (FRAG. NO:1173) (SEQ. ID NO:1182)
 20 5'-TCTGGTCGGTTGTC GCTCG-3' (FRAG. NO:1174) (SEQ. ID NO:1183)
 5'-GGGCTCCGTGGGTCCCTGGC-3' (FRAG. NO:1175) (SEQ. ID NO:1184)
 5'-GCCGTTTGTGTTTGTC-3' (FRAG. NO:1176) (SEQ. ID NO:1185)
 5'-TTTCCTCCCTGGCGT-3' (FRAG. NO:1177) (SEQ. ID NO:1186)
 5'-CCCTGTGCCCTCTCCTCTCCTCTGCTTCTC-3' (FRAG. NO:1178) (SEQ. ID NO:1187)
 25 5'-GCTCTCTTTGTGGG-3' (FRAG. NO:1179) (SEQ. ID NO:1188)
 5'-GCCCTCCCTGCTGCT-3' (FRAG. NO:1180) (SEQ. ID NO:1189)
 5'-CTTGGTTTGGGCT-3' (FRAG. NO:1181) (SEQ. ID NO:1190)
 5'-TTTTTCTCTCCTCTTTTC-3' (FRAG. NO:1182) (SEQ. ID NO:1191)
 5'-GTGCGTGGGCCTCC-3' (FRAG. NO:1183) (SEQ. ID NO:1192)
 30 5'-GCACGCCCTCT TGCCACCTCC TGCGCAGGGC AGCGCCTTGG GGCCAGCGCC GCTCCCGGCG CGGCCAGCAG
 GGCAGCCAGC AGCGCGCAGC CGACGGCCAG CATGCTTCC CCTCGGCTAC CACTCCATGG TCCCGCAGAG
 GCGGACAGGC-3' (FRAG. NO:1185) (SEQ. ID NO:1194)
 5'-GCBGCGCTCT TGCCBCCCTCC TGCGCBGGC BGCGCCTTGG GGCCBGCGCC GCTCCCGGCG CGGCCBGCBG
 GGCGBCCBG CBGCGCGCBG CCGBCGGCCB GCBTGCTTCC TCCTCGGCTB CCBCTCCBTG GTCCCGCGBGB
 35 5'-GGCGBCBGG C-3' (FRAG. NO:1187) (SEQ. ID NO:1196)

Human IL-6 Nucleic Acid and Antisense Oligonucleotide Fragments

5'-GGGGTGGCT TCTGCCGCG TCTCTGGGCC GTCCCGTCCC TCGGCCCCGC GCGCGCTCG GCTCCTCTCC
 CTCTGGCCCG GCTCGGGCG GGGCGGGCG GTGGCGGGC GCGCCTGCC TGCGCGCGC GCTGGCCCT
 GCTGGCCGTC GGCGTGCAGC TGCTGGCTGC CCTGCTGGCC GCGCCGGGC CTGTCGCGCT CTGCGGGCGC
 40 5'-TGTCTCTGG CTTGCTTCC GGCTCTCTG CTGGGGTGGG GCTGGCGGC CGGCCGGGTG CTGGGGCTCC
 TCGGGGGGGG GGGCTCTTCC GGGCTGTCTC CCTCCGGGC GGGGGTTCT GGCCGTGGGG GTCTTGCCTG
 GCCTCCGGGC TCCGTCTGT CTTGCCTTCC TTCTCTGGTC GGTGTGGCT CGGGGCTCCG TGGGTCCCTG
 GCGCCCGTT GTGTTTGTC TTTTCCCCTG GCGTCCCTGT GCCCCTCTCC TCTCCTCCCT CTGCTTCTCG
 CTCTCCTTGT TGGGCCCTC CCTGCTGCTC TTGGTTTGG GCTTTTTTC TCTTCCCTCCT TTTTCGTGCG
 45 5'-GGGGCCTCC GCACGCCCTCT TGCCACCTCC TGCGCAGGGC AGCGCCTTGG GGCCAGCGCC GCTCCCGGCG
 CGGCCAGCAG GGCAGCCAGC AGCGCGCAGC CGACGGCCAG CATGCTTCC CCTCGGCTAC CACTCCATGG
 TCCCGCAGAG GCGGACAGGC GCBGCGCTC TTGCCBCCTC CTGCGCBGG CBGCGCCTTG GGGCCBGCGC
 CGCTCCCGC GCGGCCBGBG GGGCBGCCBG CBGCGCGCBG CCGBCGGCCB GCBTGCTTCC TCCTCGGCTB
 CCBCTCCBTG GTCCCGBGB GGCGBCBGG C-3' (FRAG. NO:1772) (SEQ. ID NO:1785)
 50 5'-GGGGCBGG-3' (FRAG. NO:1773) (SEQ. ID NO:1786)
 5'-GBBGGCBG CBGGC 3' (FRAG. NO:1774) (SEQ. ID NO:1787)
 5'-CCBGGBGBG CCCC-3' (FRAG. NO:1775) (SEQ. ID NO:1788)
 5'-BGGG BGBBGGCBG-3' (FRAG. NO:1776) (SEQ. ID NO:1789)
 5'-GCT TCT CTT TCG 'TC CCG GTG GGC TCG-3' (FRAG. NO:1188) (SEQ. ID NO:1197)
 55 5'-GTG GCT GTC TGT GTG GGG CGG CT-3' (FRAG. NO:1189) (SEQ. ID NO:1198)
 5'-GTG CCT CTT TGC TGC TTT C-3' (FRAG. NO:1190) (SEQ. ID NO:1199)
 5'-GAT TCT TTG CCT TTT TCT GC-3' (FRAG. NO:1191) (SEQ. ID NO:1200)
 5'-CTCCTGGGG TBCTGGGCB GGGBBGGCBG CBGGCBCBC CBGGBGBGC CCCBGGGBGB BGGCBBCCTGG BCCGBGGCG
 CTTGTGGBGB BGGBGTCTBT BGCTGGGCTC CTGGBGGGB GBTBGBGC-3' (FRAG. NO:1777) (SEQ. ID NO:1790)

60 Human Monocyte-derived Neutrophil Chemotactic Factor

Nucleic Acid and Antisense Oligonucleotide Fragments

5'-GGGGTGGBBB GGTTTGGGBT BTGTCCTTBT GCBCTGBCBT CTBBGTTCTT TBGCBCTCCT TGGCBBBBCT
GCBCCCTCBC BCBGBGCTGC BGBBBCTBGG BBGGCTGCCB BGBGBGCCBC GGCCBGCTTG GBBGTCBTGT
TTBCBCBCBG TGBGBTGGTT CCTTCCGGGC TTGTGTGCTC TGCTGTCTCT TGGTCCCTC CGGTGGTTTC
5 TTCCCTGGCTC TTGTCCTTTC TCTTGG CCCT TGGC-3' (FRAG. NO:1778) (SEQ. ID NO: 1791)
5'-GGBGT BTG-3' (FRAG. NO:1779) (SEQ. ID NO: 1792)
5'-GCBCTGBCBT CT-3' (FRAG. NO:1780) (SEQ. ID NO:1793)
5'-CCG GTG G-3' (FRAG. NO:1781) (SEQ. ID NO: 1794)
5'-GG CCC TTG GC-3' (FRAG. NO:1782) (SEQ. ID NO: 1795)
10 5'-GCT TGT GTG CTC TGC TGT CTC T-3' (FRAG. NO:1192) (SEQ. ID NO:1201)
5'-TGG TTC CTT CCG GTG GTT TCT TCC TGG CTC TTG TCC T-3' (FRAG. NO:1193) (SEQ. ID NO:1202)
5'-TTC TCT TGG CCC TG GC-3' (FRAG. NO:1194) (SEQ. ID NO:1203)
5'-GGGGTGGBBB GGTTTGGGBT BTGTCCTTBT GCBCTGBCBT CTBBGTTCTT TBGCBCTCCT TGGCBBBBCT
GCBCCCTCBC BCBGBGCTC-3' (FRAG. NO:1783) (SEQ. ID NO: 1796)

Human Neutrophil Elastase (Medullasin) Nucleic Acid and Antisense Oligonucleotide Fragments

15 5'-GGGCTCCCGC CGCGBGBGGT TBTGGGCTCC CBGGBCCBCC CGCBBCCGCGC GGBCGTTBC BTTCGCCBCG
CBGTGCCCGG CCGFCBTGBC GBBGTTGGGC GCBBTCBGGG TGGCGCCGCB GBBGTTGGCCT CCGCGCBGCT
GCBGGGBCBC CBTGBBGGGC CBCGCGTGGG GCCGCGCTCG CCGGCCCCCCC BCBBTCTCCG BGGCCBGGCG
GGTGCCCGCC BGBCBGCBGGG CCGGCBGGBC BCBGGCGBGG BGBCBCGCGB GTCGGCGGCC GBGGGTCBTG
20 GTGGGGCTGG GGC CCGGGG TCTCTGCCCG TCCGTGCTGG TGGGGCTGGG GCTCCGGGG TCTCTGCCCG
TCCGTGCCGC GTGGGGCCGC GCTCGCCGGC CCCCCCCTGC CGGGTGGGCT CCCGCCGCGC GCCGGCCTGC
CGGCCCTCG TGGGTCCTGC TGGCCGGGTC CGGGTCCCGG GGGTGGGGCG CGBGTGGCG GCCBGGGTC-3'
(FRAG. NO:1784) (SEQ. ID NO: 1797)
5'-GG TGG GGC-3' (FRAG. NO:1785) (SEQ. ID NO: 1798)
25 5'-G GGG CCG -3' (FRAG. NO:1786) (SEQ. ID NO:1799)
5'- GGC CGG GTC CGG G-3' (FRAG. NO:1787) (SEQ. ID NO: 1800)
5'-TGG TGG GGC TGG GGC TCC GGG GTC TCT GCC CCT CCG TGC-3' (FRAG.NO:1195)(SEQ.ID NO:1204)
5'-CGC GTG GGG CCG CGC TCG CCG GCC CCC C-3' (FRAG. NO:1196) (SEQ. ID NO:1205)
5'-CCT GCC GGG TGG GCT CCC GCC GCG-3' (FRAG. NO:1197) (SEQ. ID NO:1206)
30 5'-CGC CGG CCT GCC GGG CCC TC-3' (FRAG. NO:1198) (SEQ. ID NO:1207)
5'-GTG GGT CCT GCT 3GC CGG GTC CGG GTC CCG GGG GTG GGG-3'(FRAG.NO:1199)(SEQ.ID NO:1208)
5'-CGC GBG TCG GCG GCC GBG GGT C-3' (FRAG. NO:1200) (SEQ. ID NO:1209)
5'-GGGCTCCCGC CGCGBGBGGT TBTGGGCTCC CBGGBCCBCC CGCBBCCGCGC GGBCGTTBC BTTCGCCBCG
CBGTGCCCGG CCGFCBTGBC GBBGTTGGGC GCBBTCBGGG TGGCGCCGCB GBBGTTGGCCT CCGCGCBGCT
35 GCBGGGBCBC CBTGBBGGGC CBCGCGTGGG GCCGCGCTCG CCGGCCCCCCC BCBBTCTCCG BGGCCBGGCG
GGTGCCCGCC BGBCBGCBGGG CCGGCBGGBC BCBGGCGBGG BGBCBCGCGB GTCGGCGGCC GBGGGTCBTG
GTGGGGCTGG GGCTCCGGGG TCTCTGCCCG TCCGTGCTG-3' (FRAG. NO:1788) (SEQ. ID NO: 1801)

Human Neutrophil Oxidase Factor Nucleic Acid and Antisense Oligonucleotide Fragments

40 5'-CGGGGBTGGG GGTCTGGBC GGCCTGBBG GCBTCCBGGG CTCCCTTCB GTCCCTCTTG TCCGCTGCCB
GCBCCCCCTTC BTTCGBGBGG CTGBTGGCCT CCBCBGGGB CBTGBTBGG TBGBBBCTBG GBGGCCGGCC
TCCBCBGGG BCBTGGTCTT TCTTGTCCGC TGCTCTCTG GGGTTTCGG TCTGGGTGGG CTTTCCTCCT
GGGGCTGCTG CTGGGCTCTT CTTTTGTT CTGGCCTGGT GCTCTCTCG GCCCTTCCC TTGGGTGTCT
TGTGTTTG TG GCCTCCBCCB GGGBCBTG-3' (FRAG. NO:1789) (SEQ. ID NO: 1802)
5'-CGGGGBTGGG GG-3' (FRAG.NO:1790) (SEQ. ID NO: 1803)
45 5'-GCCBGCBCCCC-3' (FRAG.NO:1791) (SEQ. ID NO: 1804)
5'-C CBC CBG-3' (FRAG.NO:1792) (SEQ. ID NO: 1805)
5'-GGC CTC CBC CBG GGB CBT G-3' (FRAG. NO:1201) (SEQ. ID NO:1210)
5'-GTC CTT CTT GTC CGC TGC C -3' (FRAG. NO:1202) (SEQ. ID NO:1211)
5'-TCT CTG GGG TTT TCG GTC TGG GTG G-3 (FRAG. NO:1203) (SEQ. ID NO:1212)
50 5'-GCT TTC CTC CTG GGG CTG CTG CTG-3' (FRAG. NO:1204) (SEQ. ID NO:1213)
5'-GGC TCT TCT TTT GT TTC TGG CCT GGT G-3' (FRAG. NO:1205) (SEQ. ID NO:1214)
5'-CTC TCT CGT GCC CTT TCC-3' (FRAG. NO:1206) (SEQ. ID NO:1215)
5'-CTT GGG TGT CTT GTT TTT GT-3' (FRAG. NO:1207) (SEQ. ID NO:1216)
5'-GGC CTC CBC CBG 3GB CBT G-3' (FRAG. NO:1208) (SEQ. ID NO:1217)
55 5'-CGGGGBTGGG GGTCTGGBC GGCCTGBBG GCBTCCBGGG CTCCCTTCB GTCCCTCTTG TCCGCTGCCB
GCBCCCCCTTC BTTCGBGBGG CTGBTGGCCT CCBCBGGGB CBTGBTBGG TBGBBBCTBG GBGGCC-3' (FRAG.
NO:1793) (SEQ. ID NC: 1806)

Human Cathepsin G Nucleic Acid and Antisense Oligonucleotide Fragments

5'-CCCTCCBCBT CTGCTCTGBC CTGCTGGBC CTGGBTCTGB BGBTBCGCCB TGTBGGGGCG GGBGTGGGGC

CTGCTCTCCC GGCC'TCCGBT GBTCTCCCT GCCTCBGCC CBGTGGGTBG GBGBBBGGCC BGCBGBGCB
 GGBGTGGCTG CBTCTTCCT GGTGGGGCCT GCTCTCCCG CCTCCGTGTG TTGCTGGGTG TTTTCCCGTC
 TCTGGTCTGC CTTCGGGGT CGT-3' (FRAG. NO:1794) (SEQ. ID NO: 1807)
 5'-GGBGBTBCGCC-3' (FRAG. NO:1795) (SEQ. ID NO: 1808)

5 5'-CBGCCCCBG-3' (FRAG. NO:1796) (SEQ. ID NO: 1809)
 5'-TCC CGT CTC TGG-3' (FRAG. NO:1797) (SEQ. ID NO: 1810)
 5'-GTG GGG CCT GCT CTC CCG GCC TCC G-3' (FRAG. NO:1209) (SEQ. ID NO:1218)
 5'-TGT GTT GCT GG GTG TTT TCC CGT CTC TGG-3' (FRAG. NO:1210) (SEQ. ID NO:1219)
 5'-TCT GCC TTC GGG GGT CGT-3' (FRAG. NO:1211) (SEQ. ID NO:1220)

10 5'-CCCTCCBCBT CTGCTCTGBC CTGCTGGBC CTGGBTCTGB BGBTBCGCCB TGTBGGGGCG GGBGTGGGCG
 CTGCTCTCCC GGCC'TCCGBT GBTCTCCCT GCCTCBGCC CBGTGGGTBG GBGBBBGGCC BGCBGBGCB
 GGBGTGGCTG-3' (FRAG. NO:1798) (SEQ. ID NO: 1811)

Human Defensin 1 Nucleic Acid and Antisense Oligonucleotide Fragments

15 5'-CCGGGGCTGC BGCBBCCTCB TCBGCTCTTG CCTGGGBTGG CTCBGCCCTGG GCCTGCBGGG CCBCCBGBGB
 BBTGGCBGCB BGGGBTGGCGB GGGTCCTCBT GGCTGGGGTC BCBGBTCCCT TBGCTBGGCB GGGTGBCCBG
 BGBGGGC GGG TCC TCB TGG CTG GGG GCC TGG GCC TGC BGG GCC GCT CTT GCC TGG BGT GGC TC GCC CBG
 BGT CTT CCC TGG T GCTCAGCCTC CAAAGGAGCC AGCCTCTCCC CAGTTCTGA AATCTGAGT GTTGCCTGCC
 AGTCGCCATG AGA\ACTTCT ACCTTCTGCT GTTACTCTC TGCTTACTTT TGTCTGAGAT GGCCTCAGGT
 GGTAACTTT TCACAGGCCT TGGCACACAGA TCTGATCATT ACAATTGCGT CAGCAGTGGA GGGCAATGTC
 20 TCTATTCCTGC CTGCCCGATC TTACACAAA TTCAAGGCAC CTGTTACAGA GGGAAAGGCCA AGTGCTGCAA
 GTGAGCTGGG AGTGACCAGA AGAAATGACG CAGAAAGTGA ATGAACTTT TATAAGCATT CTTTAATAA
 AGGAAAATTG CTTTGAAGT AT CTGCAGTGGT AAAAAGATTG TATATCTGCT GTTGTATGAA TGCAAGCACCC
 ACTAGCCACA TAGIGCTCGT GAGCACTTGC AATGCGGCTA GGGTGATTTC AATTAACCTA AAAGAGAAC
 GCCACAGGGG GCA\GTGGCT GCCATATTGG ATGGTGCTGC TTTGAGAACAA ATATGAGAGA AATGAAGCCT
 25 25 CTATTTACCT TGGTGGCGG AACACATTGA AGGGACTCTG TATTGATACC AGGCTTCAA CTTTGGGAAG
 TGTACTGGCC AACTTAAACA CATCCACAGG AGAAATGAGA GGGTTGGGAA GGGACCAGAA ACCAGGCATT
 GAGGACAATG AGA\GAGTTT TTCAAAAGTG GAATTACTGC AAAAAGTGGA AAAATAGCCT TTGGATGGAA
 GTTACTGATG AGAC AATTTC CATCGGTGTG AAAGCCATCT TTCCAACAGA GATCTGCAAC ATGAGAATGT
 ACTGTCTCCT AGGC TAGCGA TGGCCTCTTG TATTAGTCG CTCAGGCTAC CAGATTATTC GTTAAACTG
 30 CCCATAAAACA GACCAGGCAG TTAAACAAAC AGAAAATTAT TTCTCTCGAG TCCTGGAGGC AGGAAGTCTG
 CGATCAAGGT GGA\GCAGGG TTGGCTTCTT CTCAGGTGTC TGTCTTGGC TGGTAGATGA CCGCCGCC
 CCTGGGTCTC CACATGGTCT TTCCCTGTG TGTCTGTG CCAATCTCTT CTTATAAGGA TGCAAGTCTT
 ATGGATCAGA GCACACCCCCA ATGACCGTGT TAAACTTGA TCACCTCTT AAAGTTCTC TCTCCAAATA
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 35 AAAACGCCTA CCAC TGGAGA CTTGCAACAT GGCGGCCTGC TGGTCCCTCG CCAGGAATAT CACAGGC
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 40 TTCCACATTT CTAA AACACA GGATGTGATT TTGGGGTGTG TTGAGACAAG GCAGAAAAC TGTGGGAAA
 AATAACTTGA ATTCCCTGCA CATTAAAAT CTCTCAGCAG AAGAAAACCC CACTCAGAAC CCCACTGTT
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 45 TCCCTCTTA CAGGTGGTAA CTTTCTCACA GGCCTTGGCC ACAGATCTGA TCATTACAAT TGCCTCAGCA
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 50 GCCTGCCCTGG AAA\GGGGAG TGACGTCTA GGCTTCAGTG ATGTCACCTC CACTTGTGTT GATCCACAAA
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 GAGTGTGCC TGCCAGTCGC CATGAGAACT TCCTACCTC TGCTGTTAC TCTCTGCTTA CTTTTGTCTG
 AGATGGGCTC AGG\GGTAAAC TTTCTCACAG GCCTTGGCCA CAGATCTGAT CATTACAATT GCGTCAGCAG
 TGGAGGGCAA TGTCTCTATT CTGCTGCC GATCTTAC AAAATTCAAG GCACCTGTTA CAGAGGGAAAG
 55 GCCAAGTGC GCAAGTGAGC TGGGAGTGAC CAGAAGAAAT GACGAGAAC TGAAATGAAC TT -3'
 (FRAG.NO:1799) (SEQ. ID NO: 3010)
 5'-GTCAGCTAG CC\CCAAAGG AGCCAGCCTC TCCCCAGTT TCAGAAC CCTCTGTT ACAGAGGGAA
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 TTTCTCACAG GCCTTGGCCA CAGATCTGAT CATTACAATT GCGTCAGCAG TGGAGGGCAA TGTCTCTATT
 60 CTGCTGCCCTGG GATC\TTAC AAAATTCAAG GCACCTGTTA CAGAGGGAAAG GCCAAGTGC GCAAGTGAGC
 TGGGAGTGAC CAGA\GAAAT GACGAGAAC TGAAATGAAC TT-3' (FRAG.NO:_) (SEQ. ID NO: 2475)

5'-CTGCA GTGGT AAAAAGATT C TATATCTGCT GTTTGATGAA TGCAGCACCC ACTAGCCACA TAGTGCTCGT
 GAGCACTTGC AATC CGGCTA GGGTGATTC AATTAACCTA AAAGAGAACAA GCCACAGGGAA GCATGTGGCT
 GCCATATTGG ATGCTGCTGC TTTGAGAACAA AAATGAGAGA AATGAAGCCT CTATTTACCT TGTTGGCGG
 AACACATTGA AGGGACTCTG TATTGATACC AGGCTCAA A CTTTGGGAAG TGTACTGGCC AACTTAAACA
 5 CATCCACAGG AGAA TGAAGA GGTTTGGGAA GGGACCAAGA ACCAGGCATT GAGGACAATG AGAAGAGTT
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 CATCGGTGTG AAAGCCATCT TTCCAACAGA GATCTGCAAC ATGAGAACATG ACTGCTCCT AGGGTAGCGA
 TGGCCTTGT TATTAGTCCG CTCAGGCTAC CAGATTATC GTTTAAACTG CCCATAAACAA GACCAGGCAG
 TTTAAACAAAC AGAA ATTATAT TTCCCTCGAG TCCTGGAGGC AGGAAGTCTG CGATCAAGGT GGAAGCAGGG
 10 TTGGCTCTT CTCAGGTGTC TGTCTTGGC TGGTAGATGA CCGCCGCTC CCTGGGTCTC CACATGGTCT
 TTCCCTGTG TGTGCTGTC CCAATCTT CTTATAAGGA TGCAAGTCTT ATGGATCAGA GCACACCCCA
 ATGACCGTGT TAACTTGAA TCACCTCTT AAAGTTTCTC TCTCCAAAATA CAATCACCTC CTGAGGCAC
 GTTAGGGCTT CGAC'ACAGGA ATTCTTTCC TAGGGGATTG AGTCAGTCC AAAACGCCTA CCAGTGGAGA
 15 CTTGCAACAT GGCGGCCTGC TGGTCCCCTCG CCAGGAATAT CACAGGCAC TGTTCCCTGT TGCAATGGAAAT
 AGAAGGCTAT TCCAGAGTAC TGTCTCTATT TATCAGATCT GGGATACTGG GAGAAGGGCA AAATAAAGTC
 CAAGTAGAAA AAAA AACTAT GAAAGTTTA GAGAGTAACC ATAATTTCAG CCCGATGTGA AACGATCCTA
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 20 CATTAAAAT CTCTCAGCAG AAGAAAAACCC CACTCAGAAC CCCACTGTT ATTCCCTGGC TTGTATTTGG
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 AATCATGGGC CAA TTCTTG GAAGAGAAAGA CTCTCCGGTG TTTTGAGTT ATTGTTCTG CTTTCGCGAG
 ATGTTCTCAA ATCC TTGCAAG CTCAGGCA TGAGTCTGAA GTGTTGTGT TCCCTCCTTA CAGGTGGTAA
 CTTTCTCACA GGCC TGGGCC ACAGATCTGA TCATTACAAT TGCGTCAGCA GTGGAGGGCA ATGTCCTAT
 25 TCTGCCTGCC CGATCTTAC CAAAATTCAA GGCACTGTT ACAGAGGGAA GGCAAGTGC TGCAAGTGA
 CTGAGAGTGA CCAGAAGAAA TGACGCAGAA GTGAAATGAA CTTTTTATAA GCATTCCTT AATAAAGGAA
 AATTGCTTT GAAGTATACC TCCTTGGGC CAAAATGAAT CTTGTGTCTC AATTGGAAGA GGTAAAGAAG
 TAGGGGGTTA GGGTGCATGG GTTGGAACGT GAGACAGGT GAACACACAA GCCTGCCTGG AAAAGGGGG
 TGACGTCTTA GGCTCAGTG ATGTCACCTC CACTTTGTT GATCCACAAA CCAACAGGTG ACTGATTTG-3'
 30 (FRAG.NO:____) (SEQ. ID NO: 2474)
 5'-GCTCAGCCTC CA AAGGAGCC AGCCTCTCCC CAGTTCCGTAA AATCCTGAGT GTTGCTGCC AGTCGCCATG
 AGAACTTCCCT ACC TCTGCT GTTTACTCTC TGCTTACTTT TGTCTGAGAT GGCCTCAGGT GGTAACITTC
 TCACAGGCCT TGGC'CACAGA TCTGATCATT ACAATTGCGT CAGCAGTGGA GGGCAATGTC TCTATTCTGC
 CTGCCGATC TTACCAAAA TTCAAGGCAC CTGTACAGA GGGAAGGCCA AGTGTGCAA GTGAGCTGGG
 35 AGTGACCAAGA AGA AATGACG CAGAAGTGAA ATGAACTTTT TATAAGCATT CTTTAATAA AGGAAAATTG
 CTTTGAAAGT AT-3' (FRAG.NO:____) (SEQ. ID NO: 2472)
 5'-CCGGGGC-3' (FRAG.NO:1800) (SEQ. ID NO: 1813)
 5'-GG GCCTGCBGGG CC-3' (FRAG.NO:1801) (SEQ. ID NO: 1814)
 5'-GGCGBCB BGG-3' (FRAG.NO:1802) (SEQ. ID NO: 1815)
 40 5'-GGG TCC TCB TGG CTG GGG-3' (FRAG. NO:1212) (SEQ. ID NO:1221)
 5'-GCC TGG GCC TGC BGG GCC-3' (FRAG. NO:1213) (SEQ. ID NO:1222)
 5'-GCT CTT GCC TGG 3GT GGC TC-3' (FRAG. NO:1214) (SEQ. ID NO:1223)
 5'-GCC CBG BGT CTT CCC TGG T-3' (FRAG. NO:1215) (SEQ. ID NO:1224)
 45 5'-CCGGGGCTGC BGCBBCCTCB TCBGCTCTG CCTGGBGTGG CTCBGCTGG GCCTGCBGGG CCBCCBGBG
 BBTGGCBGB BGGTGGCGB GGGTCTCTB GGCTGGGTC BCBGBTCTC TBGCTBGGCB GGGTGBCCBG
 BGBGGC-3' (FRAG.NO:1803) (SEQ. ID NO: 1816)

Human Defensin 2 Nucleic Acid and Antisense Oligonucleotide Fragments

5'-ATCCTTAAG TCAATGGACT TTGCATCACT CACACCATCT TTTGTTACTT TGGACTTCCC CAGCTATGTT
 CAATAATTAC TGTCTTCCC TTGGGCCCA TTGTAATGGC TACAGCCTCG ACAAAAAGTC TACACTTGA
 50 AGCATTAAAG CTCCGACATC AGCACAAAT TTTACATCTT TACCATCACT TCAAGTGGAG TGAGGAGCCA
 GTAGCCTGGA CACTGGTCTC ATCTGGTGA AGACTGTGGG TAATGGAAGC ATTCTGTGG GGTGCTGGCA
 GGACATGTGC ATGCCGAGGC AGGTCACTAG CAGCAAGTGA GAGCTGCCTC TTACTTTCTA AAGGTGACAT
 AGCAAATATA CAA AAAAAAA TAAATAAATT ATTAATTAG GTAGAGCACA TAAAGGCTTT ATTTCATATT
 CCATTTCTCT GTATGTTTC TTCACCAAGGA AGAAATAGTT TTAGTGTCAAG GAATGAATGA GTCTGCCCT
 55 CAATTCCAGC CTGCTCAACA CACAAGGAAA CAAAGCCCTG ACAATCAGAG TGACTCCCTG GTGACTAAGC
 TCCCAGTCCT GGAT'GCATAT TTGTTTAGCA GTTCTGACAG CATTGACCC AGCCCTCTCT CTGCATATCC
 CATCAGAACCC TTC TTTTTT TTTTTTTCTT TGAGACTGAG TCTTGCTCTG TCGGAAGCGA CTCCGTGCC
 TCAGCCTCCC AAAATACCTGG AATTATAGGC GTAAGCCATC ATGCCTGGCT AATTGTTGTA TTTTCATGG
 AGATGGGGTT TTGC'CATGTT GGTCAAATTG GTCTCACACT CCTGACCTCA TGTGATCCAC CTGCTCAGC
 60 CTCCCAAACCT GCTC GGATGA CAGGTGAAG CCACCATGCT AGGCTCAGAA ATTCCTTTT ATAAAATGTT
 CATTAAGGAT CTTC GCTGCA CAATATCGTT ACCAGCTCC TTTAAATCCA CTTCTGGCCT GCCAGGAATC

	AGGTTCTTCA	GAACCTGACA	TTTTAAATGA	AGAGGTCAGG	CAGTCATGA	GGAAAGCCTC	ATTGTCCCCA
	TGTCTCTGTC	ACTGCTGCAC	CCCTGAGACA	TCACAGACAT	GGACACTGGG	GCCTGCTTGT	TTCTCAAAC
	GCCCTTAGAT	CGAAGAGGG	AGGAACCAGG	ATGAATGCCA	CTCATTTCC	CAAGAAAGGC	CCTCTCCTGA
5	GTGCCCGGGA	TGGGGCTCTG	TCCATTGCC	GGGCCGCCA	ATTGCTACTC	TGGGTTACGG	AGGAAGGACA
	GGGTCTGAG	AGACACCAGA	GACCTCACAC	AGCCCTGAAA	ACATGGGGCT	CCTTCATAAG	TGTTTCCCCT
	CACCAACAGG	GAGACCACGT	GGAGGCCCTG	CAGCCCCACT	CGGTGCTTCT	CCACCAAATC	CCAAGGGCAG
	TGACGCTGAC	GTCIGTGGAA	AGCAGAGAAA	GCCCTGGCTC	CCAAAGCCT	GAAGTCCCTG	TGGAGCTGAC
	ATTCCCTGAG	TGACGGTGTG	AATGGAAGGA	ACTCAAGTGC	GGGTGGTAGG	CCACCTCCTG	GCCCAGGCCT
10	GGGTGAACTC	TGACGGGACA	CATGTAGTCA	CAATCCCCTC	CTCCCATTCT	CCTTCCTCAGA	GGAAGGAAGT
	GGGCATCCAT	CTGCCTCATC	TCTCTCCCGT	GGGGAAAGATG	GGGAGTTCA	GGGGAACTTT	CACATAAAATT
	TCACCAGCTC	AGA1CTCCTG	TGAGGATGGG	GCCCACCATG	CTCCCGTGC	TGCCAGAGGC	CCTGAGCCCC
	TCCCAGGGTC	CCTGGGTTTG	AGCCAGCCCT	GTATCATCCC	CAGGAGCTGA	ATGTCAGAGC	AATGGATAGA
15	ATTAGATGGA	AAGAGCTCTC	AATTGACCT	GAGACTGTCC	CCAGATACTC	AGGAAAAAAC	GGACGTCGCA
	CAGAGTGGGC	ACGAGGTGAG	TGGCAGGTTA	TAGGCCTGTA	GGTTGAGTTT	GTTCTCACGT	GAGACAGACC
	CAGCCCCCTA	CTCCATTCA	ACACTGGGTT	TTAAATGGTG	CAAGATAGGA	GCAATTTCCT	GGTCCCAAGA
	GCAGGAGGAA	GGGATTTTCT	GGGGTTTCC	GAGTCAGAT	TTGCATAAGA	TCTCTGAGT	GTGCATTGTT
	CTTGAGGAC	CATI CTCTGA	CTCACCAAGGT	AAGTGGCTGA	ATTCTAACCT	CTGTAATGAG	CATTGCACCC
	AATACCAAGTT	CTGA ACTCTA	CCTGGTGACC	AGGACCAGG	ACCTTATAA	GGTGGAAAGC	TTGATGTCTC
20	CCCCAGACTC	AGCCTCTGGT	GAAGCTCCA	GCCATCAGCC	ATGAGGGTCT	TGTATCTCCT	CTTCTCGTTC
	CTCTTCATAT	TCCTGATGCC	TCTTCCAGGT	GAGATGGGCC	AGGGAAATAG	GAGGGTTGGC	CAAATGGAAG
	AATGGCGTAG	AAGITCTCTG	TCTCCTCTCA	TTCCCCCTCA	CCTATCTC	CCTCATCCCT	CTCTCTCCTT
	CCTCTCTCTG	TGTCTCCCT	CCATCCTTT	CTCTGCTTC	TCTCTCTCT	TCCTCTCTC	TCTTTTCTT
	GTCTTTCTT	TTCCCTCTCTC	CCTAGAGCAT	GTCTTCTTT	CTTCTCTTT	CCTTCTCTCT	ACCCACACTT
	TTAGACTGAA	TGCCCTATTT	AATTGAACAA	AGCATTGCTT	CCTTCAATAG	AAAAGGAGTT	TGAGAACCCA
25	ATGGACACCT	CACTCGTTCT	TCTAAGCCAA	TATGAAGGAG	CCCAGTAGCT	TGTAATATAC	ATCTCTCAC
	TGCTTCCAT	GCTACAACGT	CTGAGACTAT	GGTTGAAACC	TGTTAGGTG	CTTTTAAAT	AAAAGGCAGA
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	ACCAATCTTA	TTATGAGTC	CTGGGTTTG	TGAGAACAT	GGGGTTCTGA	GAGGCACCAG	AGACCTCATG
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35	GGAGGCGGGC	AGG1GGGGAG	GGAGGGACGG	AAGGAGGGAG	GGAGGGAGGG	AGGGAGGGAG	GGAGGGATAA
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	CTTTTATACC	CATCTCAGGT	CAAATACTTA	ACAGACTAAA	TGATTGAAA	AAGCAAAAGT	TTACTGGCTT
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40	TCGTTGCTGA	GCTCTTACCA	GACCCACCT	GGAGGCCCA	GTCACTCAGG	AGAGATCAGG	GTCTTTCACA
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	CAAATGACTG	ACTCGCGTCT	CATTATCATG	ATGGAAAAGC	CCAGGCTTGA	GAAAAGGCC	CGCTGCGGAT
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	GCTCTTTTG	TGTGTTTTT	CCCTGTTAGG	TGTTTTGGT	GGTATAGGCG	ATCCTGTTAC	CTGCCTTAAG
45	AGTGGAGCCA	TATGTCATCC	AGTCTTTGC	CCTAGAAAGGT	ATAAAACAAAT	TGGCACCTGT	GGTCTCCCTG
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	TCCCTCATCA	GAGACGTGCG	ACATGTAAAC	CAAATTAAAC	TATGGTGTCC	AAAGATAACGC	AATCTTATC
	CTAGTAATTG	TGGTCATTGG	GTGATGTTGG	TTGGGCAGG	CCATCTCTAA	TATCCTGAA	ACACCTTTT
	CTGCTCTCCA	GGAA GGGGTC	AGGGCTGCCA	CAGGGGGCT	TGGAGTGTCT	TCCAGGGTCA	CAGGCATCTG
50	TATTCTTGG	ATTCCTTGAC	CTTCCCCATT	TATTCCCGC	ATTTCTAA	AACGTGTGCT	TTGCTCCTCC
	TGCATCCTCC	CCTT3CATGC	CCTCACCTAC	CCCACATCTT	CCCTAAAAAA	AGCAAGCCCA	ACTCAAAGAC
	CAGTTCCCTC	ATGGAATCAT	AGTGGATCTG	CCAAGGGAGG	GGATGCCAG	TCCTCTGTT	TTCACAAGAC
	TCCCTCTTC	TGGCTAAGGT	TTCTTATGCA	ATTAT GAATTACAT	TTCTCACCTT	TTGATGTATT	AAGAAAGTAT
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55	TCCTTACTG	TGATGATGCC	CTTCTTCCA	AACTTTTCA	TTGCATCAGA	GATGATGTTA	CCAATTCTT
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	CCAGTCTCTC	CATITGTGTT	ATTGGCAACA	TCTGGACAA	GTTCAGCTCC	AATGCTTTTA	TATTTATCCT
60	TTAAGTCAAT	TGACTTTGCA	TCAGTCACAC	CATCTTTGT	TACTTTGGGA	CTTCCCCAGC	TATGTTCAAT
	AATTACTGTT	CTTCCCTTTG	GCCCCATTGT	AATGGCTACA	GCATCGACAA	AAAGTCTACA	CTTTGAAGCA
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 10 10 GTGCTGGGAT GACGGGTGTA AGCCACCATG CTAGGCTCAG AAATTCCTT TTATAAAAAT GTCATTAAGG
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 15 15 GGATGGGCT CTGTCATTG CCTGGGCCG CCAATTGCTA CTCTGGTTA CGGAAGAAGG ACAGGGCTCT
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 35 35 AGTAGACTGA ATGCCCTATT TAATTGAACC AAGCATTGCT TCTTCAATA GAAAAGGAGT TTGAGAACCC
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 45 45 TTTCCAAAAC CTAGAACAGT ATAATGAAGG AAGGAGGGAA GGAGGGAGGG AGGGAGGGAA GGAGGGAGG
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 50 50 TGGAGCTGAA TTCA CAAGAG ATCGTTGCTG AGCTCCTGCC AGACCCACC TGGAGGCCCT AGTCACTCAG
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 TCCATGTCAG AAACTTAGAT CCAAATGACT GACTCGCGTC TCATTATCAT GATGGAAAAG CCCAGGCTTG
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 TGATGCGGAT TCAC AAAGGG CTCCCTCATC AGAGACGTGC GACATGAAA CCAAATTAAA CTATGGTGTG
 CAAAGATACG CAACTCTTAT CCTAGTAATT GTGGTCATTG GGTGATGTTG GTTGGCAG GCCATCTCTA
 ATATCCTGA AACACCTTT TCTGCTCTCC AGGAAGGGGT CAGGGCTGCC ACAGCAGGGC TTGGAGTGC-3'
 60 60 (FRAG. NO: ____) (SEQ. ID NO:3011)
 5'-GAATTACAT TTCTCACCTT TTGATGTATT AAGAAAGTAT GGAGAAATAT ATCCTCTATC AAATTTCTAT
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	AACTTTTCA	TTGCATCAGA	GATGATGTTA	CCAATTCTT	TGTCTCCATT	TGCAGAAATT	GTAGCAACCT
	GTGCAATTTC	TTCAAGTTTG	GTCACAGGT	TAGACTGCTT	TTTAAGTCA	GCAATTACAG	CATCAACAGC
	TAACATACA	CCTCTTGTGA	TTTCCACTGG	ATTAGCACCT	TTGCTAACCT	TCTGGAAGGC	TTATTTGGAA
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	TCCCTCCATT	CTCCCTCTCA	GAGGAAGGAA	GTGGGATCC	ATCTGCCTCA	TCTCTCTCCC	GTGGGAAAGA
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Human Defensin 3 Nucleic Acid and Antisense Oligonucleotide Fragments

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 GGCAAGCAA ACAGGTGATA GTACCTCTGG GGAACCAT GCGCGTGTG CATCAGATC TCAGGAGAAC
 CCAAAAATGT CTGTTCCACA TAGCAACAGA AGCCCAGGT GCACTCAGTC TCACCTGGGT GTTCTCAAAC
 30 ATCCCAGCTC AGCCAAATGG CTTTCATTAG TTTTATGGT TAGACCCAG GTCCTCGGGA CACTGTTA
 GAAACACATT CCAAATCCTC CTCTGTGTG AGGTGGCATT CCTATCCAA TCTCTTGCA GGGCGTATAC
 TGTGATACGC AGCCAGGTG TCCCAGAGGC CTTAAATATT CCCTCTGGC AGGTAGTTCA GCTTAGCCAC
 AGCCAATGCA TCACAGGGT AACTGTGTTA GGAGCCATTG AGAATCCATA GTTGGTTGCT GCCTGGCCT
 GGCAAGGGCT GACCAAGGTA GATGAGAGGT TCCTCTGTGG AGTTCTACTT TAACCTCACC TTCCCACCAA
 35 ATTTCTAAC TGTCTTGCC ACCACAATTG TTTAATGGAC CCAACAGAAA GTAACCCCGG AAATTAGGAC
 ACCTCATCCC AAAA' GACCTT TAAATAGGGG AAGTCCACTT GTGCACGGCT GCTCTTGCT ATAGAAGACC
 TGGGACAGAG GACCTGTC TGCCCTCTCT GGTACCCCTG CCTAGCTAGA GGATCTGTAA GTACTACAAA
 ACTTAAACTT TACACTGAGT TTTCATCATT GAAGCTATGC CTCAATCTG ACCTCTGACT GTGGGTGACT
 CCCAGAGGGTA CCCAGGGGT GAATCCCTGC TAGGAACGTC TGTCCGGACC GCTGGGGACG
 40 ATGGCTTCCA GCTRACTAA TAGAGAAACT CAAGCAGTT CCTTCTAAAT ACACATGTCA CATGCTCTGG
 TTGACATGTC CAGTAAGAAG ACTATCACAG GTCTTTGGAA CATTCTTTG AGAGAAACCT ATTAGGTCC
 TTGGTCTGTT TTCAATCAG GTTGTGTTG TTTTGTCTT GAGTTGTTGG AATTCTTAT GTATTCAAGAT
 ATTTGCCCT TCTCCATGTT AGGTTTGCA AATATTCTT CTCAATTCTT GGGTTATCTT TTCACTCGGT
 TGATTGTTTC CTTGCTGTG CAGATGCTT AGCGTTAAC TGAAGCCACAC TTGCTATT TCCCTTTAT
 45 TGCCTGTGCC TTTGGTGTCA TAGCCAAGAA ATCATTACCT ACATCAATGT CAAAGCTTT ATCCTTCTAT
 ACACTCTAG TAGTTATGG TTTCAGTTGT TACATTAGG TTTTCAATTG ATTCTGAGTT GATGTTCTTA
 CATGGTGTGA GATAAAGATT TAAATACATA CATATATAAA ATCATGAGGT AGTGTACACT ATAAATATAC
 AATTGTTAAT TGTIACTCAA GTCTAAGTAG AGGTGGAAAT AATAAACCTT CTTTTTTTA CTTAAACAC
 TCTGTGTAC TGACCTGATT TCACCTTAG CCTGATAAAA TCATTGTCCT CTCCACCCCTG ATTCCCTACAG
 50 GAGACTACTC ACCCCATAAC CTCAAAACCT TCTTCATGAG GATGGTAAGT CACCTGAATC CTGAAGTGA
 TTACTCGCTA TTCCATTGGA ACTCATATAG GACACCAGAA TCTAGACCTC CAGAGAACAG CAGGACCCAT
 CTTCAGAAAA TAAAGAAGCAT TTGTTCCCTG AGCCTGTTGA ATCAAAGTC AATTCTTATT CTTTTGGAA
 TGTTAAAAG TGAATCATAA TATTTAACAGA GGTGAACCCA CGAGTAACAT AGCAGGGTCT TTCTTGTCT
 TATTAGCTCC AACCTAGCAC AGACATTAAA GGTACAGAT TATACTAGCA TGAAACTGGG AGAACAGGAG
 55 CATTGAGCA ACCITGAGAC CAATGGGCCCT CTCTTATAAA ATGCACACCT CCTCTCACTG AGATTGAGGA
 AGGTTCTTG TCTCCGAGCC TTCTCCAGT AGAGCTATAA ATCCAGGTG GCTCCTCCCT CCCCACACAG
 CTGCTCTGC TCTCCCTCT CCAGGTGACC CCAGCCATGA GGACCTCGC CATCCTTGCT GCCATTCTCC
 TGTTGGCCCT GCACGCCAG GCTGAGCCAC TCCAGGCAAG AGCTGATGAG GTTGTGTCAG CCCCAGGAGCA
 GATTGAGCGC GACATCCCCAG AAGTGGTGT TTCCCTTGCA TGGGACGAA GCTTGGCTCC AAAGCATCCA
 60 GGTGAGAGAG GCAGGCATGC AGAGCTGCTA AGTCTAGAGG GAAGGACGGG AGAGAGGTTG CAGAGTTGGG

TCTCAGCA GT CTAIGTCACT GAGGTGGCTT CACTTAGAAT CTCTGGGCAT TGATTTCTC ATCTAGAAAT
 TGAACAGAGA GCCAAATAAA CCTGAGAAC TTTATTTCTC CAAAGACTG ATTCCAAGAA ACATCTGTGA
 AATTCACTAA GTTIAAGATA TGAAGAGACA GACTAGTTAT TTCTGGATCT AAACAAGTAG ACTTAGTTGT
 AAAGAGAACAA TTTACTCTA TCTACAGAAC AGCTTTAAA AACTGCAGCC AAGCCTGAGG GTAAGTTCAG
 5 GTGTGTGTG GATGGGGCAG GAATGAAAAA ATGAGAGCAA AGGAGAAATGA GTCTCAAATT CTGTGTGACA
 AGCACTGCTC TGCC TGTTA TTCCATCGA CTGAGGTTGT TCGTGTACCG GGCTGCAATG CAGCCAGCAT
 CACCTGTCA GCTACATGTG ACTTCCCCGA GATTCTTTT CTTACCCACT GCTAACTCCA TACTCAATT
 CTCATGCTCT CCCTGTCCCCA GGCTCAAGGA AAAACATGGA CTGCTATTGC AGAATACCAG CGTGCATTGC
 10 AGGAGAACGT CGCTATGGAA CCTGCATCTA CCAGGGAAAGA CTCTGGGCAT TCTGCTGCTG AGCTTGAGA
 AAAAGAAAAA TGAIGCTCAAA ATTGCTTG AGAGCTACAG GGAATTGCTA TTACTCCTGT ACCTTCTGCT
 CAATTCCCTT TCCTCATCTC AAATAAATGC CTTGTTACAA GATTCTGTG TTTCCACCTC TTTAATGTGT
 GATATGTGTC TGTGCAAGA CACTTGGGAT ACACGTACCA AAACGCAAAA TCAAATTAA GAACAATATA-3'
 (FRAG. NO:____) (SEQ. ID NO:2477)
 15 5'-GGCBGCBGG-3' (FRAG. NO:1805) (SEQ. ID NO:1818)
 5'-GG CTG GGG-3' (FRAG. NO:1806) (SEQ. ID NO:1819)
 5'-GGGGTCBCC-3' (FRAG. NO:1807) (SEQ. ID NO:1820)
 5'-GGG TCC TCB TGG CTG GGG TC-3' (FRAG. NO:1216) (SEQ. ID NO:1225)
 5'-CCT CTC TCC CGT CCT-3' (FRAG. NO:1217) (SEQ. ID NO:1226)
 20 5'-CGTGCBCBTC TGCTCCGGGG CTGCBGCBBC CTCBCTBGCTC TTGCTGGBGTG GCTCBGCTGG GCCTGCBGGG
 CCBCCBGGBGB BTGGCBGCBG GBTGGCBGGG TCCTCBTGGC TGGGTCBCCT GGBGGBGGGB GBGCBGG-3'
 (FRAG. NO:1808) (SEQ. ID NO:1821)

Human Macrophage Inflammatory Protein-1-alpha/RANTES Receptor Nucleic Acid and Antisense Oligonucleotide Fragments

25 5'-GTCTTTGTTT CTCGGCTCGT GCCCCBCTCCC GGCTCTCTC TGGTCCGTC CTCTGTGGTG TTTGCCCTG
 CTTCTTTTG CCTGTGAGG GGGCAGCACT TGGGCCCCAA AGGCCCTCTC GTTCACCTTC TGACGGAGTT
 GCATCCCCATA GTCAAACACT GTGGTCGTGT CATAGCCTC TGTGGTGTG GGAGTTCCA TCCCAGCTTC
 TCTCTGGTTC CAACGGAGB GGGGGCBGB GTGGGGCCCC BBBGGCCCTC TCGTTCBCCCT TCTGGCBGG
 BTTGCBTCC CCBTBGTCBB BCTCTGTGGT CGTGTCTBGG TCCTCTGTGG TGTTGGBGT TTCCBTCCCC
 GCTTCTCTCT GTTCCCBGG GB-3' (FRAG. NO:1809) (SEQ. ID NO:1822)
 30 5'-GGGCC CC-3' (FRAG. NO:1810) (SEQ. ID NO:1823)
 5'-GGGGGCBGC-3' (FRAG. NO:1811) (SEQ. ID NO:1824)
 5'-CCCGGCTTC-3' (FRAG. NO:1812) (SEQ. ID NO:1825)
 5'-GTC TTT GTT TCT GGG CTC GTG CC-3' (FRAG. NO:1218) (SEQ. ID NO:1227)
 5'-CCB TCC CGG CTT CTC TCT GGT TCC-3' (FRAG. NO:1219) (SEQ. ID NO:1228)
 35 5'-GTC CTCTGT GGT GTT TGG-3' (FRAG. NO:1220) (SEQ. ID NO:1229)
 5'-CCC TGC TTC CTT TG CCT GTT-3' (FRAG. NO:1221) (SEQ. ID NO:1230)
 5'-GAGGGGGCAG CAGTTGGGCC CCAAAGGCC TCTCGTTCAC CTTCTGGCAC GGAGTTGCAT CCCCATAGTC
 AAACTCTGTG GTCGT-3' (FRAG. NO:1222) (SEQ. ID NO:1231)
 5'-GTCATAGTCCTCTC TTGTTGGAGTTCCATCCGGCTCTCTGGTCCAAGGGA-3' (FRAG. NO:1223) (SEQ. ID
 40 NO:1232)
 5'-GBGGGGCBG CB GTGGGCC CCBGGGCC TCTCGTTCBC CTTCTGGCBC GGBGTTGCBT CCCCBTBGTC
 BBBCTCTGTG GTCGT-3' (FRAG. NO:1224) (SEQ. ID NO:1233)
 5'-TCBTBGTCCCTCTGTGTTGGAGTTCCBTCCCGCTCTCTGGTCCBGG-3' (FRAG. NO:1225) (SEQ. ID
 NO:1234)

RANTES Antisense Oligonucleotide Fragments

45 5'-GGGCBGGGG CB GTGGGCC GCBBTGTBGG CBBGCBGB GGGTGTGGTG TCCGBGGBBT BTGGGGBGGC
 BGBTGCBGB GCGCGBGBGG CBGTBGCCTB GBGBTGBCB GCGBGGCGTG CGCGGBGBGC CTTCBTGGTB
 CCTGTGGBGB GGCIGTCGGB GGGGGTGTGG TGTCCGCTTG GCGGTTCTTT CGGGTGTTC TTCTCTGGGT
 TGGCCTGCTG CTGCTCGTGGT CGCTCCGCTC CGGGGTTCTG CTCGCTCTGT CGCCCTTCC TTCCCTGTG
 50 TGTTCTCTCC TTCTCTGTG-3' (FRAG. NO: 1813) (SEQ. ID NO: 1826)
 5'-GGGTTGGC-3' (FRAG. NO: 1814) (SEQ. ID NO: 1827)
 5'-CGGGG CBG-3' (FRAG. NO: 1815) (SEQ. ID NO: 1828)
 5'-CCCGGGTTCG-3' (FRAG. NO: 1816) (SEQ. ID NO: 1829)
 5'-GGGTGTGGTG-3' (FRAG. NO: 1817) (SEQ. ID NO: 1830)
 55 5'-GGGCBGGGG CB GTGGGCC GCBBTGTBGG CBBGCBGB GGGTGTGGTG TCCGBGGBBT BTGGGGBGGC
 BGBTGCBGB GCGC-3' (FRAG. NO:1226) (SEQ. ID NO:1235)
 5'-BGBGGGCBGTB GCBBTGBGG TBGBGCBGB GCGTGCCGCG GBGBCTTCB TGGTBCTGT GGBGBGGCTG
 TCGGBGG-3' (FRAG. NO:1227) (SEQ. ID NO:1236)
 5'-GGGTGTGGTGTCCTGTTGGCGGTCTTCGGGTGTTCTCTGGGTTGGCCTGCTGCTCGTGGTC-3' (FRAG.
 60 NO:1228) (SEQ. ID NO:1237)

5'-GCTCCGCTCCGGCTTCGTCTCGCTCTGCGCCCTTCCCTTGCGTTCCCTCCCTGCCTCT-3' (FRAG. NO:1229) (SEQ. ID NC:1238)

5'-GGGTGTGGTGTCCG-3' (FRAG. NO:1230) (SEQ. ID NO:1239)

5'-CTTGGCGGTTCTTCGGGTG-3' (FRAG. NO:1231) (SEQ. ID NO:1240)

5'-TTTCTCTCTGGGTGGC-3' (FRAG. NO:1232) (SEQ. ID NO:1241)

5'-CTGCTGCTCGTCGTCGG-3' (FRAG. NO:1233) (SEQ. ID NO:1242)

5'-GCTCCGCTCCGGCTTC-3' (FRAG. NO:1234) (SEQ. ID NO:1243)

5'-GTCTCGCTCTGTGCC-3' (FRAG. NO:1235) (SEQ. ID NO:1244)

5'-CTTCCTTCCTTGTGCTC-3' (FRAG. NO:1236) (SEQ. ID NO:1245)

10 5'-GTGTTCTCCCTTCCTTGCGCTCT-3' (FRAG. NO:1237) (SEQ. ID NO:1246)

5'-GGGCBGGGG CBGTGGCGG GCBBTGTBGG CBBBGCBGB GGGTGTGGT TCCGBGBBT BTGGGGBGGC BGBTGCBGBB GCGBGBGGG CBGBTGCBBT GBGBTGBCB GCGBGGCGT CCGCGBGBBC CTTCBTGGTB CCTGTGGBGB GGCTGTCGGB GG-3' (FRAG. NO:1818) (SEQ. ID NO:1831)

Human Muscarinic Acetylcholine Receptor HM1* Nucleic Acid and Antisense Oligonucleotide Fragments

15 5'-GCTGCCCGGC GGGGTGTGCG CTTGGCGCTC CCGTGCTCGG TTCTCTGTCT CCCGGTCCCC CTTGCCTGGC GTCTCGGGCC TTCGTCTCT TCCTCTTCTT CCTTCGCTC CGTGGGGGCT GCTTGGTGGG GCCCTGTGCCT CGGGGTCCCCG GGGCCTCTGG CCCTTGCCGT TCATGGTGGC TAGGTGGGGC GTTCBTGGT GCTBGGTGGG GC-3'(FRAG. NO:1819)(SEQ. ID NO: 1832)

5'-GGTGGGGC-3' (FRAG. NO:1820) (SEQ. ID NO: 1833)

20 5'-GCCCGCGGGG-3' FRAG. NO:1821) (SEQ. ID NO: 1834)

5'-CGG GGC TTC TGG CCC-3' (FRAG. NO:1822) (SEQ. ID NO: 1835)

5'-GTT CBT GGT GGC TBG GTG GGG C-3' (FRAG. NO:1238) (SEQ. ID NO:1247)

5'-GCT GCC CGG CGG GGT GTG CGC TTG GC-3' (FRAG. NO:1239) (SEQ. ID NO:1248)

5'-GCT CCC GTG CTC 3GT TCT CTG TCT CCC GGT-3' (FRAG. NO:1240) (SEQ. ID NO:1249)

25 5'-CCC CCT TTG CCT GGC GTC TCG G-3' (FRAG. NO:1241) (SEQ. ID NO:1250)

5'-GCC TTC GTC CTC TTC CTC CTT CC-3' (FRAG. NO:1242) (SEQ. ID NO:1251)

5'-GCT CCG TGG GGG CTG CTT GGT GGG GGC CTG TGC CTC GGG GTC C-3' (FRAG. NO:1243) (SEQ. ID NO:1252)

5'-CGG GGC TTC TGG CCC TTG CC-3' (FRAG. NO:1244) (SEQ. ID NO:1253)

5'-GTT CAT GGT GGC TAG GTG GGG C-3' (FRAG. NO: 1245) (SEQ. ID NO:1254)

30 **Human Muscarinic Acetylcholine Receptor HM3* Nucleic Acid and Antisense Oligonucleotide Fragments**

5'-GGG GTG GGT BGG CCG TGT CTG GGGGTT GGC CBT GTT GGT TGC CTCT TGG TGG TGC GCC GGG CGCG TCT TGG CTT TCT TCT CCT TCG GGC CCT CGG GGT GCT TGT GGGCT CCT CCC GGG CGG CCT CCC CGG GCG GGG GCT TCT TGGCG CTG GCG GGG GGG CCT CCTGCT CTG TGG CTG GGC GTT CCT TGG TGT TCT GGG TGGTGG CGG GCG TGG TGG CCT CTG TGCCCC CCC GCG GCT GCB GGG GTTG CCT GTC TGC TTC GTCCTT TGC GCT CCC GGG CGG CGG CGGG GTG GGT AGG CCG TGT CTG GGGGTT GGC CAT GTT GGT TGC CGGG CCC GCG GCT GCA GGG G-3' (FRAG. NO:1823) (SEQ. ID NO:1836)

5'-CCC GGG CGG-3' (FRAG. NO:1824) (SEQ. ID NO:1837)

5'-G GCG GGG GGG CC-3' (FRAG. NO:1825) (SEQ. ID NO:1838)

5'-CCC GGG CCG CC-3' (FRAG. NO: 1826) (SEQ. ID NO: 1839)

40 5'-GG CCG TGT-3' (FRAG. NO:1827) (SEQ. ID NO:1840)

5'-GGG GTG GGT BGG CCG TGT CTG GGG-3' (FRAG. NO:1246) (SEQ. ID NO:1255)

5'-GTT GGC CBT GTT GGT TGC C-3' (FRAG. NO:1247) (SEQ. ID NO:1256)

5'-TCT TGG TGG TGC 3CC GGG C-3' (FRAG. NO:1248) (SEQ. ID NO:1257)

5'-GCG TCT TGG CCT TCT CCT TCG GGC CCT CGG GCC GGT GCT TGT GG-3'(FRAG.NO:1249)(SEQ.ID NO:1258)

45 5'-GCT CCT CCC GGG CGG CCT CCC CGG GCG GGG GCT TCT TG-3' (FRAG. NO:1250) (SEQ.ID NO:1259)

5'-GCG CTG GCG GGG GGG CCT CCT CC-3' (FRAG. NO:1251) (SEQ. ID NO:1260)

5'-GCT CTG TGG CTG GGC GTT CCT TGG TGT TCT GGG TGG C-3' (FRAG. NO:1252) (SEQ. ID NO:1261)

5'-TGG CGG GCG TGG TGG CCT CTG TGG TGG-3' (FRAG. NO:1253) (SEQ. ID NO:1262)

50 5'-GGG CCC GCG GCT GCB GGG G-3' (FRAG. NO:1254) (SEQ. ID NO:1263)

5'-TTG CCT GTC TGC TTC GTC-3' (FRAG. NO:1255) (SEQ. ID NO:1264)

5'-CTT TGC GCT CCC GGG CCG CC-3' (FRAG. NO:1256) (SEQ. ID NO:1265)

5'-GGG GTG GGT AGC CCG TGT CTG GGG-3' (FRAG. NO:1257) (SEQ. ID NO:1266)

5'-GTT GGC CAT GTT GGT TGC C-3' (FRAG. NO:1258) (SEQ. ID NO:1267)

55 5'-GGG CCC GCG GCT GCA GGG G-3' (FRAG. NO:1259) (SEQ. ID NO:1268)

Human Fibronectin* Antisense Oligonucleotide Fragments

5'-CGG TTT CCT TTG CGG TC TTG GCC CGG GCT CGG GGT G CCC GCC CGC CCG CGG GCC GC CCC GCC GGG CTG TCC CGG CCC CGC CCC GGC CGG CGG GG CGG CCC TCC CGC CCC TCT GG GCC GGC GCG GGC GTC GG CGG CCT GCG CCT GGG GTT CCC TCT CCT CCC CCT GTG C GCC TGC CTC TTCTGC GTC

CGC TGC CTT CTC CC CTC TCC TCG GCC GTT GCC TGT GC TGT CCG TCC TGT CGG CCT TCC GTG GTG C TGT
 TGT CTC TTC TGC CCT C GGT GTG CTG GTG CTG GTG GTG CCT CTG CCC GTG CTC GCCCTG CCT GGG CTG
 GCC TCT TCG GGT G'TG GCT TTG GGG CTC TCT TGG TTG CCC TTT CTT CTC GTG GTG CCT CTC CCT GGC
 TTG GTC GT TGT CTG GGG TGG TGC TCC TCT CCC TGC TGG CCG TTT GT CCT GTT TTC TGT CTT
 5 CCT CT TTC CTC CTC TTT CTC CGT TTG GCT TGC TGC TTG CGG GGC TGT CTC C CTT GCC CCT GTG GGC TTT
 CCC TGG TCC GGT C TT CTC CTT GGG GGT C GCC CTT CTT GGT GGG CTGGCT CGT CTG TCT TTT TCC TTC C
 TGG GGG TGG CGG TTG TGG GCG GTG TGG TCC GCC T TGC CTC TGC TGG TCT TTC-3' (FRAG. NO:1828) (SEQ.
 ID NO: 1841)
 5'-GGCCCCGGC-3' (FRAG. NO:1829) (SEQ. ID NO: 1842)
 10 5'-GCCGGCGCGGGCG 3' (FRAG. NO:1830) (SEQ. ID NO:1843)
 5'-GCCTGGGCTGGCC-3' (FRAG. NO:1831) (SEQ. ID NO: 1844)
 5'-GGGGG TGGCCG-3' (FRAG. NO:1832) (SEQ. ID NO: 1845)
 5'-GG GGG TGG CCG TTG TGG GCG G-3' (FRAG. NO:1833) (SEQ. ID NO: 1846)
 5'-CGG TTT CCT TTG CGG TC-3' (FRAG. NO:1260)(SEQ. ID NO:1269)
 15 5'-TTG GCC CGG GCT CCG GGT G-3' (FRAG. NO:1261)(SEQ. ID NO:1270)
 5'-CCC GCC CGC CCG CCG GCC GC-3' (FRAG. NO:1262)(SEQ. ID NO:1271)
 5'-CCC GCC GGG CTG TCC CCG CCC CGC CCC-3' (FRAG. NO:1263)(SEQ. ID NO:1272)
 5'-GGC CCG GGG CGC GGG GG-3' (FRAG. NO:1264)(SEQ. ID NO:1273)
 5'-CGG CCC TCC CGC CCC TCT GG-3' (FRAG. NO:1265)(SEQ. ID NO:1274)
 20 5'-GCC GGC GCG GGC GTC GG-3' (FRAG. NO:1266)(SEQ. ID NO:1275)
 5'-CCG CTC GCG CCT GGG GTT CCC TCT CCT CCC CCT GTG C-3' (FRAG. NO:1267)(SEQ. ID NO:1276)
 5'-GCC TGC CTC TTG CTC TTC-3' (FRAG. NO:1268)(SEQ. ID NO:1277)
 5'-TGC GTC CGC TGC CTT CTC CC-3' (FRAG. NO:1269)(SEQ. ID NO:1278)
 5'-CTC TCC TCG GCC CTT GCC TGT GC-3' (FRAG. NO:1270)(SEQ. ID NO:1279)
 25 5'-TGT CCG TCC TGT CGC CCT TCC GTG GTG C-3' (FRAG. NO:1271)(SEQ. ID NO:1280)
 5'-TGT TGT CTC TTC GC CCT C-3' (FRAG. NO:1272)(SEQ. ID NO:1281)
 5'-GGT GTG CTG GTG CTG GTG GTG-3' (FRAG. NO:1273)(SEQ. ID NO:1282)
 5'-CCT CTG CCC GTG CTC GCC-3' (FRAG. NO:1274)(SEQ. ID NO:1283)
 5'-CTG CCT GGG CTG GCC TCT TCG GGT-3' (FRAG. NO:1275)(SEQ. ID NO:1284)
 30 5'-GTG GCT TTG GGG CTC TCT TGG TTG CCC TTT-3' (FRAG. NO:1276)(SEQ. ID NO:1285)
 5'-CTT CTC GTG GTG CCT CTC CCT GGC TTG GTC GT-3' (FRAG. NO:1277)(SEQ. ID NO:1286)
 5'- TGT CTG GGG TGG TGC TCC TCT CCC-3' (FRAG. NO:1278)(SEQ. ID NO:1287)
 5'-TTT CCC TGC TGG CCG TTT GT-3' (FRAG. NO:1279)(SEQ. ID NO:1288)
 5'-CCT GTT TTC TGT CTT CCT CT-3' (FRAG. NO:1280)(SEQ. ID NO:1289)
 35 5'-TTC CTC CTG TTT CTC CGT-3' (FRAG. NO:1281)(SEQ. ID NO:1290)
 5'-TTG GCT TGC TGC TTG CGG GGC TGT CTC C-3' (FRAG. NO:1282)(SEQ. ID NO:1291)
 5'-CTT GCC CCT GTG GGC TTT CCC-3' (FRAG. NO:1283)(SEQ. ID NO:1292)
 5'-TGG TCC GGT CTT CTC CTT GGG GGT C-3' (FRAG. NO:1284)(SEQ. ID NO:1293)
 5'-GCC CTT CTT GGT GGG CTG-3' (FRAG. NO:1285)(SEQ. ID NO:1294)
 40 5'-GCT CGT CTG TCT TTT TCC TTC C-3' (FRAG. NO:1286)(SEQ. ID NO:1295)
 5'-TGG GGG TGG CGG TTG TGG GCG GTG TGG TCC GCC T-3' (FRAG. NO:1287)(SEQ. ID NO:1296)
 5'-TGC CTC TGC TGG TCT TTC-3' (FRAG. NO:1288)(SEQ. ID NO:1297)

Human Interleukin-1 (IL-1) Nucleic Acid and antisense Oligonucleotide Fragments

45 5'-AAGCTCTAC CC AGTCTGG TGCTACACTT ACATTGCTTA CATCCAAGTG TGGTTATTTC TGTGGCTCCT
 GTTATAACTA TTATAGCACC AGGTCTATGA CCAGGAGAA TAGACTGGCA TAAATCAGA ATAAGAGATT
 TTGCACCTGC AATAGACCTT ATGACACCTA ACCAACCCCA TTATTTACAA TTAAACAGGA ACAGAGGGAA
 TACTTTATCC AACTCACACA AGCTGTTTC CTCCCAGATC CATGCTTTT TGCGTTTATT ATTTTTAGA
 GATGGGGCT TCACATATGTT GCCCCACACTG GACTAAAAGT CTGGGCCTCA AGTGATTGTC CTGCCTCAGC
 CTCCTGAATA GCTGGGACTA CAGGGCATG CCATCACACC TAGTTCATTT CCTCTATTTA AAATATACAT
 50 GGCTTAAACT CCAA CTGGGA ACCCAAAACA TTCATTGCT AAGAGTCTGG TGTCTACCA CCTGAACTAG
 GCTGCCACA GGA ATTATAA AAGCTGAGAA ATTCTTTAAT AATAGTAACC AGGCAACATC ATTGAAGGCT
 CATATGTAAA AAC TCATGCC TTCTTTCTC CCAATCTCCA TTCCCAAAC TAGCCACTGG TTCTGGCTGA
 GCCCTTACGC ATAC CTCCCG GGGCTTGAC ACACCTTCTT CTACAGAAGA CACACCTTGG GCATATCCTA
 CAGAAGACCA GGC TCTCTC TGGCTCTGG TAGAGGGCTA CTTTACTGTA ACAGGGCCAG GGTGGAGAGT
 55 TCTCTCTGA AGCT CCATCC CCTCTATAGG AAATGTGTTG ACAATATTCA GAAGAGTAAG AGGATCAAGA
 CTTCTTGTG CTCA AATACC ACTGTTCTCT TCTCTACCCCT GCCCTAACCA GGAGCTTGTC ACCCCAAACT
 CTGAGGTGAT TTATGCCCTA ATCAAGCAA CTTCCCTCTT CAGAAAAGAT GGCTCATTTT CCCTCAAAG
 TTGCCAGGAG CTGCCAAAGTA TTCTGCCAAT TCACCCCTGGA GCACAATCAA CAAATTCAAG CAGAACACAA
 CTACAGCTAC TATTAGAACT ATTATTATTA ATAAATTCCCT CTCCAAATCT AGCCCTTGA CTTCGGATTT
 60 CACGATTCT C CCCCCTCTCC TAGAAACTTG ATAAGTTTCC CGCGCTTCCC TTTTCTAAG ACTACATGTT
 TGTCTCTTA TAAA GCAAAG GGGTGAATAA ATGAACCAAA TCAATAACTT CTGGAATATC TGCAAACAA

	AATAATATCA	GCTATGCCAT	CTTTCACTAT	TTTAGCCAGT	ATCGAGTTGA	ATGAACATAG	AAAAATACAA
	AACTGAATTG	TTCCCTGTAA	ATTCCCCGTT	TTGACGACGC	ACTTGTAGCC	ACGTAGCCAC	GCCTACTTAA
	GACAATTACA	AAACGCGAAG	AAGACTGACT	CAGGCTTAAG	CTGCCAGGCC	GAGAGGGAGT	CATTTCATTG
5	GCGTTTGA	CAGCAAAGGT	ATTGTCCTCA	CATCTCTGGC	TATTAAGTA	TTTCTGTGTT	TTGTTTTCT
	CTTTGGCTGT	TTTCCTCTCAC	ATTGCCTCT	CTAAAGCTAC	AGTCTCTCT	TCATTTGCT	GTCCCCTCC
	GGTTTGGTAT	GTGACCTAGA	ATTACAGTC	GATTTCAGAA	AATGATTCTC	TCAACACTCT	GATAAGGACT
	GATCTGTTT	ACTGAGGGAC	GGCAGAACTA	GTTTCCTATG	AGGGCATGGG	TGAATACAAAC	TGAGGCTTCT
	CATGGGAGGG	AATCTCTACT	ATCCA AAAATT	ATTAGGAGAA	AATTGAAAAT	TTCCAACACTCT	GTCTCTCTCT
10	TACCTCTGTG	TAAC GCAAAT	ACCTTATTCT	TGTGGTGT	TTGTAACCTC	TCACAACTTT	CATTGATTGA
	ATGCCGTGTC	TGGCAATACA	TTAGGTTGGG	CACATAAGGA	ATACCAACAT	AAATAAAACA	TTCTAAAAGA
	AGTTTACGAT	CTAA TAAAGG	AGACAGGTAC	ATAGCAAAC	AATTCAAAGG	AGCTAGAAGA	TGGAGAAAAT
	GCTGAATGTG	GACTAAGTCA	TTCAACAAAG	TTTCAGGAA	GCACAAAGAG	GAGGGGCTCC	CCTCACAGAT
	ATCTGGATTA	GAGC CTGGCT	GAGCTGATGG	TGGCTGGTGT	TCTCTGTGTC	AGAAGTCAAG	ATGGCCAAG
15	TTCCAGACAT	GTTGAAGAC	CTGAAGAAC	GTACAGGTA	AGGAATAAGA	TTTATCTCTT	GTGATTAAAT
	GAGGGTTTCA	AGGC TCACCA	GAATCCAGCT	AGGCATAACA	GTGGCCAGGC	TGGGGCAGG	CCGGCAGAGG
	TTGTAAGAGAT	GTGTAAGTAGT	CCTGAAGTC	GAGCAGGTT	AGAGAAAGACC	CAGAAAAAACT	AAGCATTCA
	CATGTTAACAC	TGAC ATTACA	TTGGCAGGGA	GACCGCCATT	TTAGAAAAAT	TATTTTGAG	GTCTGCTGAG
	CCCTACATGA	ATATCAGCAT	CAACTTAGAC	ACAGCCTCTG	TTGAGATCAC	ATGCCCTGAT	ATAAGAATGG
20	GTTTACTGG	TCCA TTCTCA	GGAAAACCTG	ATCTCATTCA	GGAACAGGAA	ATGGCTCCAC	AGCAAGCTGG
	GCATGTGAAAC	TCACATATGC	AGGCAAATCT	CACTCAGATG	TAGAAGAAAG	GTAATGAAC	ACAAAGATAA
	AATTACGGAA	CATATTTAACAC	TAACATGATG	TTTCATTAT	CTGTAGTAAA	TACTAACACA	AACTAGGCTG
	TCAAAATTTC	GCCTGGATAT	TTTACTAAGT	ATAAAATTATG	AAATCTGTT	TAGTGAATAC	ATGAAAGTAA
	TGTGTAACAT	ATAA TCTATT	TGGTTAAAAT	AAAAAGGAAG	TGCTTCAAAA	CCTTCTTTT	CTCTAAAGGA
25	GCTTAACATT	CTTCCCTGAA	CTTCAATTAA	AGCTCTCAA	TTTGTAGCC	AAGTCAATT	TTTACAGATA
	AAGCACAGGT	AAAGCTCAA	GCCTGTCTG	ATGACTACTA	ATTCCAGATT	AGTAAGATAT	GAATTACTCT
	ACCTATGTG	ATGTGTAGAA	GTCCTTAAT	TTCAAAGATG	ACAGTAATGG	CCATGTGTAT	GTGTGTGACC
	CACAACATC	ATGC TCATTA	AAAGTACATTG	GCCAGAGACC	ACATGAAATA	ACAAACAATT	CATTCTCATC
	ATCTTATTTC	GACAGTGA	ATGAAGAAGA	CAGTTCCTCC	ATTGATCATC	TGTCTCTGAA	TCAGGTAAGC
30	AAATGACTGT	AAATCTCATG	GGACTGCTAT	TCTTACACAG	TGGTTCTTC	ATCCAAAGAG	AACAGCAATG
	ACTTGAATCT	TAAT TACTTT	TGTTTACCC	TCACTAGAGA	TCCAGAGACC	TGTCTTCTAT	TATAAGTGA
	ACCAGCTGCC	TCTCTAAACT	AATAGTTGAT	GTGCATTGGC	TTCTCCCAGA	ACAGAGCAGA	ACTATCCCAA
	ATCCCCTGAGA	ACTC GAGTCT	CCTGGGGCAG	GCTTCATCAG	GATGTTAGTT	ATGCCATCCT	GAGAAAGCCC
	CGCAGGCCGC	TTCA CCAGGT	GTCTGTCCTC	TAACGTGATG	TGTTGTGTT	GTCTCTCTG	ACACCAGCAT
35	CAGAGGTAG	AGAA AGTCTC	CAAACATGAA	GCTGAGAGAG	AGGAAGCAAG	CCAGCTGAAA	GTGAGAAGTC
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40	CTGGAAGGAG	GAAGGAAGGT	GAGACAAAAG	GGAGAGAGGG	AGGAAGCCT	AATGAAACAC	CAGTTACCTA
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	GACCATGAAC	AGCCTCTCAG	CTTCTGTTT	CCTTCCTCAG	AGAAATCCTT	CTATCATGTA	AGCTATGGCC
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	GAGCTAGCTG	GGCCCTCTCTG	ACTGTTATAA	AGATTAATG	AGTCAACATC	CCCTAACCTTC	TGGACTAGAA
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	ACAATGAACA	TCTGTATAAA	TAATATTCA	TTCTCTCAC	CCTTTATTTC	CTTAGAATAT	ATTCCTAGAA
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	GCAATGTGAA	ATACAACTTT	ATGAGGATCA	TCAAATACGA	ATTACATCTG	AATGACGCC	TCAATCAAAG
	TATAATTGCA	GCCATGATC	AGTACCTCAC	GGCTGCTGCA	TTACATAATC	TGGATGAAGC	AGGTACATTA
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	TCAGTGGCAA	ACAGGGTGC	AAGTAATCT	GATTAAAGA	CTACTTTCCC	ATTACAAGTC	CCTCCAGCCT
	TGGGACCTGG	AGGCATATCCA	GATGTGTTGT	TGCAAGGGCT	TCCTGCAGAG	GCAAATGGGG	AGAAAAGATT
30	CCAAGCCCAC	AATA.CAAGGA	ATCCCTTGC	AAAGTGTGGC	TTGGAGGGAG	AGGGAGAGCT	CAGATTTAG
	CTGACTCTGC	TGGGCTAGAG	GTTAGGCTC	AAAGATCCAAC	AGGGAGCACC	AGGGGCCA	CCTGCCAGGC
	CTAGAATCTG	CCTCTGGAC	TGTTCTGCGC	ATATCACTGT	GAAACTGCC	AGGTGTTCA	GGCAGCTTTG
	AGAGGCAGGC	TGT'TGCACT	TTCTTATGAA	CAGTCAGTC	TTGTACACAG	GGAAGGAAAA	ATAAACCTGT
	TTAGAAGACA	TAA'TGAGAC	ATGTCCTGT	TTTATTACAA	GTGGCAATGA	GGATGACTTG	TTCTTGAAG
35	CTGATGCC	TAACAGATG	AAGGTAAGAC	TATGGGTTTA	ACTCCCCAAC	CAAGGAAGGG	CTCTAACACA
	GGGAAAGCTC	AAAGAAGGGAA	GTTCTGGGCC	ACTTGTATGC	CATGGTATTT	TGTTTAGAA	AGACTTTAAC
	CTCTTCCAGT	GAGA CACAGG	CTGCACCACT	TGCTGACCTG	GCCACTTGGT	CATCATATCA	CCACAGTCAC
	TCACTAACGT	TGGTGGTGGT	GGCCACACTT	GGTGGTGACA	GGGGAGGAGT	AGTATAATG	TTCCCATITC
	ATAGTAGGAA	GACAAACCAAG	TCTTCACAT	AAATTGATT	ATCCTTTAA	GAGATGGATT	CAGCCTATGC
	CAATCACTG	AGTIAAAACTC	TGAAACCAAG	AGATGATCTT	GAGAACTAAC	ATATGTCTAC	CCCTTTGAG
40	TAGAATAGTT	TTTCTTAC	TGGGGTGAAG	CTTATAACAA	CAAGACATAG	ATGATATAAA	CAAAAAGATG
	AATTGAGACT	TGAAGAAAAA	CCATTCACTT	GCTGTTTGAC	CTTGACAAGT	CATTTCACCC	GCTTTGGACC
	TCATCTGAAA	AATAAAGGGC	TGAGCTGGAT	GATCTCTGAG	ATTCCAGCAT	CCTGCAACCT	CCAGTTCTGA
	AATATTTCA	GTTGAGCTA	AGGGCATTG	GGCAGCAAAT	GGTCATTTTT	CAGACTCATC	CTTACAAAGA
	GCCATGTTAT	ATTCTGCTG	TCCCCTCTGT	TTTATATGAT	GCTCAGTAGC	CTTCCTAGGT	GCCCAGCCAT
45	CAGCCTAGCT	AGG'CAGTTG	TGCAGGTGG	AGGCAGCCAC	TTTCTCTGG	CTTATTTTA	TTCCAGTTG
	TGATAGCCTC	CCCTAGCCTC	ATAATCCAGT	CCTCAATCTT	GTAAAAAAACA	TATTCTTTA	GAAGTTTAA
	GAETGGCATA	ACTCTTGGC	TGCAGCTGTG	GGAGGGAGCCC	ATTGGCTGTG	CTGCCCTGGCC	TTTGCCCCCC
	ATTGCCTCTT	CCAC CAGCTT	GGCTCTGCTC	CAGGCAGGAA	ATTCTCTCTC	GCTCAACTTT	CTTTTGTGCA
	CTTACAGGTC	TCTTAACTG	TCTTCAAGC	CTTGAACCA	TTATCAGCCT	TAAGGCAACC	TCAGTGAAGC
50	CTTAATACGG	AGCITCTCTG	AATAAGAGGA	AAGTGGTAAC	ATTTCACAAA	AAGTACTCTC	ACAGGATTG
	CAGAATGCCT	ATGAGACAGT	GTTATGAAA	AGGAAAAAAA	AGAACAGTGT	AGAAAAATTG	AATAACTGCT
	GAGTGAGCAT	AGG'GAATGG	AAAATGTTAT	GGTCATCTGC	ATGAAAAAAGC	AAATCATAGT	GTGACAGCAT
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55	GCCTCTACCT	GCTC TGTGCC	CTTGAGTACA	CCCTTAACCT	CCTTGAGCTT	CAGAGAGGGA	TAATTTTT
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	TTCCCTAGTC	TCCTGAATAG	CTAGGATTAC	AGGTGCACCC	CACCACACCC	AGCTAATT	TGTATTTTTA
	GTAGAGAAGG	GGT'TCGCCA	TGTTGGCCAG	GCTGGTTTG	AAGTCCTGAC	CTAAATGATT	CATCCACCTC
60	GGCTTCCAA	AGTC CTGGGA	TTACAGGCAT	GAGCCACCAC	GCCTGGCCCA	GAGAGGGATG	ATCTTTAGAA
	GCTCGGGATT	CTTCAAGCC	CTTCTCTCT	CTCTGAGCTT	TCTACTCTCT	GATGTCAAAG	CATGGTTCTC
	GGCAGGACCA	CCTCACCAAGG	CTCCCTCCCT	CGCTCTCTCC	GCAGTGCTCC	TTCCAGGACC	TGGACCTCTG

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5	TGTGTCTCT	TGGAAGTCAT	CAAGCCCCAG	CCAACATCAAT	TCCCCCAGAG	CCAAAGCCCT	TTAAAGGTAG
	AAGGCCAACG	GGGGAGACAA	AACAAAGAAG	GCTGGAAACC	AAAGCAATCA	TCTCTTAGT	GGAAACTATT
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	ATTGTCACCA	GAGGTTCGTA	ACCTCCCTGT	GGGCTAGTGT	TATGACCATC	ACCATTTCAC	CTAAGTAGCT
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10	TGTTCTTAGC	CACCCCACTC	CCAGCTTCAT	CCCTACTGGT	GTTGTCATCA	GACTTTGACC	GTATATGCTC
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	CAGTGACACA	ATGCTTCC	TCCTTCTTC	CTTCAGCATT	TAACATGTAG	ACCCCTTTTC	ATTCTCCGTT
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30	GCTATTGTCT	GTGAGAAGTC	AAGTTATCCT	GTGTCTTAGG	CCAAGGAACC	TCACTGTGGG	TTCCCACAGA
	GGCTACCAAT	TACATGTATC	CTACTCTCGG	GGCTAGGGGT	TGGGGTGA	CTGCATGCTG	TGTCCCTAAC
	CACAAGACCC	CCTCTTCT	TCAGTGGTGT	TCTCCATGTC	CTTTGTACAA	GGAGAAGAAA	GTAATGACAA
	AATACCTGTG	GCCTTGGGCC	TCAAGGAAA	GAATCTGTAC	CTGTCCTCG	TGTTGAAAGA	TGATAAGCCC
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	TCATTTGCC	GATGTTATA	TGTCTACCA	TAGTTACAAC	CCCAACAGAT	TATATATTGT	TAGGGCTGCT
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40	CATAAGGAAA	AATAACAATAA	AAAGCCCCCTG	GAAACTAGGT	ACTTCAAGAA	GCTCTAGCTT	AATTTCACC
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50	GCCAGGACAG	TCA/GCTCTCT	CCTTTCAGGG	CCAATCCCCA	GCCCTTTGT	TGAGCCAGGC	CTCTCTCACC
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	TGGCTTATTA	CAGTGGCAAT	GAGGATGACT	TGTTCTTGA	AGCTGATGCC	CCTAACAGA	TGAAGTGCTC
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10	AAGGGCTTCA	GGCA.GGCCGC	GTCAGTTGTT	GTGCCATGG	ACAAGCTGAG	GAAGATGCTG	GTTCCCTGCC
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	ATCCCAGCCC	TTTT GTT GAG	CCAGGCCTCT	CTCACCTCTC	CTACTCACT	AAAGCCGCC	TGACAGAAAC
	CAGGCCACAT	TTTC GTT CTA	AGAAACCCCTC	CTCTGTCATT	CGCTCCACAA	TTCTGATGAG	CAACCGCTC
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	CGGAGCGTGG	AGCCCGCAA	GCTCGAGCT	AGCTTCGCT	TGCCGTCCAC	CACTGCCCAC	ACTGTCGTT
	GCTGCCATCG	CAGA CCTGCT	GCTGACTTCC	ATCCCTCTGG	ATCCGGCAAG	GGCCTGCGAT	TTTGACAATG
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25	CTAAAATTAC CGTC ATTCTA AGAACATCTAA AAACATCAATT GTATGTGACT GCCCAAGATG AAGACCAACC	AGTGCTGCTG AAGGAGATGC CTGAGATACC CAAACCCATC ACAGGTAGTG AGACCAACCT CCTCTTCTTC
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55	5'-AAGCTTCTAC CCTAGTCTGG TGCTACACTT ACATTGCTTA CATCCAAGTG TGGTATTTC TGTGGCTCCT	GTTATAACTA TTATAGCACC AGGTCTATGA CCAGGAGAAT TAGACTGCA TTAAATCAGA ATAAGAGATT
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 ACCTCAGTT TATCATTTC AAAATGGAGG GAATAATACC TAAGCCTTCC TGCCGCAACA GTTTTTATG
 20 CTAATCAGGG AGGT'CATTTT GGTAAAATAC TTCTCGAAGC CGAGCCTCAA GATGAAGGCA AAGCACGAAA
 TGTATTTTT TAATFATTAT TTATATATGT ATTATAAAT ATATTTAAGA TAATTATAAT ATACTATATT
 TATGGGAACC CCTICATCCT CTGAGTGTGA CCAGGCATCC TCCACAATAG CAGACAGTGT TTTCTGGGAT
 AAGTAAGTTT GATTCATTA ATACAGGGCA TTTGGTCCA AGTTGTGCT ATCCCATAGC CAGGAAACTC
 TGCAATTCTAG TACTGGGAG ACCTGTAATC ATATAATAAA TGTACATTA TTACCTTGAG CCAGTAATTG
 25 GTCCGATCTT TGACTCTTT GCCATTAAAC TTACCTGGGC ATTCTTGTCTT CATTCAATT CACCTGCAAT
 CAAGTCTTAC AAGCTAAAAT TAGATGAAC CAACTTGAC AACCATGAGA CCACTGTTAT CAAAACTTTC
 TTTTCTGGAA TGTAATCAAT GTTCTCTA GGTTCTAAAA ATTGTGATCA GACCATAATG TTACATTATT
 ATCAACAAATA GTGA'TGATA GAGTGTACT AGTCATAACT AAATAAGCT TGCAACAAAA TTCTCTG-3' (FRAG.
 NO:) (SEQ. ID NO:2515)

30 Human Interleukin-1 Receptor (IL-1 R) Nucleic Acids and Anti-sense Oligonucleotide Fragments

5'-GCCACGTGCT GCTGGGTCTC AGTCCTCCAC TTCCCGTGTCT CTCTGGAAGT TGTCAAGGAGC AATGTTGCGC
 TTGTACGTGT TGGTAATGGG AGTTTCTGCC TTCACCCCTTC AGCCTGCGGC ACACACAGGG GCTGCCAGAA
 GCTGCCGGTT TCGTGGGAGG CATTACAAGC GGGAGTTCAAG GCTGGAAAGGG GAGCCTGTAG CCCTGAGGTG
 35 CCCCCAGGTG CCCIACTGGT TGTGGGCCCT TGTCAAGCCCC CGCATCAACCC TGACATGGCA TAAAATGAC
 TCTGCTAGGA CGGICCCAGG AGAAGAAAGAG ACACGGATGT GGGCCCAAGGA CGGTGCTCTG TGGCTTCTGC
 CAGCCTGCA GGAGGACTCT GGCACCTACG TCTGCACTAC TAGAAATGCT TCTTACTGTG ACAAATGTC
 CATTGAGCTC AGAGTTTTG AGAATACAGA TGCTTCTCTG CCGTTCATCT CATACCCGCA AATTAAACC
 TTGTCAACCT CTGGGGTATT AGTATGCCCT GACCTGAGTG AATTCAACCCG TGACAAAAGT GACGTGAAGA
 TTCAATGGTA CAAAGATTCT CTTCTTTGG ATAAAGACAA TGAGAAATT TGAGAAATT CTAAGTGTGA GGGGGACCAC
 40 TCACTTACTC GTACACGATG TGGCCCTGGAG AGATGCTGGC TATTACCGCT GTGCTGTGAC ATTTGCCAT
 GAAGGCCAGC AATAAACAT CACTAGGAGT ATTGAGCTAC GCATCAAGAA AAAAAAAAGAA GAGACCATTC
 CTGTGATCAT TTCCCCCTC AAGACCATAT CAGCTTCTCT GGGGTCAAGA CTGACAATCC CGTGTAAAGGT
 GTTCTGGGA ACCCGCACAC CCTTAACCCAC CATGCTGTGG TGGACGGCCA ATGACACCCCA CATAGAGAGC
 GCCTACCCGG GAGGCCGCGT GACCGAGGGG CCACGCCAGG AATATTCAAG AAATAATGAG AACTACATTG
 45 AAGTGCCTT GATTTTGTAT CCTGTCACAA GAGAGGATT GCACATGGAT TTTAAATGTG TTGTCCATAA
 TACCCCTGAGT TTTCAGACAC TACGCACCCAC AGTCAAGGAA GCCTCTTCA CGTCTCTTG GGGCATTGTG
 CTGGCCCCAC TTTCACTGGC CTTCTTGGTT TTGGGGGGAA TATGGATGCA CAGACGGTGCA AAACACAGAA
 CTGGAAAAGC AGA'TGGTCTG ACTGTGCTAT GGCCTCATCA TCAAGACTTT CAATCCTATC CCAAGTGAAA
 TAAATGGAAT GAAATTAATC AAACACAAAA AAAAAAAA AAAAAAAA GCGGGAGCCG ACTCGGAGCG
 50 CGCGGGCGGG CCGCGAGGAG CCGAGCCGC CGGGCGCGGC GTGGGGGGCG CCGCTGCCCG GCGCGCCAG
 GGAGCGGCAG GAA'TGTGACA ATCGCGCGCC CGCACCGTAG CACTCCTCGC TCGGCTCTA GGGCTCTCGC
 CCTCTGAGCT GAGCGGGTT CCGCCCCGGC TGGGATCCCA TCACCCCTCA CGGCCGTCCG TCCAGGTAGA
 CGCACCTCT GAAACATGGT ACTCCCTCT GAGAAGCTGG ACCCCCTGGT AAAAGACAAG GCCTTCTCCA
 AGAAGAATAT GAAAGTGTGTA CTCAGACTTA TTTGTTTCAT AGCTCTACTG ATTCTCTCTC TGGAGGCTGA
 55 TAAATGCAAG GAAAGTGAAG AAAAAATAAT TTTAGTGTCA TCTGCAAATG AAATTGATGT TCGTCCCTGT

	CCTCTTAACC	CAAATGAACA	CAAAGGCACT	ATAACTTGGT	ATAAAAGATGA	CAGCAAGACA	CCTGTATCTA
	CAGAACAAAGC	CTCC'AGGATT	CATCAACACA	AAGAGAAAATC	TTGGTTTGTG	CCTGCTAAGG	TGGAGGATTC
5	AGGACATTAC	TATIGCGTGG	TAAGAAAATTC	ATCTTACTGC	CTCAGAATT	AAATAAGTGC	AAAATTGTTG
	GAGAATGAGC	CTAACTTATG	TTATAATGCA	CAAGCCATAT	TTAACAGAA	ACTACCCGTT	GCAGGAGACG
	GAGGACTTGT	GTGC CTTAT	ATGGAGTTT	TTAAAAAATGA	AAATAATGAG	TTACCTAAAT	TACAGTGGTA
	TAAGGATTGC	AAAACCTCAC	TTCTTGACAA	TATACACTTT	AGTGGAGTC	AAGATAGGCT	CATCGTGTG
	AATGTGGCTG	AAAAAGCATAG	AGGGAACTAT	ACTTGTATG	CATCCTACAC	ATACTTGGGC	AAGCAATATC
	CTATTACCCG	GGTAATAGAA	TTTATTACTC	TAGAGGAAAA	CAAACCCCA	AGGCCTGTGA	TTGTGAGCCC
10	AGCTAATGAG	ACAA.TGGAAG	TAGACTTGGG	ATCCAGATA	CAATTGATCT	GTAAATGTCAC	CGGCCAGTTG
	AGTGCACATTG	CTTACTGGAA	GTGGAATGGG	TCAGTAATG	ATGAAGATGA	CCCAGTGCTA	GGGAAAGACT
	ATTACAGTGT	GGAA AATCCT	GCAAAACAAA	GAAGGAGTAC	CCTCATCACA	GTGCTTAATA	TATCGGAAT
	TGAAAGTAGA	TTTIAAAAC	ATCCATTTC	CTGTTTGCG	AAGAATACAC	ATGGTATAGA	TGCAGCATAT
	ATCCAGTAA	TATATCCAGT	CACTAATTTC	CAGAACACAA	TGATTGGTAT	ATGTGTACG	TTGACAGTCA
15	TAATTGTGT	TTCTGTTTTC	ATCTATAAAA	TCTTCAGAT	TGACATTGTG	CTTTGGTACA	GGGATTCTG
	CTATGATTT	CTCCCATAA	AAGCTTCAGA	TGGAAAGACC	TATGACGCA	ATATACTGTA	TCCAAGACT
	GTTGGGAAG	GGTCTACCTC	TGACTGTGAT	ATTTTGTGT	TTAAAGTCTT	GCCTGAGGTC	TTGGAAAAC
	AGTGTGGATA	TAAC CTGTC	ATTTATGGAA	GGGTGACTA	CGTTGGGGAA	GACATTGTTG	AGGTCTTAA
	TGAAAACGTA	AAG/AAGCA	GAAGACTGAT	TATCATTITA	GTCAAGAGAA	CATCAGGCTT	CAGCTGGCTG
20	GGTGGTTCAT	CTGAAGAGCA	AATAGCCATG	TATAATGCTC	TTGTTTCAGGA	TGGAATTAAA	GTTGCTCTG
	TTGAGCTGGA	GAAP ATCAA	GACTATGAGA	AAATGCCAGA	ATCGATTAAT	TTCATTAAGC	AGAAACATGG
	GGCTATCCGC	TGGTCAGGGG	ACTTTACACA	GGGACCACAG	TCTGCAAAGA	CAAGTTCTG	GAAGAATGTC
	AGGTACCCACA	TGCC AGTCCA	GCGACGGTC	CCTCATCTA	AACACCAAGT	ACTGTCACCA	GCCACTAAGG
	AGAAAATGCA	AAG/GAGGCT	CACGTGCCTC	TCGGGTAGCA	TGGAGAAAGT	GCCAAGAGTT	CTTTAGGTGC
25	CTCCGTCTT	ATGG CGTTGC	AGGCCAGGTT	ATGCCCTCATG	CTGACTTGCA	GAGTCATGG	AATGTAACTA
	TATCATCCTT	TATCCCTGAG	GTCACCAGGA	ATCAGG-3'	(FRAG NO:) (SEQ. ID NO:2520)		
	5'-GCCACGTGCT	GCTGGGTCTC	AGTCCTCCAC	TTCCCGTGTG	CTCTGGAAGT	TGTCAAGGAC	AATGTTGCGC
	TTGTACGTGT	TGGTAATGGG	AGTTTCTGCC	TTCACCCCTTC	AGCCTGCGC	ACACACAGGG	GCTGCCAGAA
	GCTGCCGTT	TCGT GGGAGG	CATTACAAGC	GGGAGTTCA	GCTGGAAGGG	GAGCCTGTAG	CCCTGAGGTG
	CCCCCAGGTG	CCCI ACTGGT	TGTGGGCTC	TGTCAAGCCC	CGCATCAACC	TGACATGGCA	AAAAATGAC
30	TCTGCTAGGA	CGG TCCCAGG	AGAAGAAAG	ACACGGATGT	GGGCCAGGA	CGGTGCTCTG	TGGCTTCTG
	CAGCCTTGCA	GGAG/GACTCT	GGCACCTACG	TCTGCACTAC	TAGAAATGCT	TCTTACTGTG	ACAAAATGTC
	CATTGAGCTC	AGAC TTTTG	AGAATACAGA	TGCTTCTCTG	CCGTTCATCT	CATACCCGCA	AATTAAACC
	TTGTCAACCT	CTGGGGTATT	AGTATGCCCT	GACCTGAGTG	AATTACCCG	TGACAAAACT	GACGTGAAGA
	TTCAATGGTA	CAAC GATTCT	CTTCTTTGG	ATAAAGACAA	TGAGAAATT	CTAAGTGTGA	GGGGGACAC
35	TCACTTACTC	GTACACGATG	TGGCCCTGGA	AGATGCTGGC	TATTACCGCT	GTGCTCTGAC	ATTGCCCCAT
	GAAGGCCAGC	AATA CAACAT	CACTAGGAGT	ATTGAGCTAC	GCATCAAGAA	AAAAAAAGAA	GAGACCATTC
	CTGTGATCAT	TTCCCCTCTC	AAGACCATAT	CAGCTCTCT	GGGGTCAAGA	CTGACAATCC	CGTGTAAAGGT
	GTTCCTGGGA	ACCGGCACAC	CCTTAACCAC	CATGCTGTGG	TGGACGGCCA	ATGACACCCA	CATAGAGAGC
	GCCTACCCGG	GAGC CCGCGT	GACCGAGGGG	CCACGCCAGG	AATATTCA	AAATAATGAG	AACTACATG
40	AAGTGCCATT	GATTTTGAT	CCTGTACAA	GAGAGGATT	GCACATGGAT	TTAAATGTTG	TTGTCCTAA
	TACCCCTGAGT	TTTCAGACAC	TACGCACCAC	AGTCAGGAA	GCCTCTCCA	CGTTCTCTG	GGGCATTGTG
	CTGGCCCCAC	TTTC ACTGGC	CTTCTTGTT	TTGGGGGAA	TATGGATGCA	CAGACGGTGC	AAACACAGAA
	CTGGAAAAGC	AGA/GGTCTG	ACTGTGCTAT	GGCCTCATCA	TCAAGACTTT	CAATCCTATC	CCAAGTGAAA
	TAAATGGAAT	GAAT/AATT	AAACACAAAA	AAAAAAAAAA	AAAAAAAAA-3'	(FRAG. NO:) (SEQ. ID NO:2518)	
45	5'-GCCGGAGCCG	AC'CGGAGCG	CGCGGGCGCG	CCGGGAGGAG	CCGAGCGCGC	CGGGCGCGC	GTGGGGCGC
	CGGCTGCC	CGCG GCCCC	GGAGCGGCAG	GAATGTGACA	ATCGCGCGCC	CGCACCGTAG	CACTCCTCGC
	TCGGCTCTA	GGGC TCTCG	CCTCTGAGCT	GAGCCGGGTT	CCGCCCCGGC	TGGGATCCCA	TCACCCCTCCA
	CGGCGTCCG	TCCA GGTAGA	CGCACCCCT	GAAGATGGTG	ACTCCCTCCT	GAGAAGCTGG	ACCCCTTGGT
	AAAAGACAAG	GCC TCTCCA	AGAAGAATAT	GAAAGTGT	CTCAGACTTA	TTTGTTCAT	AGCTCTACTG
50	ATTTCTTCTC	TGGA/GGCTGA	TAATGCAAG	GAACGTGAAG	AAAAAATAAT	TTTATGTGTC	TCTGCAAATG
	AAATTGATGT	TCG TCCCTGT	CCTCTTAACC	CAAATGAACA	CAAAGGCACT	ATAACTTGGT	ATAAAGATGA
	CAGCAAGACA	CCTGTATCTA	CAGAACAAAGC	CTCCAGGATT	CATCAACACA	AAGAGAAACT	TTGGTTTGTG
	CCTGCTAAGG	TGGAGGATT	AGGACATTAC	TATTGCGTGG	TAAGAAATTC	ATCTTACTGC	CTCAGAATTA
	AAATAAGTGC	AAA/TTTGTG	GAGAATGAGC	CTAACTTATG	TTATAATGCA	CAAGCCATAT	TTAAGCAGAA
55	ACTACCCGTT	GCAC GAGACG	GAGGACTTGT	GTGCCCTTAT	ATGGAGTTT	TTAAAAATGA	AAATAATGAG
	TTACCTAAAT	TACAGTGGTA	TAAGGATTGC	AAACCTCTAC	TTCTTGACAA	TATACACTTT	AGTGGAGTC
	AAGATAGGCT	CATC GTGATG	AATGTGGCTG	AAAAGCATAG	AGGGAACTAT	ACTTGTATG	CATCCTACAC
	ATACTTGGC	AAGC AAATATC	CTATTACCCG	GGTAATAGAA	TTTATTACTC	TAGAGGAAAA	CAAACCCACA
	AGGCCTGTGA	TTGIGAGCCC	AGCTAATGAG	ACAATGGAAG	TAGACTTGGG	ATCCAGATA	CAATTGATCT
60	GTAATGTAC	CGGC CAGTTG	AGTGACATTG	CTTACTGGAA	GTGGAATGGG	TCAGTAATTG	ATGAAGATGA
	CCCAGTGCTA	GGGC AAGACT	ATTACAGTGT	GGAAAATCCT	GCAAAACAAA	GAAGGAGTAC	CCTCATCACA
	GTGCTTAATA	TATCGGAAAT	TGAAAGTAGA	TTTATAAAC	ATCCATTAC	CTGTTTGCC	AAGAATACAC

ATGGTATAGA TGCAGCATAT ATCCAGTTAA TATATCCAGT CACTAATTTC CAGAAGCACA TGATTGGTAT
 ATGTGTCACG TTGACAGTC TAATTGTGT TTCTGTTTC ATCTATAAAA TCTTCAGAT TGACATTGTG
 CTGGTACA GGGATTCTCG CTATGATTT CTCCAATAA AAGCTTCAGA TGAAAGACC TATGACGCAT
 ATATACTGTA TCCAAAGACT GTTGGGAAG GGTCTACCTC TGACTGTGAT ATTTTGTTGTT AAAGTCTT
 5 GCCTGAGGTC TTGCAAAAAAC AGTGTGGATA TAAGCTGTT ATTTATGGAA GGGATGACTA CGTTGGGAA
 GACATTGTTG AGGTCAATTAA TGAAAACGTA AAGAAAAGCA GAAGACTGAT TATCATTAA GTCAGAGAAA
 CATCAGGCTT CAGCTGGCTG GGTGGTTCAT CTGAAGAGCA AATAGCCATG TATAATGCTC TTGTTCAGGA
 TGGAAATTAAA GTTCCTCTGC TTGAGCTGGA GAAAATCCAA GACTATGAGA AAATGCCAGA ATCGATTAAA
 10 TTCATTAAGC AGAPACATGG GGCTATCCGC TGGTCAGGG ACTTTACACA GGGACACAG TCTGCAAAGA
 CAAGGTTCTG GAAGAATGTC AGGTACCCAA TGCCAGTCCA GCGACGGTCA CCTTCATCTA AACACCAAGTT
 ACTGTACCCA GCCCTAAAG AGAAAATGCA AAGAGAGGCT CACGTGCCCTC TCAGGTAGCA TGGAGAAGTT
 GCCAAGAGTT CTTTAGGTGC CTCCGTCTT ATGGCGTTGC AGGCCAGGTT ATGCCCTCATG CTGACTTGCA
 GAGTTCATGG AATGAACTA TATCATCCTT TATCCCTGAG GTCACCAGGA ATCAGG-3' (FRAG. NO:_) (SEQ. ID
 NO:2519)

Human Interleukin-8* Fragments Antisense Oligonucleotide Fragments

15 5'-GBTGTTGTT BCCBBGCBT CBBGBTBGC TTTGCTBTCT BBGGBCTBCB TTTBGBCTB GGBBBBCGCT
 GTBGGTCBGBB BGBIGTGCTT BCCTTCBCB BGBGCTGCBG BBBTCBGGBBGG CTGCCBGBGBG CBCGCGCCBGC
 TTGGBGTCBT GTTTCBCBC BGTGBGGTGC TCCGGTGGCT TTTGCTTGT GTGCTCTGCT GTCTCTG TTC
 CTTCCGGTGG TTTCTCCTG GCTCTTGTCC TTCTCTTGG CCCTGGCCC-3' (FRAG. NO:1834) (SEQ. ID NO:1847)
 20 5'-G CTC CGG-3' (FRAG. NO:1835) (SEQ. ID NO:1848)
 5'-CBBGBTBGC-3' (FRAG. NO:1836) (SEQ. ID NO:1849)
 5'-CBCBC BGTGBGGTGC-3' (FRAG. NO:1837) (SEQ. ID NO:1850)
 5'-BCCBBGCBT CBBCBBTBGC-3' (FRAG. NO:1838) (SEQ. ID NO:1851)
 25 5'-GCCBBGBGBG CCBGGCCBGC-3' (FRAG. NO:1839) (SEQ. ID NO:1852)
 5'-GTG CTC CGG TGG CTT TTT-3' (FRAG. NO:1289) (SEQ. ID NO:1298)
 5'-GCT TGT GTG CTC TGC TGT CTC TG-3' (FRAG. NO:1290) (SEQ. ID NO:1299)
 5'-TTC CTT CCG GTG GTT TCT TCC TGG CTC TTG TCC T-3' (FRAG. NO:1291) (SEQ. ID NO:1300)
 30 5'-TTC TCT TGG CCC TTG GCC C-3' (FRAG. NO:1292) (SEQ. ID NO:1301)
 5'-GBTGTTGTT BCCBBGCBT CBBGBTBGC TTTGCTBTCT BBGGBCTBCB TTTBGBCTB GGBBBBCGCT
 GTBGGTCBGBB BGBIGTGCTT BCCTTCBCB BGBGCTGCBG BBBTCBGGBBGG CTGCCBGBGBG CBCGCGCCBGC
 TTGGBGTCBT GTTTCBCBC BGTGBGGTGC TCCGGTGGCT TTTGCTTGT-3' (FRAG. NO:1840) (SEQ. ID NO:1853)

Human IL-8 Receptor Alpha Antisense Oligonucleotide Fragments

35 5'-ACAGGGCTG TAATCTTCATC TGCAGGTGGC ATGCCAGTGA AATTTAGATC ATCAAAATCC CACATCTGTG
 GATCTGTAAT ATTIGACATG TCCTCTTCAG TTTCAGCAAT GGTTTGATCT AACTGAAGCA CGGGCCAGGB
 CBGGGCTGT BBTCTTCBTC TGCBGGTGGC BTGCCBGTGB BTTTTBGBTB BTCBBBBTCC CBCBTCTGTG
 GBTCTGTBBT BTTTGBCBTG TCCTCTTCBG TTTCBGCBB TGGTTTGBTCT BBTCTGBGC BCCGGCCBGG
 TGGCTCGGTG CTTCTGCCCC TTGTTGTTGCG GCGCTCGGTT GGTGTGGCCC CTGTTGTCCT TCCTTTCCCC
 CTCTTCTCT TTGTTGGGG TTCTTGTGG CGGGCTGCTT GTCTCGTTCC-3' (FRAG. NO:1841) (SEQ. ID NO:1854)
 40 5'-CBGGGGC-3' (FRAG. NO:1842) (SEQ. ID NO:1855)
 5'-GCBGGTGGC-3' (FRAG. NO:1843) (SEQ. ID NO:1856)
 5'-GCGCGCTC-3' (FRAG. NO:1844) (SEQ. ID NO:1857)
 5'-TGGCTCGGTGCTTCTGCCCC (FRAG. NO:1293) (SEQ. ID NO:1302)
 5'-TGGCTCGGTGCTC (FRAG. NO:1294) (SEQ. ID NO:1303)
 45 5'-GGTTGGTGTGGCCCTG (FRAG. NO:1295) (SEQ. ID NO:1304)
 5'-GGGTGCTTCGTTTC (FRAG. NO:1296) (SEQ. ID NO:1305)
 5'-CCCTCTTCTCTTCTTCTC (FRAG. NO:1297) (SEQ. ID NO:1306)
 5'-GGGGGTTCTTGTGGC (FRAG. NO:1298) (SEQ. ID NO:1307)
 5'-GGGCTGCTTGTCTCGTCC (FRAG. NO:1299) (SEQ. ID NO:1308)
 50 5'-ACAGGGGCTG TAATCTTCATC TGCAGGTGGC ATGCCAGTGA AATTTAGATC ATCAAAATCC CACATCTGTG
 GATCTGTAAT ATTIGACATG TCCTCTTCAG TTTCAGCAAT GGTTTGATCT AACTGAAGCA CGGGCCAGG-3'
 (FRAG. NO:1845) (SEQ. ID NO:1858)
 5'-B CBGGGGCTGT BBTCTTCBTC TGCBGGTGGC BTGCCBGTGB BTTTTBGBTB BTCBBBBTCC CBCBTCTGTG
 GBTCTGTBBT BTTTGBCBTG TCCTCTTCBG TTTCBGCBB TGGTTTGBTCT BBTCTGBGC BCCGGCCBGG-3' (FRAG.
 NO:1846) (SEQ. ID NO:1859)

Interleukin-11 (IL-11) Nucleic Acid and Antisense Oligonucleotide Fragments

55 5'-GCTCAGGGCA CAIGCCTCCC CTCCCCAGGC CGCGGCCAG CTGACCCCTCG GGGCTCCCCC GGCAGCGGAC
 AGGGAAGGGT TAAAGGCCCTG CGGCTCCCTG CCCCTGCCCT TGGGAAACCC CTGGCCCTGT GGGGACATGA
 ACTGTGTTG CCGCCTGGTC CTGGTCGTGC TGAGCCTGTG GCCAGATACA GCTGTCGCCCT GGGGCCACC

	ACCTGGCCCC	CCTCGAGTTT	CCCCAGACCC	TGGGGCCGAG	CTGGACAGCA	CCGTGCTCCT	GACCCGCTCT
	CTCCCTGGCGG	ACACGCGGCA	GCTGGCTGCA	CAGCTGAGGG	ACAAATTCCC	AGCTGACGGG	GACCACAACC
	TGGATTCCCT	GCCCCACCCTG	GCCATGAGTG	CGGGGGCACT	GGGAGCTCTA	CAGCTCCCAG	GTGTGCTGAC
5	AAGGCTCGA	GCGGACCTAC	TGTCTACCT	GC GG CAC GTG	CAGTGGCTGC	GCCGGGCAGG	TGGCTCTTCC
	CTGAAGACCC	TGGAGGCCGA	GCTGGGCACC	CTGCAGGCC	GACTGGACCG	GCTGCTGC	CGGCTGCAGC
	TCCTGATGTC	CCGCTGGCC	CTGCCCAGC	CACCCCGGA	CCCGCCGGCG	CCCCCGCTGG	CGCCCCCCTC
	CTCAGCCTGG	GGGC GCATCA	GGGCCGCCA	CGCCATCCTG	GGGGGGCTGC	ACCTGACACT	TGACTGGGCC
10	GTGAGGGGAC	TGCT'GCTGCT	GAAGACTCGG	CTGTGACCCG	GGGCCCAAAG	CCACCAACGT	CCTTCCAAAG
	CCAGATCTTA	TTTATTATT	TATTCAGTA	CTGGGGCGA	AACAGCCAGG	TGATCCCCC	GCCATTATCT
	CCCCCTAGTT	AGACACAGTC	CTTCCGTGAG	GCCTGGGGGA	CATCTGTGCC	TTATTTATAC	TTATTTATTT
	CAGGAGCAGG	GGTGGGAGGC	AGGTGGACTC	CTGGGTCCCC	GAGGAGGAGG	GGACTGGGGT	CCCGGATTCT
	TGGGCTCCA	AGAA.GTCTGT	CCACAGACTT	CTGCCCTGGC	TCTTCCCCAT	CTAGGCCTGG	GCAGGAACAT
15	ATATTATTTA	TTTAAGCAAT	TACTTTCAT	GTTGGGGTGG	GGACGGAGGG	GAAAGGGAAG	CCTGGGTTT
	TGTACAAAAA	TGTGAGAAC	CTTTGTGAGA	CAGAGAACAG	GGAATTAAAT	GTGTATACA	TATCC
	CAGCTGCAGC	ATCCCTCTGTC	TCAGAGTCTT	GGTGTCTCTG	TTCTTCCC	CTCGGGGTCT	CCCTGGGTCT
	CCCCAAGTCC	CTCCCTGCTGT	CTTCCCTCCG	CTCTCTGATC	TCTGACTCCC	AGAACCTCTC	CCTCTGTCTC
	CAGGGCTGCC	CCTCTGATCC	TCTTGTCTC	TCTGGTGTGT	CTCTCTGGCT	GCCTCCATCT	CTGTGGATCT
20	CCGTCTCCCT	GTCTCTGTCT	CAGTCTGTCC	TTCACTCTGT	GTGTGTGTGT	GTCTCTCTCT	CTCTCTCTCC
	TTCCCTTCCA	CTCCCTCTTC	CTCCGTCTC	CACCTCTCCA	GGCCCTGTG	TTGTCCTCC	GTCCGGCCTT
	TCTCTGCCTT	TCCGTCCTCC	TGCCTCCCCA	TCTCTCTCTG	CTAGTCCTGT	CCAGCCGGAC	CCCCACCCAC
	AGTCGGGCC	CAGC GCTTGA	GCCTGAGTGT	CTGCTCCGGC	CCGTGGAGGT	GGAGGGAGGG	GACGCCAATG
	ACCTCACCCAG	CCCCCTCTCCG	ACCACCCCCC	CCTTCCCCCT	TTCAACTTTT	CCAACCTTTTC	CTTCCGTGCC
25	CTCCTCCGAG	CGCGCGGGCG	TGAGCCCTGC	AAGGCAGCCG	CTCCGTCTGA	ATGGAAAAGG	CAGGCAGGGA
	GGGTGAGTCA	GGATGTGTCA	GGCCGGCCCT	CCCCTGCCGC	CTGCCCCCG	CCCGCCCGCC	CCAGGCCCCC
	TATATAAACCC	CCCAGGGCAGTC	CACACTCCCT	CACTGCCGCG	GGCCCTGTG	CTCAGGGCAC	ATGCCCTCCCC
	TCCCCAGCCG	CGGGCCCAGC	TGACCTCTGG	GGCTCCCCCG	GCAGCGGACA	GGGAAGGGTT	AAAGGCCCCC
	GGCTCCCTGC	CCCCTGCCT	GGGAAACCCC	TGGCCCTGTG	GGGACATGAA	CTGTAAGTTG	GTTCATGGGG
30	AGGGTGGAGG	GGACAGGGAG	GCAGGGAGGA	GAGGGACCCA	CGCGGGGGT	GGGAGCAGAC	CCCGCTGAGT
	CGCACAGAGA	GGGA CCCGGA	GACAGGCAGC	CGGGGAGGAG	AGCAGCTTG	GAGACAGGAG	GCGCGGAGG
	AGATGGCAG	AGACAGACAC	AGACAGGAGC	GGATGGAGGC	AGCCAATCAG	AGGCAGCGA	GGAGGGACGG
	GCCAGACAGG	CCCCGAGAGG	AGCGAGACGC	GAGACCGAGC	AGGGCAGGG	ACGCAGGGAC	TGGTGCCGGG
	AGGGAGGTGA	CCCCCATCGA	CCCAGGCC	AGGGAGCCCG	CGGGGACCG	GAGACTCCCT	GGGATTCCGG
35	CAGAGAGGCT	CCGCAGGGAA	ACTGAGGCAG	GGTCCGCGGA	GAGCGGAGCA	AGCCAGGGAG	TAGCGACCCC
	AGCCGGGGGG	AGGA.GAGAGA	CTGGGCGCCG	GGGAAAGCG	GGGAGAGCCG	GGCAGATGCG	GCCGACGGAG
	GCGCGGACAG	ACCCACGGCT	GGCGGCCCG	GGGGCGGGC	TGGGGGTGTG	CGAGGC	GCGGCCGGGG
	AGCGCTGATT	GGCTGGCGGG	TGGCGGGGTG	GGCGGGCGG	CGGGGGTGG	CTGCGGGGAG	CGAGCTCCGG
	ACCCCCCGC	CCCCGGCGCC	CCCCGCGCCC	CCCGCCGCCA	GCTCTCCC	TCCCGCGCC	CGGCCGGGGCC
40	ATGGCTCTGC	CCCTCTCCGC	CCAGGTGCGC	TGCGGCCCGG	GCTTCTGCG	CCCACCCGGC	GGGCTCTGG
	GAGGGCGTCT	AAGGGGTCTC	CCGTGGGAGA	GGTCCGTGTC	TCCCGGACTC	CGTCTGGG	TTTGGCTCC
	TTCCCCCTGCT	CCCA GCCAGC	TGGGGCTCCC	GGGGCCCGGG	GAGGGGGCAG	GTTCTGGCCT	GTGCCTCCCC
	CACCATCCGC	GCCCCGGGGC	CCAGATTCCG	GGTCCGGGG	GGGACGGGA	GACGCCCGGG	CCGCGTCTGC
	TCCGACGGGC	GGGC CAGCCA	GAGCCAGGG	GGGAGAGGG	AGCCCGCC	GCCCTGCCAC	CTGCCCGCGG
45	GCGTCCACC	CTGGGACTTA	AGACCTCCAG	CTCCATCC	CCTAAGGCCG	GGAGTCAGG	CCCCAGACCC
	TCCTCCCCGA	GACCAGGAG	TCCAGACCC	AGGCCTTCCT	CCCTCAGACC	TAGGAGTCCA	GGCCCCCAGC
	CTCTCCTCCC	TCAGACCCAG	GAGGAGTCCA	GACCCAGTT	CCTCCTCCC	CAGACCCGGG	AGTCCAGCCC
	AGGCCCTCC	CTCTCAGACC	CGGAGTCCAG	CCTGAGCTCT	CTGCTTATC	CTGCCCCCAG	GTGTTTGCGG
50	CCTGGTCTG	GTCGTGCTGA	GCCTGTGCC	AGATACAGCT	GTCGCCCC	GGCCACCA	TGGCCCCCCT
	CGAGTTCCC	CAGACCCCTG	GGCCGAGCTG	GACAGCACCG	TGCTCTGAC	CCGCTCTCTC	CTGGCGGACCA
	CGCGGCAGCT	GGCTGCACAG	CTGGTAGGAG	AGACTGGGCT	GGGGCCAGCA	CAGGAGTGAG	AGGCAGAGAG
	GAACGGAGAG	GAG'CTGCGG	GCAGCCACTT	GGAGGGTTC	TGGGCTCTCA	GGTGGCAGAG	TGAGGGAGGG
	GAAGAGITGG	GGGCCTGGCG	TGGGGATGG	AGGGAGCCCC	GAGGCTGGG	AGGGGCCACC	TCACAGCTT
	TTTCCCTGCC	AGAGGGACAA	ATTCCCAGCT	GACGGGGACC	ACAACCTGGA	TTCCCTGCC	ACCCTGGCCA

TGAGTCGAGG GGCACTGGGA GCTCTACAGG TAAGGGCAAG GGAGTGGGCT GGGGACAAGG TGGGAGGCAG
 GCAGTGAAGG GGGUGGGGAG GATGAGGGGC ACTGGTCGGG TGTTCTCTGA TGTCCCGGCT CTATCCCCAG
 CTCCCAGGTG TGCTGACAAG GCTGCGAGCG GACCTACTGT CCTACCTGCG GCACGTGCAG TGGCTGCGCC
 5 GGGCAGGTGG CTCITCCCTG AAGACCCTGG AGCCCGAGCT GGGCACCCCTG CAGGCCGAC TGGACCGGCT
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 CAAAATCCT GTGCCCTGAG TCCTTGAAGC CTGAGACCCC AGACCCGAGT GCAACAGCCC CGCTCTGAGA
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 ACGCTGTAA TCCCAGCACT TTGGGAGGCC GAGGCAAGTG GATCACCTGA GGTGGGAGT TCAAGACCAAG
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 GTAATCCCAG CTACTTGGGA GGCTGAGGCA GGAGAACATGC TTGAACCTGG GAGGCGGAGG TTGCAGTGAG
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 AAAAAAAA AAGAAGGAAA AGAAAACCCT GGACCTCCAG ACCCTGAGAC CCCAGGCCAG AGCCCTGAGA
 TCCTGACATC TTAAAGATCC CAGGCCCTAA GATACAAGAC CTTGACCCAA AGCCAGCCTT GGGACCCCTGG
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 AGGCCTGACG CCGUGCCTGG CTTCTTAATT GTTCTAACAG CAGCGACAAAC AACAAAAACC CAGCTCTGAG
 35 ATTCCAGCCC CGGGGACTCT AACAGTCCA GGCCGATCC CTCACCTAGA ACCGAGATGC CAGCCCTGAC
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 TCACCTCTCT CCTCTCCCCA CAGATGTCCC GCCTGGCCCT GCCCCAGCCA CCCCCGGACC CGCCGGCGCC
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 GTGATCAACA GTACCCGTAT GGGACAAAGC TGCAAGGTCA AGATGGTTCA TTATGGCTGT GTTCACCATA
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CACCCAGCCG CCCC GAGCAG GGACTGTCAT TCAGGGAGGC TAAGGAGAGA GGCTTGCTTG GGATATAGAA
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 15 CTCCTGGCGG ACACGCGCA GCTGGCTGCA CAGCTGAGGG ACAAAATTCC AGCTGACGGG GACCACAAAC
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 TGTACAAAAA TGTAAGAAC CTTTGTGAGA CAGAGAACAG GGAATTAAAT GTGTACATACA TATCC-3' (FRAG.
 NO:) (SEQ. ID NO:2521)
 30 5'-CAGCTGCGGC A'CCTCTGTC TCAGAGTCTT GGTGTCTCTG TTCCCTTCCC CTGGGGTCT CCCTGGGTCT
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 60 GTGGATCAACT GAACTCCAAG AGTTTGAGAC CGGCCTGCGA GACATGGCAA AACCTGTCT CAAAAAAAGAA
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 ATCAGCCTCC TCCTCTCAA AAATAAGCCC TCAGGAGGGG ACAAAAGTTGA CCGCTGATTG AGCCTGTCAG
 GGCTGTGCAC-3' (FRAG. NO:_) (SEQ. ID NO:2522)

5 Human GM-CSF Nucleic Acid and Antisense Oligonucleotide Fragments

5'-CTTGBGCBGG BBGCTCTGGG GCBGGGBGCT GGCBBGGCCC BGGGGGTGG CTTCTGBCB TGTCCBGBGT
 GCBCTGTGCC BCBGCBGCBG CTGCBGGGCC BTCBGCTTCB TGGGGCTCTG GGTGGCBGGT CCBGCCBTGG
 GTCTGGGTGG GGCCTGGGCTG CBGGCTCCGG GCGGTCCBGCCBTGGGTCTG GGGGCTGGG CTGCBGGCTC
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 10 GGCTGGGCTG CBGGCTCCGG GCGGGCGGGT GCGGGCTGCG TGCTGGGGC TGCCCGCAG GCCCTGC-3' (FRAG.
 NO:1847) (SEQ. ID NC: 1860)
 5'-GBGCBGG BBG-3' (FRAG. NO:1848) (SEQ. ID NO: 1861)
 5'-GCCBCBGCBCBGC-3' (FRAG. NO:1849) (SEQ. ID NO: 1862)
 5'-GGG TGC GGG C-3' (FRAG. NO:1850) (SEQ. ID NO: 1863)
 15 5'-GGT CCB GCC BTG GGT CTG GG-3' (FRAG. NO:1300)(SEQ. ID NO:1309)
 5'-GGC TGG GCT GCB GGC TCC GG-3' (FRAG. NO:1301)(SEQ. ID NO:1310)
 5'-GCG GGC GGG TGC GGG CTG CGT GCT GGG-3' (FRAG. NO:1302)(SEQ. ID NO:1311)
 5'-GGC TGC CCC GCA GGC CCT GC-3' (FRAG. NO:1303)(SEQ. ID NO:1312)
 20 5'-CTTGBGCBGG BBGCTCTGGG GCBGGGBGCT GGCBBGGCCC BGGGGGTGG CTTCTGBCB TGTCCBGBGT
 GCBCTGTGCC BCBGCBGCBG CTGCBGGGCC BTCBGCTTCB TGGGGCTCTG GGTGGCBGGT CCBGCCBTGG
 GTCTGGGTGG GGCTGGCTG CBGGCTCCGG GC-3' (FRAG. NO:1851) (SEQ. ID NO: 1864)

Human Tumor Necrosis Factor α Antisense Oligonucleotide Fragments

5'-GCBCCGCCTG GBGCCCTGGG GCCCCCTGT CTTCTGGGG BGCGCCTCCT CGGCCBGCTC CBCGTCCCCG
 BTCBTGCCTT CBGTCCTCBT GGTGCTCTTT CCBGGGBGB GBGGGGCTGG TCCTCTGCTG TCCTGCTGG
 25 TGCTCBTGGT GTCTTTCCG CCCTGGGCC CCCCTGTCTT CTTGGGCTCT CTTCCCTCTG GGGGCCGCTCT
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 TGGTTTCTC TCTCGCTGG CTGCCTGTCT GGCCTGCGCT CTTGGCCTGT GCTGTTCTC CTCCGGTTCC
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 30 CTCBTGGTGT CCTITCCGCC CTGGGGCCCC CCTGTCTCT TGGGGCTCT TCCCTCTGGG GGCCGTCTC
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 GGGTTTCTCT CTCCGCTGGC TGCCGTCTG GCCTGCGCTC TTGGCCTGTG CTGTTCTCC TCCGGTTCT
 GTCCCTCTG TCTGTCGCC CCTCTGGGT CTCCCTCTGG CGTGGTGGTC TTGTTGCTTG GGCTGGGCTC
 CGTGTCTCCB GTGCTCBTGG TGTCCGCTGB GGGBGCCTCT GCTGGC-3' (FRAG.NO:1852)(SEQ.ID NO:1865)
 35 5'-GGGGCCCCC-3' (FRAG. NO:1853) (SEQ. ID NO:1866)
 5'-GGG GGC CG TCT-3' (FRAG. NO:1854) (SEQ. ID NO:1867)
 5'-CCBGGGGBGB GBG 3GGCTGG-3' (FRAG. NO:1855) (SEQ. ID NO:1868)
 5'-GCBCCGCCTG GBGCCCTGGG GCCCCCTGT CTTCTGGGG BGCGCCTCCT CGGCCBGCTC CBCGTCCCCG
 BTCBTGCCTT CBGTCCTCBT GGTGCTCTTT CCBGGGGBGB GBGGG-3' (FRAG. NO:1304) (SEQ. ID NO:1313)
 40 5'-GCT GGT CCT CTG TCT TTG CTG GTG CTC BTG GTG TCC TTT CC GCC CTG GGG CCC CCC TGT CTT CTT
 GGG G CCT CTT CCC TCT GGG GGC CG TCT CTC TCC CTC TCT GTC TCT C TCT TTC TCT CTC TCT CTT CCC
 C TTT CCC GCT CTT TCT GTC TC GGT GTC TGG TTT TCT CTC TCC GCT GGC TGC CTG TCT GGC CTG CGC TCT T
 GGC CTG TGC TGT TCC TCC GGT TCC TGT CCT CTC TGT CTG TC GCC CCC TCT GGG GTC TCC CTC TGG C
 GTG GTG GTC TTG TTG CTT GGG CTG GGC TCC GTG TCT C CBG TGC TCB TGG TGT CC-3' (FRAG. NO:1305)
 45 (SEQ. ID NO:1314)
 5'-GCT GBG GGB GCG TCT GCT GGC GCT GGT CCT CTG CTG TCC TTG CTG GTG CTC BTG GTG TCC TTT CC GCC
 CTG GGG CCC CCC TGT CTT CTT GGG G CCT CTT CCC TCT GGG GGC CG TCT CTC TCC CTC TCT GTC TCT
 C TCT TTC TCT CTC TCT CTT CCC C TTT CCC GCT CTT TCT GTC TC GGT GTC TGG TTT TCT CTC TCC GCT GGC
 TGC CTG TCT GGC CTG CGC TCT T GGC CTG TGC TGT TCC TCC GGT TCC TGT CCT CTC TGT CTG TC GCC
 50 CCC TCT GGG GTC TCC CTC TGG C GTG GTG GTC TTG TTG CTT GGG CTG GGC TCC GTG TCT C CBG TGC TCB
 TGG TGT CC GCT GBC GGB GCG TCT GCT GGC-3'(FRAG.NO:1306)(SEQ.ID NO:1315)
 5'-GCT GGT CCT CTG CTG TCC TTG CTG-3' (FRAG. NO:1655) (SEQ. ID NO:1664)
 5'-GTG CTC BTG GTG TCC TTT CC-3' (FRAG. NO:1656)(SEQ. ID NO:1665)
 5'-GCC CTG GGG CCC CCC TGT CTT CTT GGG G-3' (FRAG. NO:1657)(SEQ. ID NO:1666)
 55 5'-CCT CTT CCC TCT GGG GGC CG-3' (FRAG. NO:1658)(SEQ. ID NO:1667)
 5'-TCT CTC TCC CTC "CT TGC GTC TCT C-3' (FRAG. NO:1659)(SEQ. ID NO:1668)
 5'-TCT TTC TCT CTC TCT CTT CCC C-3' (FRAG. NO:1660)(SEQ. ID NO:1669)
 5'-TTT CCC GCT CTT "CT GTC TC-3' (FRAG. NO:1661)(SEQ. ID NO:1670)
 5'-GGT GTC TGG TTT TCT CTC TCC-3' (FRAG. NO:1662)(SEQ. ID NO:1671)

5'-GCT GGC TGC CTG TCT GGC CTG CGC TCT T-3' (FRAG. NO:1663)(SEQ. ID NO:1672)
 5'-GGC CTG TGC TGT TCC TCC-3' (FRAG. NO:1664)(SEQ. ID NO:1673)
 5'-TCC GGT TCC TGT CCT CTC TGT CTG TC-3' (FRAG. NO:1665)(SEQ. ID NO:1674)
 5'-GCC CCC TCT GGG GTC TCC CTC TGG C-3' (FRAG. NO:1666)(SEQ. ID NO:1675)
 5 5'-GTG GTG GTC TTG TTG CTT-3' (FRAG. NO:1667)(SEQ. ID NO:1676)
 5'-GGG CTG GGC TCC GTG TCT C-3' (FRAG. NO:1668)(SEQ. ID NO:1677)
 5'-CBG TGC TCB TGG TGT CC-3' (FRAG. NO:1669)(SEQ. ID NO:1678)
 5'-GCT GBG GGB GCG TCT GCT GGC-3' (FRAG. NO:1670)(SEQ. ID NO:1679)

Human Leukotriene C4 Synthase Nucleic Acids and Antisense Oligonucleotide Fragments

10 5'-CTCGGTBDBC GCC;CTCGBBC TCGGGTGGC CGGTGGTGBG CGGC GGCGC BCB CGCGGBBGGC CCTGCGCGCC
 GBGBTBCCCTG CBGGGBBGB TBGGCTGCB GCBGBCTCC CBGGBGGGTG BCBGCBGCC GTBGBGCTBC
 CTCGTCCCTC BTGGTBCCGT CGGTGTGGTG GCBGGGCTG TGTGTGBBGG CGBGCTGGC CCCGTCTGCT
 GCTCCTCGTG CGCGCTCGTC CTTCA TGG TA CCGTCGGTGT GGTGGCCTCG GGTGGGCCGG TGTTGGGCG
 CGCGCGCTCG CGTCGCTCCG GCTCTTCTT CCCGGCTCCGT CGGCCCGGGG GCCTTGGTCT CCCTCGTCC
 15 TCBTGGTBCC G-3' (FRAG. NO:1856) (SEQ ID NO: 1869)
 5'-GCB GCBGGBC-3' (FRAG. NO:1857) (SEQ ID NO: 1870)
 5'-CCCGGCTCCG-3' (FRAG. NO:1858) (SEQ ID NO: 1871)
 5'-CGGCCCGGGG GCC-3' (FRAG. NO:1859) (SEQ ID NO:1872)
 5'-CB CGCGG-3' (FRAG. NO:1860) (SEQ ID NO: 1873)
 20 5'-GCC CCG TCT GCT GCT CCT CGT GCC G-3' (FRAG. NO:1307)(SEQ. ID NO:1316)
 5'-CCT CGT CCT TCA TGG TAC CGT CGG TGT GGT GGC-3' (FRAG. NO:1308)(SEQ. ID NO:1317)
 5'-CTC GGG TGG GCC GGT GGT G-3' (FRAG. NO:1309)(SEQ. ID NO:1318)
 5'-GGG CGC GCG CGC TCG CGT-3' (FRAG. NO:1310)(SEQ. ID NO:1319)
 5'-GGC TCC GGC TCT TCT TTC CCG GCT CCG TCG GCC CGG GGG CCT TGG TCT C-3'(FRAG.NO:1311)(SEQ.ID NO:1320)
 25 5'-CCT CGT CCT TCB TGG TBC CG-3' (FRAG. NO:1312)(SEQ. ID NO:1321)
 5'-CTCGGTBDBC GCC;CTCGBBC TCGGGTGGC CGGTGGTGBG CGGC GGCGC BCB CGCGGBBGGC CCTGCGCGCC
 GBGBTBCCCTG CBGGGBBGB TBGGCTGCB GCBGBCTCC CBGGBGGGTG BCBGCBGCC GTBGBGCTBC
 CTCGTCCCTC BTGGTBCCGT CGGTGTGGTG GCBGGGCTG TGTGTGBBGG CGBGCTGG-3' (FRAG.NO:1861)
 (SEQ ID NO:1874)

Human Endothelin-1 Nucleic Acids and Antisense Oligonucleotide Fragments

30 5'-BCCGGCGGBG CGGCCBGGGT GGBCTGGBG TGGTTTCTC CCCGCCGTT TCBCCCBCCG CGCTGBGCTC
 BGCGCCTBBG BCTGCTGTT CTGGBGCTCC TTGGCBBGCC BCBBBCBGB GBGBGBBBBT CBTGBGCBBC
 TBBTCCCTTC TGBB BBBB BBG GGBTCBBBB CCTCCCGTTC CCCGTTCGCC TGGCGCGC TGCGGGITCC
 TCGTGGGTTT CTCC CCGCCG TTCTCCGGTC TGTGCTTT GTGGGCTTCT TGTCTTTTG GCTGTTCTTT
 35 TCCCTGCTTGG CGTCTTTTCC TTTCTTTGTG CTGGTTGTG GGTCCGCTGG TCCTTTGCC CGCGTTCTC
 TGCTGCCGT TCGCCTGGCG CGCGCTGCGG GTTCCCTCGT GGTTTCTCCC CGCGTTCTC CGGTCTGTTG
 CCTTTGTGGG CTTCTTGCTC TTTTGGCTGT TCTTTCCCTG CTTGGCGTCT TTTCCTTCT TTGTGCTCGG
 TTGTGGGTCC GCTGC TCCCT TGCCCTGTGT GTTTCTGCTG-3' (FRAG. NO:1862) (SEQ. ID NO:1875)
 5'-CCGGCGGBG CGCGCBGGGT GGBC-3' (FRAG. NO:1863) (SEQ. ID NO:1876)

40 40 5'-CCGCCBGGG-3' (FRAG. NO:1864) (SEQ. ID NO:1877)
 5'-GGCGCGCGC-3' (FRAG. NO:1865) (SEQ. ID NO:1878)
 5'-GTGGGTCCGC-3' (FRAG. NO:1866) (SEQ. ID NO:1879)
 5'-CCCGTTCGCCTGGCGC-3' (FRAG. NO:1313)(SEQ. ID NO:1322)
 5'-GCGCTGCGGGTTCTC-3' (FRAG. NO:1314)(SEQ. ID NO:1323)

45 45 5'-GTGGGTTCTCCCCGCCGTTCTC-3' (FRAG. NO:1315)(SEQ. ID NO:1324)
 5'-CGGTCTGTTGCCCTGTGGGG-3' (FRAG. NO:1316)(SEQ. ID NO:1325)
 5'-CTTCTTGTCTTTTGGCT-3' (FRAG. NO:1317)(SEQ. ID NO:1326)
 5'-GTTCTTTCTGCTGGC-3' (FRAG. NO:1318)(SEQ. ID NO:1327)
 5'-GTCTTTCTTTCTT-3' (FRAG. NO:1319)(SEQ. ID NO:1328)

50 50 5'-TGTGCTCGGTTGTGGTC-3' (FRAG. NO:1320)(SEQ. ID NO:1329)
 5'-CGCTGGCTTTGCC-3' (FRAG. NO:1321)(SEQ. ID NO:1330)
 5'-CTGTGTGTTCTGCTG-3' (FRAG. NO:1322)(SEQ. ID NO:1331)
 5'-CCCGTTCGCCTGGCGC-3' (FRAG. NO:1323)(SEQ. ID NO:1332)
 5'-GCGCTGCGGGTTCTC-3' (FRAG. NO:1324)(SEQ. ID NO:1333)

55 55 5'-GTGGGTTCTCCCCGCCGTTCTC-3' (FRAG. NO:1325)(SEQ. ID NO:1334)
 5'-CGGTCTGTTGCCCTGTGGGG-3' (FRAG. NO:1326)(SEQ. ID NO:1335)
 5'-CTTCTTGTCTTTTGGCT-3' (FRAG. NO:1327)(SEQ. ID NO:1336)
 5'-GTTCTTTCTGCTGGC-3' (FRAG. NO:1328)(SEQ. ID NO:1337)
 5'-GTCTTTCTTTCTT-3' (FRAG. NO:1329)(SEQ. ID NO:1338)

60 60 5'-TGTGCTCGGTTGTGGTC-3' (FRAG. NO:1330)(SEQ. ID NO:1339)

5'-CGCTGGTCCTTGC C-3' (FRAG. NO:1331)(SEQ. ID NO:1340)
 5'-CTGTGTGTTCTGCTG-3' (FRAG. NO:1332)(SEQ. ID NO:1341)

Endothelin Receptor ET-B Nucleic Acids and Antisense Oligonucleotide Fragments

5'-GCCCTGTCGG GCGGGAAAGCC TCTCTCCTCT CCCCAGATC CGCGACAGGC CGCAGGCAAG AACCAAGCGCA
 5 ACCAGGGCGC GTCCGCACAG ACTTGGAGGC GGCTGCATGC TGCTACCTGC TCCAGAAGCG TCCGGTGGCC
 10 GCCGCGCC CTGTCGGCG GGBBGCCTCT CTCCTCTCCC CBGBTCCGCG BCBGGCCGCB GGCBGBBCC
 BGCGCBCCB GGGCGCGTCC GCBBCBGBCTT GGBGGCGGCT GCBTGCCTGCT BCCTGCTCGGGCG GGBBGCCCTCCG
 GTGGCCGCCG CGCGCTCCGGT GGCCGCCGCG CCTCTCTCCCT CTCCCCGTGG CCCTGTCGGG CGGGTCCCTGC
 CGTCCTGTCT CCTTTCTT TGCTGTCTTG TCTTCCCGTC TCTGCTTT-3' (FRAG. NO: 1867) (SEQ. ID NO: 1880)
 10 5'-CGGGCG GGBBGC-3' (FRAG. NO: 1868) (SEQ. ID NO: 1881)
 5'-CGGGCGGG-3' (FRAG. NO: 1869) (SEQ. ID NO: 1882)
 5'-CCGCBGBC-3' (FRAG. NO: 1870) (SEQ. ID NO: 1883)
 5'-GCGTCCGGTGGCCGCC-3' (FRAG. NO:1333)(SEQ. ID NO:1342)
 5'-GCCTCTCTCCTCTCCCC-3' (FRAG. NO:1334)(SEQ. ID NO:1343)
 15 5'-GTGGCCCTGTCGGCGGG-3' (FRAG. NO:1335)(SEQ. ID NO:1344)
 5'-TCCTGCCGTCTGCTCCTT-3' (FRAG. NO:1336)(SEQ. ID NO:1345)
 5'-TCTTTGCTGTCTTGT-3' (FRAG. NO:1337)(SEQ. ID NO:1346)
 5'-CTTCCCGTCTCTGCTT-3' (FRAG. NO:1338)(SEQ. ID NO:1347)
 5'-GCCCTGTCGG GCGGGAAAGCC TCTCTCCTCT CCCCAGATC CGCGACAGGC CGCAGGCAAG AACCAAGCGCA
 20 ACCAGGGCGC GTCCGCACAG ACTTGGAGGC GGCTGCATGC TGCTACCTGC TCCAGAAGCG TCCGGTGGCC
 GCCGC-3' (FRAG. NO: 1871) (SEQ. ID NO: 1884)
 5'-GCCCTGTCGG GCGGGBBGCC TCTCTCCTCT CCCCBGBTCC GCGBCBGGCC GCBGGCBBGB BCCBGCGB
 BCCBGGCGC GTCCCBCBG BCTTGGBGGC GGCTGCBTGC TGCTBCCTGC TCCBGBBGCG TCCGGTGGCC GCCGC-
 3' (FRAG. NO: 1872) (SEQ. ID NO: 1885)
 25 **Endothelin ETA Receptor Nucleic Acids and Antisense Oligonucleotide Fragments**
 5'-GTCTGTCCTC CCCGTCTCCT CCCACTGCTT CTCCCGGGGG CTTCCCGGC TTGGGGTGGC CGGTGTCCCG
 GGCTCCGGCG CGGGGGCGGC TTGGCTGCG GGTGGGTGGC GCGGGCTGCC GGGTCCGCC GGCCTGCCGG
 CCCTTGTGCT GCTTTTGCT TGTTCCGTT TGGCTGCTCC GGTCTGTGTT GTGTTGTT TGTTCTTCT
 TGGGTGTGGG CCTGCGGTT TTGGCTGTGG GCCCTTTGGG GCCTTGGCTT CTGGCTCGTC TGCTCCCG
 30 GTCTCCTCCC ACTCTTCT CCCGGGGGCT TCCCCGGCTT CGGGTGGCCG GTGTCCCGGG CTCCGGCGCG
 GCGGCGGCTT CGGGTGCAGGG TGGGTGGCGC GGGCTGCCGG GTCCGCGCG CGCTTGGGCC CTTGTGCTGC
 TTTTGCTTG TTCCGTTCTG GCTGCTCCGG TCTGTGTTGT GGTTGTTTG TTTCTTCTTG GGTGTGGGCC
 TTGCGGTTTG GGC`GTGGGC CCTTITGGGC CTTGGCTTCT GGCTCCAT CCACATGATT GCTTAGATTT
 GTGCTGTATC TCTCAGGATT ATCACTGATT ACACATCAA CCAGTGCCAG CCAAAGGAT GCCCTGAGGC
 35 AAAGGGTTTC CATTTGAGG CAAATTGAG GACBTCCBC BTGBTGCTT BGBTGTTGTC TGTTCTCTC
 BGGBTTBCB CTGETTBCBC BTCCBBCBG TGCCBGCCBB BBGGBTGCC TGBGGCBBBG GGTTCBCB
 TTGBGGCBBB TTGGBGG-3' (FRAG. NO:1873) (SEQ. ID NO: 1886)
 5'-GBGGCBBGGG-3' (FRAG. NO:1874) (SEQ. ID NO: 1887)
 5'-GCCBGCCB BBGG 3'-3' (FRAG. NO:1875) (SEQ. ID NO: 1888)
 40 5'-CGCCTGGGCC C-3' (FRAG. NO:1876) (SEQ. ID NO: 1889)
 5'-GTCTGTCCTCCCCCTCTCCTCCC-3' (FRAG. NO:1339)(SEQ. ID NO:1348)
 5'-ACTGCTTCTCCCGCGG-3' (FRAG. NO:1340)(SEQ. ID NO:1349)
 5'-GCTTCCCCGGCTTC-3' (FRAG. NO:1341)(SEQ. ID NO:1350)
 5'-GGGTGGCCGGTGTCCGGGCTCCGGCGCGGCC-3' (FRAG. NO:1342)(SEQ. ID NO:1351)
 45 5'-GGCTTCGGCTGC-3' (FRAG. NO:1343)(SEQ. ID NO:1352)
 5'-GGGTGGGTGGCGCGG-3' (FRAG. NO:1344)(SEQ. ID NO:1353)
 5'-GCTGCCGGGTCCCGCGGCCCTGGGCC-3' (FRAG. NO:1345)(SEQ. ID NO:1354)
 5'-CTTGTGCTGCTTT-3' (FRAG. NO:1346)(SEQ. ID NO:1355)
 5'-TGCTTGTCTCCGTT-3' (FRAG. NO:1347)(SEQ. ID NO:1356)
 50 5'-TGGCTGCTCCGGTCTGTGTTGTTGTTTG-3' (FRAG. NO:1348)(SEQ. ID NO:1357)
 5'-TTTCTTCTTGGGTGTTG-3' (FRAG. NO:1349)(SEQ. ID NO:1358)
 5'-CCTTGCGGTTTGCG-3' (FRAG. NO:1350)(SEQ. ID NO:1359)
 5'-CTGTGGGCCCTTC-3' (FRAG. NO:1351)(SEQ. ID NO:1360)
 5'-GGGCCTGGCTTCGGCTC-3' (FRAG. NO:1352)(SEQ. ID NO:1361)
 55 5'-CATCCACATG ATGCTTAGA TTTGTGCTGT ATCTCTCAGG ATTATCACTG ATTACACATC CAACCAGTGC
 CAGCCAAAAG GATC CCCTGA GGCAAAGGGT TTCCCATCTTG AGGCAAATTG GAGGA-3' (FRAG.NO:1353)
 (SEQ.ID NO:1362)
 5'-CBTCCBCBTG BTGCTTBGB TTTGTGCTGT BTCTCTCBGG BTTBTCBCTG BTTBCBCBTC CBBCCBGTGC
 CBGCCBBBG GBTGCCCTGB GGCBGGGGT TTCCBTCTTG BGGCBBTTT GBGGB-3' (FRAG. NO:1354)(SEQ. ID NO:1363)

Endothelin Receptor A Nucleic Acid and Antisense Oligonucleotide Fragments

5	GCCACCATGG	AAACCCTTG	CCTCAGGGCA	TCCTTTGGC	TGGCACTGGT	TGGATGTGTA	ATCAGTGATA
	ATCCTGAGAG	ATACAGCACA	AATCTAACGA	ATCATGTGGA	TGATTTCAC	ACTTTCTGTG	GCACAGAGCT
	CAGCTTCCTG	GTTCACACTC	ATCAACCCAC	TAATTGGTC	CTACCCAGCA	ATGGCTCAAT	GCACAACATAT
5	TGCCACAGC	AGACTAAAAT	TACTTCAGCT	TTCAAATACA	TTAACACTGT	GATATCTTGT	ACTATTTICA
	TCGTGGGAAT	GGTCGGGAAT	GCAACTCTGC	TCAGGATCAT	TTACCAAGAAC	AAATGTATGA	GGAATGGCCC
	CAACCGCCTG	ATAGCCAGTC	TTGCCCTGG	AGACCTTATC	TATGTGGTCA	TTGATCTCCC	TATCAATGTA
10	TGGCTGGCG	CTGGCCTTTT	GATCACAAATG	ACTTTGGCGT	ATTCTTTGC	AAGCTGTTCC	CCTTTTGCA
	GAAGTCCTCG	GTGGGGATCA	CCGCTCTAA	CCTCTGCGCT	CTTAGTGTG	ACAGGTACAG	AGCAGTTGCC
10	TCCTGGAGTC	GTGTTCAGGG	AATTGGGATT	CCTTGGTAA	CTGCCATTGA	AATTGCCCTC	ATCTGGATCC
	TGTCCTTAT	CCTGGCCATT	CCTGAAGCGA	TTGGCTTCGT	CATGGTACCC	TTTGAATATA	GGGGTGGACA
	GCATAAAAAC	TGTATGCTCA	ATGCCACATC	AAAATTATCG	GAGTTCTACC	AAGATGTAAA	GGACTGGTGG
15	CTCTTCGGGT	TCTATTCTG	TATGCCCTTG	GTGTCACTG	CGATCTTCTA	CACCCCTCATG	ACTGGTGAGA
	TGTTGAACAG	AAGGAATGGC	AGCTTGAGAA	TTGCCCTCAG	TGAACATCTT	AAGCAGCGTC	GAGAAGTGGC
15	AAAAACAGTT	TTCGCTTGG	TTGTAATTTC	TGCTCTTGC	TGGTCCCTC	TTCATTTAAG	CCGTATATTG
	AAGAAAATG	TGTATAACGA	GATGGACAAG	AACCGATGTG	AATTACTTAG	TTTCTTACTG	CTCATGGATT
	ACATCGGTAT	TAACCTGGCA	ACCATGAATT	CATGTATAAA	CCCCATAGCT	CTGTATTTG	TGAGCAAGAA
20	ATTTAAAAAT	TGTITCCAGT	CATGCCCTCT	CTGCTGCTGT	TACCACTCCA	AAAGTCTGAT	GACCTCGGTC
	CCCATGAACG	GAACAAGCAT	CCAGTGGAAAG	AACCACGATC	AAAACAACCA	CAACACAGAC	CGGAGCAGCC
20	ATAAGGACAG	CATGAACCTGA	CCACCCCTAG	AAGCACTCCT	GAATTGGGGA	AAAAGTGAAG	GTGTAAAAGC
	AGCACAAGTG	CAAAGAGAGA	TATTTCTCA	AATTGCGCTC	AAGATGGAAA	CCCTTGCCT	CAGGGCATCC
	TTTGGCTGG	CACTGGTTGG	ATGTGTAATC	AGTGATAATC	CTGAGAGATA	CAGCACAAAT	CTAAGCAATC
	ATGTGGATGA	TTTCACCACT	TTTCGTGGCA	CAGAGCTCAG	CTTCCCTGGTT	ACCACTCATC	AACCCACTAA
25	TTTGGTCCCTA	CCCAGCAATG	GCTCAATGCA	CAACTATTGC	CCACAGCAGA	CTAAAATTAC	TTCAAGCTTTC
	AAATACATTA	ACACTGTGAT	ATCTTGACT	ATTTTATCG	TGGGAATGGT	GGGGATGCA	ACTCTGCTCA
	GGATCATTTA	CCACAAACAA	TGTATGAGGA	ATGGCCCCAA	CGCGCTGATA	GCCAGTCTTG	CCCTTGGAGA
	CCTTATCTAT	GTGCTCATTC	ATCTCCCTAT	CAATGTATTT	AAGCTGCTGG	CTGGCGCTG	GCCTTTGAT
	CACAATGACT	TTGGCGTATT	TCTTGCAG	CTGTTCCCT	TTTGCGAGAA	GTCCCTGGTG	GGGATCACCG
30	TCCTCAACCT	CTGCGCTCTT	AGTGTGACA	GGTACAGAGC	AGTTGCCCTC	TGGAGTCGTG	TTCAAGGGAT
	TGGGATTCCT	TTGCTAACTG	CCATTGAAAT	TGCTCTCATC	TGGATCTGTG	CCTTATTCCT	GGCCATTCT
	GAAGCGATTG	GCTTCGTAT	GGTACCCCTT	GAATATAGGG	GTGAACAGCA	TAAAACCTGT	ATGCTCAATG
	CCACATCAA	ATTCTATGGAG	TTCTACCAAG	ATGTAAAGGA	CTGGTGGCTC	TTGGGTTCT	ATTCTGTAT
	GCCCTGGTG	TGCACTGCGA	TCTTCTACAC	CCTCATGACT	TGTGAGATGT	TGAACAGAAAG	GAATGGCAGC
35	TTGAGAATTG	CCCTCAGTGA	ACATCTTAA	CAGCGTCGAG	AAGTGGCAAA	AACAGTTTC	TGCTTGGTTG
	TAATTTTGC	TCTTGTCTGG	TTCCCTCTTC	ATTTAAGCCG	TATATTGAAG	AAAACTGTGT	ATAACGAGAT
	GGACAAGAAC	CGATGTGAAT	TACTTAGTT	CTTACTGTC	ATGGATTACA	TCGGTATTAA	CTTGGCAACC
	ATGAATTATC	GTATAAACCC	CATAGCTCG	TATTTGTA	GCAAGAAATT	AAAAAATTGT	TTCCAGTCAT
	GCCTCTGCTG	CTGCTGTTAC	CAGTCCAAA	GTCTGATGAC	CTCGGTCCTC	ATGAACGGAA	CAAGCATCCA
40	GTGGAAGAAC	CACGATCAA	ACAACCAAA	CACAGACCGG	AGCAGCCATA	AGGACAGCAT	GAACTGACCA
	CCCTTAGAAG	CACCTCTCGG	TACTCCCATA	ATCCTCTCGG	AGAAAAAAAT	CACAAGGCAA	CTGTGAGTCC
	GGGAATCTCT	TCTCTGATCC	TTCTTCCTA	ATTCACTCCC	ACACCCAAAGA	AGAAATGCTT	TCCAAAACCG
	CAAGGTAGA	CTGGTTTATC	CACCCACAAAC	ATCTACGAAT	CGTACTCTT	TAATTGATCT	AATTACATA
	TTCTCGCTGT	TGTAATCAGC	ACTAAAAAAAT	GGTGGGAGCT	GGGGGAGAAT	GAAGACTGTT	AAATGAAACC
45	AGAAGGATAT	TTTACTACTT	TGCATAAAAA	TAGAGCTTTC	AAGTACATGG	CTAGCTTTA	TGGCAGTTCT
	GGTGAATGTT	CAATGGGAAC	TGGTCACCAT	GAAACTTTAG	AGATTAACGA	CAAGATTTC	TACTTTTTT
	AAAGTATTTC	TTTGTCCTTC	AGCCAAACAC	AATATGGGT	CAAGTCACCT	TTATTGAAA	TGTCATTGG
	TGCCAGTATC	CCGAATTTC	GAATTGGGAA	AAAAGTGAAG	GTGAAAAGC	AGCACAAGTG	CAATAAGAGA
	TATTCCTCA	AATTGCTTC	AAGATGGAAA	CCCTTGGCT	CAGGGCATCC	TTTGGCTGG	CACTGGTTGG
50	ATGTGAATC	AGTCATAATC	CTGAGAGATA	CAGCACAAAT	CTAACGCAATC	ATGTGGATGA	TTTCACCACT
	TTTCGGCA	CAGTCCTCAG	CTTCTGGTT	ACCACTCATC	AACCCACTAA	TTTGGCTCTA	CCCAGCAATG
	GCTCAATGCA	CAACTATTGC	CCACAGCAGA	CTAAAATTAC	TTCAGCTTC	AAATACATTA	ACACTGTGAT
	ATCTTGACT	ATTTTCATCG	TGGGAATGGT	GGGGAAATGCA	ACTCTGCTCA	GGATCATTAA	CCAGAACAAA
	TGTATGAGGA	ATGGCCCAA	CGCGCTGATA	GCCAGTCTTG	CCCTTGGAGA	CCTTATCTAT	GTGGTCATTG
55	ATCTCCCTAT	CAAATGTATT	AAGCTGCTG	CTGGCGCTG	GCCTTTGAT	CACATGACT	TTGGCGTATT
	TCTTGCAG	CTGTCCTCCT	TTTTCAGAA	GTCTCGGTG	GGGATCACC	TCCTCAACCT	CTCGCTCTT
	AGTGTGACA	GGTACAGAGC	AGTTGCCCTC	TGGAGTCGTG	TTCAGGGAAT	TGGGATTCC	TTGGTAACG
	CCATTGAAAT	TGTCTCCATC	TGGATCTGT	CCTTATCTC	GGCCATTCT	GAAGCGATTG	GCTTCGTAT
	GGTACCCCTT	GAATATAGGG	GTGAACAGCA	TAAAACCTGT	ATGCTCAATG	CCACATCAA	ATTCATGGAG
60	TTCTACCAAG	ATGTAAAGGA	CTGGTGGCTC	TTGGGTTCT	ATTCTGTAT	GCCCTTGGTG	TGCACTGCGA
	TCTTCTACAC	CCTCATGACT	TGTGAGATGT	TGAACAGAAAG	GAATGGCAGC	TTGAGAATTG	CCCTCAGTGA
	ACATCTTAAAG	CAGCGTCGAG	AAAGTGGCAAA	AACAGTTTC	TGCTTGGTT	TAATTTCG	TCTTTGCTGG

TTCCCTCTTC ATTTAAGCCG TATATTGAAG AAAACTGTGT ATAACGAGAT GGACAAGAAC CGATGTGAAT
 TACTTAGTTT CTTAATGCTC ATGGATTACA TCGGTATTAA CTTGGCAACC ATGAATTCAT GTATAAACCC
 CATAGCTCTG TATTTGTGA GCAAGAAAATT TAAAATTGT TTCCAGTCAT GCCTCTGCTG CTGCTGTTAC
 CAGTCCAAAAA GTCIGATGAC CTCGGTCCCC ATGAACGGAA CAAGCATCCA GTGGAAGAAC CACGATCAA
 5 ACAACCACAA CACAGACCGG AGCAGCCATA AGGACAGCAT GAACTGACCA CCCTAGAAG CACTCCTCGG
 TACTCCCATA ATCCCTCTCGG AGAAAAAAAT CACAAGGCAA CTGTGAGTCC GGGAAATCTCT TCTCTGATCC
 TTCTTCTTA ATTCACTCCC ACACCCAAGA AGAAATGCTT TCCAAAACCG CAAGGGTAGA CTGGTTTATC
 CACCCACAAC ATCTACGAAT CGTACTTCTT TAATTGATCT AATTACATA TTCTCGTGTT TGTATTCA
 ACTAAAAAAAT GGTCGGAGCT GGGGGAGAAT GAAGACTGTT AAATGAAACC AGAAGGATAT TTACTACTT
 10 TGCAATGAAAA TAGAGCTITC AAGTACATGG CTAGCTTTA TGGCAGTTCT GGTGAATGTT CAATGGGAAC
 TGGTCACCAT GAAACTTITAG AGATTAACGA CAAGATTTTC TACTTTTTT AAGTGAATT TTTGTCTTC
 AGCCAACAC AATA'GGGCT CAAGTCACTT TTATTTGAAA TGTCAATTGG TGCCAGTATC CCGAATTTC-3' (FRAG.
 NO: __) (SEQ ID NO: 3014)
 5'-GAATTGGGA AAAAGTGAAG GTGTAAAAGC AGCACAAGTG CAATAAGAGA TATTTCTCA AATTGCTC
 15 AAGATGAAA CCCTTGCCT CAGGGCATCC TTTGGCTGG CACTGGTTGG ATGTGAATC AGTGATAATC
 CTGAGAGATA CAGCACAAAT CTAAGCAATC ATGTGGATGA TTTCACCACT TTCTGGGCA CAGAGCTCAG
 CTTCTGGTT ACCACTCATC AACCCACTAA TTGGTCTTA CCCAGCAATG GCTCAATGCA CAACTATTGC
 CCACAGCAGA CTAATTAC TTCAGCTTC AAATACATTA ACACGTGAT ATCTTGACT ATTTCATCG
 20 TGGGAATGGT GGGGAATGCA ACTCTGCTCA GGATCATTAA CCAGAACAAA TGTATGAGGA ATGGCCCCAA
 CGCGCTGATA GCCAGTCTTG CCCTTGGAGA CCTTATCTAT GTGGTCATTG ATCTCCCTAT CAATGTATTT
 AAGCTGCTGG CTGGGCGCTG GCCTTTGAT CACAATGACT TTGGCGTATT TCTTGCAAG CTGCGCTCTT
 TTTTGAGAAA GTCTCGGTG GGGATCACC CGTCAACCT TTGGTAACTG AGTGGTACCA GGTACAGAGC
 AGTTGCCCTC TGGATCTGT CTTTATCCT GGCCATTCTT GAAGCGATTG GCTTCGTAC GGTACCCCTT
 25 GTGAACAGCA TAAACCTGT ATGCTCAATG CCACATCAA ATTCACTGGAG TTCTACCAAG ATGTAAGGA
 CTGGTGCTC TTCCGGTCT ATTTCTGTAT GCCCCTGGTG TGCACTGGCA TCTTCTACAC CCTCATGACT
 TGTGAGATGT TGAAAGAGA GAATGGCAGC TTGAGAATTG CCCTCAGTGA ACATCTTAAG CAGCGTCGAG
 AAGTGGCAA AACAGTTTC TGCTTGGTT TAATTTTGC TCTTGCTGG TTCCCTCTTC ATTAAAGCCG
 TATATTGAAG AAACTGTGT ATAACGAGAT GGACAAGAAC CGATGTGAAT TACTTAGTTT CTTACTGCTC
 30 ATGGATTACA TCGCTATTAA CTTGGCAACC ATGAATTCAT GTATAAACCC CATAGCTCTG TATTTGTGA
 GCAAGAAAATT TAAATTGT TTCCAGTCAT GCCTCTGCTG CTGCTGTTAC CAGTCCAAAA ACAACCACAA
 CTCGGTCCCC ATGAACGGAA CAAGCATCCA GTGGAAGAAC CACGATCAA ACAAGACCGG ATCCTCTCGG
 AGCAGCCATA AGGACAGCAT GAACTGACCA CCCTAGAAG GCTTCGTAC TCTTGCAAG GAAACTTAG
 AGAAAAAAAT CACAGGCAA CTGTGAGTCC GGGAAATCTCT TTCTTCCTT ATTCACTCCC
 35 ACACCCAAAGA AGAAATGCTT TCCAAAACCG CAAGGGTAGA CTGGTTTATC CACCCACAAC ATCTACGAAT
 CGTACTTCTT TAATTGATCT AATTACATA TTCTCGTGTT TGATTCAGC ACTAAAAAAAT GGTGGGAGCT
 GGGGGAGAAT GAAAGACTGTT AAATGAAACC AGAAGGATAT TTACTACTT TGCAATGAAA TGTACAGAGC
 AAGTACATGG CTAGCTTTA TGGCAGTTCT GGTGAATGTT CAATGGGAAC TGGTCACCAT GAAACTTTAG
 AGATTAACGA CAAAGATTTTC TACTTTTTT AAGTGAATT TTTGTCTTC AGCCAACAC AATATGGGCT
 40 CAAGTCACTT TTATTTGAAA TGTCAATTGG TGCCAGTATC CCGAATTTC-3' (FRAG. NO: __) (SEQ ID NO: 2482)
 5'-GAATTGGGA AAAAGTGAAG GTGTAAAAGC AGCACAAGTG CAATAAGAGA TATTTCTCA AATTGCTC
 AAGATGAAA CCCTTGCCT CAGGGCATCC TTTGGCTGG CACTGGTTGG ATGTGAATC AGTGATAATC
 CTGAGAGATA CAGCACAAAT CTAAGCAATC ATGTGGATGA TTTCACCACT TTCTGGGCA CAGAGCTCAG
 CTTCTGGTT ACCACTCATC AACCCACTAA TTGGTCTTA CCCAGCAATG GCTCAATGCA CAACTATTGC
 45 CCACAGCAGA CTAATTAC TTCAGCTTC AAATACATTA ACACGTGAT ATCTTGACT ATTTCATCG
 TGGGAATGGT GGGGAATGCA ACTCTGCTCA GGATCATTAA CCAGAACAAA TGTATGAGGA ATGGCCCCAA
 CGCGCTGATA GCCAGTCTTG CCCTTGGAGA CCTTATCTAT GTGGTCATTG ATCTCCCTAT CAATGTATTT
 AAGCTGCTGG CTGGGCGCTG GCCTTTGAT CACAATGACT TTGGCGTATT TCTTGCAAG CTGTTCCCT
 TTTTGAGAAA GTCTCGGTG GGGATCACC CGTCAACCT TTGGTAACTG AGTGGTACCA GGTACAGAGC
 50 AGTTGCCCTC TGGAGTCGTG TTCAGGGAAAT TGGGATTCTT GGTCAGTAC GGTACCCCTT GAATATAGGG
 TGGATCTGT CTTTATCCT GGCCATTCTT GAAGCGATTG ATTCACTGGAG TTCTACCAAG ATGTAAGGA
 GTGAACAGCA TAAACCTGT ATGCTCAATG CCACATCAA TGCACTGGCA TCTTCTACAC CCTCATGACT
 CTGGTGCTC TTCCGGTCT ATTTCTGTAT GCCCCTGGTG CCCTCAGTGA ACATCTTAAG CAGCGTCGAG
 TGTGAGATGT TGAAAGAGA GAATGGCAGC TTGAGAATTG TCTCTGCTGG TTCCCTCTTC ATTAAAGCCG
 55 AAGTGGCAA AACAGTTTC TGCTTGGTT TAATTTTGC CGATGTGAAT TACTTAGTTT CTTACTGCTC
 TATATTGAAG AAAACTGTGT ATAACGAGAT GGACAAGAAC GTATAAACCC CATAGCTCTG TATTTGTGA
 ATGGATTACA TCGCTATTAA CTTGGCAACC ATGAATTCAT CTGCTGTTAC CAGTCCAAAA GTCTGATGAC
 GCAAGAAAATT TAAATTGT TTCCAGTCAT GCCTCTGCTG CACGATCAA ACAACCACAA CACAGACCGG
 CTCGGTCCCC ATGAACGGAA CAAGCATCCA GTGGAAGAAC CACTCCTCGG TACTCCATA ATCCTCTCGG
 60 AGCAGCCATA AGGACAGCAT GAACTGACCA CCCTAGAAG TCTCTGATCC TTCTTCCTT ATTCACTCCC
 AGAAAAAAAT CACAGGCAA CTGTGAGTCC GGGAAATCTCT CACCCACAAC ATCTACGAAT
 ACACCCAAAGA AGAAATGCTT TCCAAAACCG CAAGGGTAGA CACCCACAAC ATCTACGAAT

CGTACTTCCTT TAATTGATCT AATTACATA TTCTCGTGT TGTATTCAAGC ACTAAAAAAAT GGTGGGAGCT
 GGGGGAGAAT GAA³GACTGTT AAATGAAACC AGAAGGATAT TTACTACTT TGATGAAAAA TAGAGCTTC
 AAGTACATGG CTAGCTTTA TGGCAGTTCT GGTGAATGTT CAATGGGAAC TGGTCACCAT GAAACTTAG
 AGATTAACGA CAA³GATTTTC TACTTTTTT AAGTGATTIT TTTGTCCTTC AGCCAAACAC AATATGGGCT
 5 CAAGTCACCT TTATTGAAA TGTCAATTGG TGCCAGTATC CCGAATT-3' (FRAG. NO: __) (SEQ ID NO: 2470)
 5'-GCCACCATGG AAACCCCTTG CCTCAGGGCA TCCTTTGGC TGGCACTGGT TGGATGTGTA ATCAGTGATA
 ATCCTGAGAG ATACAGCACA AATCTAACCA ATCATGTGGA TGATTTCAC ACTTTCTG GCACAGAGCT
 CAGCTTCTG GTTACCACTC ATCAACCCAC TAATTGGTC CTACCCAGCA ATGGCTCAAT GCACAACTAT
 10 TGCCCCACAGC AGA³TAAAAT TACTTCAGCT TTCAAATACA TTAACACTGT GATATCTTGT ACTATTTCA
 TCGTGGGAAT GGT³GGGAAT GCAACTCTGC TCAGGATCAT TTACCAAGAAC AAATGTATGA GGAATGGCCC
 CAACCGCCTG ATAGCCAGTC TTGCCCCTGG AGACCTTATC TATGTTGTC TTGATCTCCC TATCAATGTA
 TGGCTGGCG CTGGCCTTT GATCACAATG ACTTTGGCGT ATTTCTTGC AAGCTGTTCC CCTTTTGCA
 GAAGTCCCTG GTGGGGATCA CCGTCCTCAA CCTCTGCGCT CTTAGTGTG ACAGGTACAG AGCAGTTGCC
 15 TCCTGGAGTC GTGT³CAGGG AATTGGGATT CCTTTGGTAA CTGCCATTGA AATTGGCTTCC ATCTGGATCC
 TGTCTTTAT CCTGGCCATT CCTGAAGCGA TTGGCTTCGT CATGGTACCC TTTGAATATA GGGGTGGACA
 GCATAAAACC TGT³TGCTCA ATGCCACATC AAAATTCTATG GAGTTCTACC AAGATGTAAA GGACTGGTGG
 CTCTTCGGGT TCTATTCTG TATGCCCTG GTGTGACTG CGATCTCTA CACCCCTCATG ACTGGTGAGA
 20 TGTTGAACAG AAGGAATGGC AGCTTGAGAA TTGCCCTCAG TGAACATCTT AAGCAGCGTC GAGAAGTGGC
 AAAAACAGTT TTC³GCTTGG TTGTAATT TTGCTCTTGC TGGTCCCTC TTCACTTAAG CCGTATATTG
 AAGAAAATG TGT³TAACGA GATGGACAAG AACCGATGTG AATTACTTAG TTTCTTACTG CTCATGGATT
 ACATCGGTAT TAACTGGCA ACCATGAATT CATGTATAAA CCCATAGCT CTGTATTITG TGAGCAAGAA
 ATTAAAAAT TGT³TCCAGT CATGCCCTG CTGCTGCTGT TACCACTCA AAAGCTGAT GACCTCGGT
 CCCATGAACG GAAC³AAGCAT CCAGTGGAAAG AACACAGATC AAAACAACCA CAACACAGAC CGGAGCAGCC
 ATAAGGACAG CATGAACTGA CCACCCCTAG AAGCACTCCT-3' (FRAG. NO: __) (SEQ ID NO: 2469)

Substance P Antisense Nucleic Acids and Oligonucleotide Antisense Oligonucleotide Fragments

25 5'-CTGCTGBGGC TTGGGTCTCC GGGCGBTCT CTGCBGBBGB TGCTCBBBG GCTCCGGCBG TTCCCTCTG
 BTCTGGTCGCT GTC³GTBCCBG TCGGBCBGT BBTTCBGBTC BTCTBTTGGCT CCTBTTTCTT CTGCBBBCBG
 CTGBGTGGBG BCBHBBBBB BGBCTGCCB GGCCBCGBGG BTTTTCBTGT TGGBTTTGC GBCGGBCBGT
 CCCCGGGGT GCTGAGTTTC TCTGGTTCTT CCGBGCGCCTC GTGGTCGCTC CGCGTTTCTC TGGTTCTCC
 30 GGTCCCGCGG GGTGCTGTCT GGTCGCTGTC GTGGCTTGGG TCTCCGGCG GTTTCCCTCC TTTTCCGC-3' (FRAG.
 NO:1877) (SEQ ID NO: 1890)
 5'-CTCC GGGCGB-3' (FRAG. NO:1878) (SEQ ID NO: 1891)
 5'-GGCCBCGBGG-3' (FRAG. NO:1879) (SEQ ID NO: 1892)
 5'-GGGTCTCCGGCG 3' (FRAG. NO:1880) (SEQ ID NO: 1893)
 35 5'-GGG TCTCCGGCG G-3' (FRAG. NO:1881) (SEQ ID NO:1894)
 5'-CGTGGTCGCTCCG-3' (FRAG. NO:1355)(SEQ. ID NO:1364)
 5'-GTTTCTCTGGTTCC TCCG-3' (FRAG. NO:1356)(SEQ. ID NO:1365)
 5'-GTCGGCGGGGTGCTG-3' (FRAG. NO:1357)(SEQ. ID NO:1366)
 5'-TCTGGTCGCTGTCC-3' (FRAG. NO:1358)(SEQ. ID NO:1367)
 40 5'-GGCTTGGGTCTCCGGCG-3' (FRAG. NO:1359)(SEQ. ID NO:1368)
 5'-GTTTCTCTCCCTTCCG-3' (FRAG. NO:1360)(SEQ. ID NO:1369)
 5'-CTGCTGBGGC TTGGGTCTCC GGGCGBTCT CTGCBGBBGB TGCTCBBBG GCTCCGGCBG TTCCCTCTG
 BTCTGGTCGCT GTC³GTBCCBG TCGGBCBGT BBTTCBGBTC BTCTBTTGGCT CCTBTTTCTT CTGCBBBCBG
 CTGBGTGGBG BCBHBBBBB BGBCTGCCB GGCCBCGBGG BTTTTCBTGT TGGBTTTGC GBCGGBCBGT
 45 CCCCGGGGT GCTGAGTTTC TCTGGTTCTT CCGBGCGC-3' (FRAG. NO:1882) (SEQ ID NO: 1895)

Substance P Receptor Nucleic Acids and Antisense Oligonucleotide Fragments

5'-GGGCTBBGBT GB³CCBCBTC BCTBCCBCGT TGCCCBCC BGBGGTCBC BCBBTGBCCG TGTBGGCBGC
 TGCCCBGGG BCB³TTGCC BGGCTGGTG CBCGBCBCTG TTGGGTTCCG BGGTGTBGT GGBGBTGTTT
 50 GGGGBGBGGT CTG³GTCCBC CGGGBGBCG TTBTCCBTG CGBBGCTBGG CGGTBBBGCC CTBCTBTCTG
 TBCBCBCCC CCC³CTGCBG CBGBGTCTG TCGTGGCGCC TGGGGCTCBG GGTCCGGGC TAAGATGATC
 CACATCACTA CCAC³GTTGCC CACACAGAG GTCACCAAA TGACCGTGT GGCAGCTGCC CAAAGGACAA
 TTTGCCAGGC TGG³TGCACG AACTGATGG GTTCCGAGGT GTTAGTGGAG ATGTTGGGG AGAGGTCTGA
 GTCCACCGGG AGGACGTTAT CCATTTCGAA GCTAGGCGGT AAAGCCCTAC TATCTGTACA CAACCCCCCT
 CTGCAGCAGA GTCCCTGTCGT GGCGCCTGGG GCTCAGGGTC CGTCCTGTCG TGGCGCCTGG GGCTCTTCTT
 55 TTGTGGGCTC TTTCGTGGCT GTGGCTGTGG TCTCTGTGGT TGCTGCCCTG GGTCTGGGGG TGTGGCCTTG
 GGGCCGTCTT CTGGCTCCTC CTCGTGGGCC CCC-3' (FRAG. NO:1883) (SEQ. ID NO:1896)
 5'-GGGBGBBCG-3' (FRAG. NO:1884) (SEQ. ID NO:1897)
 5'-GGGTC CG-3' (FRAG. NO:1885) (SEQ. ID NO:1898)
 5'-GGGCC CCC-3' (FRAG. NO:1886) (SEQ. ID NO:1899)
 60 5'-GTCCTGTCGTGGCGCCTGGGCC-3' (FRAG. NO:1361)(SEQ. ID NO:1370)

5'-TTCTTTGTGGGCT-3' (FRAG. NO:1362)(SEQ. ID NO:1371)
 5'-CTTGGTGGCTGTCGCTG-3' (FRAG. NO:1363)(SEQ. ID NO:1372)
 5'-TGGTCTCTGTTG-3' (FRAG. NO:1364)(SEQ. ID NO:1373)
 5'-CTGCCCTGGGTCTG-3' (FRAG. NO:1365)(SEQ. ID NO:1374)

5 5'-GGGTGTGGCCTTGGGCCCTCCTGGCTCCTCGTGGCCCC (FRAG.NO:1366)(SEQ.ID NO:1375)
 5'-GGGCTAAGAT GAATCCACATC ACTACCACGT TGCCCACAC AGAGGTCAAC ACAATGACCG TGTAGGCAGC
 TGCCCAAAGG ACAATTGCC AGGCTGGTT CACGAACCTGA TTGGGTTCCG AGGTGTTAGT GGAGATGTT
 GGGGAGAGGT CTGAATGCC ACAGGAGGACG TTATCCATTTC GAAGCTAGGC GGTAAAGCCC TACTATCTGTA
 CACAACCCCC CTCTCAGCA GAGTCCTGTC GTGGCGCCTG GGGCTCAGGGTCC-3'(FRAG.NO:1367)(SEQ.ID NO:1376)
 10 5'-GGGCTBBGBT GBATCCBCBT BCTBCCBCGT TGCCCBCBC BGBGGTCBC BCBBTGBCCG TGTBGGCBGC
 TGCCCBGGG BCBBTTGCC BGGCTGGTT CBGCBCTGB TTGGGTTCCG BGGTGTBGT GGBGBTGTT
 GGGGBGBGGTC TGTGTCCBCC GGGBGBGCCT GTGGCGCCTG GGGCTCBGGG TCC-3' (FRAG. NO:1368) (SEQ. ID NO:1377)

Chymase Antisense Nucleic Acids and Oligonucleotides Antisense Oligonucleotide Fragments

15 5'-GGBGCTGBTB CTGCBGATT CBGBGGGBB BBCCCTGBTB CTCBCCBGC TCBGCTCTGG BGCBCCBGBG
 BBBGBGCBGC BGGCGGBGBG GBBGBGCBG CBCTTCCCB GBGBGGCTGC CTGBGCBBBT GCTGGTTTC
 CTTTCCBGTC TTGCGTTTB TBBCTCCCB BBGGCBGBG BGGGGCBBGG CGTTTCTTC TCTCGCTGGT
 TTTCCCTTCC TGGCAGTGGG TGGGGGGGGG GGTGGGGTGG CTTCCCTGTT CCTGGGGGTG TCCTCTTGCT
 CTGGGCTTTT CTCCCTCTT CCTCCCTGTC TGTTTCTG GGGCTCTCCT CTGTCCTGT GTCCTTGCCC
 20 TGGCCCTCTT CCCTCTCTG TCTCCCTGTC CTGTGTTCCG CCCGCTCTCC
 CTCTCCTGAC CTCCCTTTCC TCCGCTGGG GGGGCCCTGC CTGTCCTG CTCCCTGGCT TGGGGTTCT
 TCTGTGTGTC TTCITCCTCT GTGGCTGGC TTCTCCTTC TTGTCCTTC CTGGGTGCC CTTCTCTT
 TCTGGGGTCC TTGGTGCTTG GGCTGGG TCCCAGTTAA TACATAATCA ATATGCAATT TATTAATACA
 25 TCTCTCCATG TCCAATCCCC CTGTATCTTG CCATTCTTGA CCTGCATTTC CATCCTCCTT ACCTTCCCTA
 GAGGCCAACT CATTTCTTT GAAAAACCTG GCATTCTCCA GAAAAAAAAG TGAGGGCTG GGAGCTGTCC
 GTTGTCTGAA TTGCTCCCT CTGCCCTGTC TTCCAAATGT GGTGGAAAG AAGCACTATT GAAAATCCC
 TAAACGCCACC CCTCGCAGGGT TGGCTCTACC CTGTAGCCAT GGACACATGC TGTGATACC ACCTGCCTCA
 TGAGTCTCAC ATAATTGCC CTTTCACACT ATCTACCCCA TCAGCCTTAC CAAACCCATA CCTGCATCCT
 GGGCAGCATC TGCCCTTCAA GAGACTAAGG AATCTCCTTG CAACCAAGAA TGACTAGACC AATGAGACAC
 30 CCTTTAAGGC CCCAGCACAA TATAGAAATC CCACAATATG GTAATCCCAG TAAGGAGCTA TCAAGCCATT
 GCAGGACCAT CTAGAAATACA ACTAGAGTAT AGTCCTTTC AATCCAGGAA CTATACTCTA ACAGCTTGGC
 TCACAGAAC CAGAAAGTGA GATGATGAGG ATCAGGGCTG AGCTGTGAG CACCAGCTCC ACCACTGACA
 CCAACCACAG ATTAAACAAG CATTTGTGG ACCCCCTGGGA TGGAAAGAAT AGTTGTTGCC TTATCAACT
 CCCCCACAGC CCACACAGAA AAGATAAAAT CATCATGGCT ACAGTGTAC AGAAGATGAT GACCCAAGGA
 35 GTAGGCCCTGC CTGAGTGAAT GCTGAGAGTG ATAATGGGAG CAGTAGCATC TCAGAGACTA CAGCAGAAC
 CATCCACATA AAGAGCTTTG CCCAAACTTA TGATAAAGGG CACCCTCAGA GACTCTCCCT ACTTTAATAT
 TAGCCCATTG CAGAAATGGT GAGTGGAAAG AGAAATCTTA GGAAGAACCC CTTAAAAAAG CAAATGCTT
 TTTAGGTTG TGCTGAAGAG CCTGGAAAAG AAATAAGGAC ACACACGCTG AGAAATCTTC CTCCTGCC
 AACACTGGGA TAACTCCAA GGATCTCTCC ATATCTCATT CTCCTGGATA CACTGTCCAC TCAGAAATAT
 40 TGTGCAGAGT GCACTAATTG AAAAGTGAGC TATTGTGTTA GGAGTGAAGG CAAGAGTATC GTAAAATAAA
 TCAAATTGAA AATGAAATTCT CTTAAATTGC TTTATAGATG TAGAAACAGG CAGGACTTAT TGCGAGGGCA
 AAACCTAAA TTCAAGAAAA ACTTGGTCAT TCAGAAACTA AGTGCCTGAGC AGTGCCTGAG AGGATGTACT
 AACACAGAGT GAGCTCCAGC CTGCTTCAGG AAAATCTGCC TCCCTGACCC ACAGGAGTTC TTTAGAAGAG
 CACTGCACTA CTGCTCAGTA TGAGCCCCATG CCATCAGCTG ACTCGAGGGT TAAAACAAGT TGCAAGAAA
 45 ACTGGTCAAC AAAAGTTCT AGGGTGTGTT ATACCTGCCA TAAACAGCCT GGCAGCACAT GAATGAATAG
 TGCTCAATCA AGAAAGACAC AGTCATTACT CAGAGAATAA CATAACAGAT GTTAATCTGT AATGTGTTA
 AAAAAAGATG TTACATGCAA AGCATGAAAT AACCAAATTC AAAAATTATA GCCAATGAGG ATATATCTAT
 GGAGAATTAA GAGGAAGTAT AAGATTATT CTTTCATCAA ACACAAAGGA ATAAAACCAA CGTTTATTAA
 CAATTATCCA TCAAGTGGTG ATATGGCAGC ACAAGTAAAG ATTCTGAAAA AAATCCTTGT ACTGTATCAT
 50 GAACCAATCA TGTGGCATTT CACATTGAGC ATCATATTAA ATTCTGAAAA AAATCCTTGT ACTGTATCAT
 TCTTCATATT TTATGGATGC AGTAACCTAAG GCTGAGAACT TAAATTTT TCCTAAGTTC AGACACATAG
 CTAAGTGGCA GAACCAAGAT TCAAACCTAC CCCATCTAAC TGCGAGGCAA ACTGCATGCC TTAAATGTCA
 AAGTGAATAC TAGCACAGTT AATACAATGT TTGAAACTC AGAGAAGGAA TGATCCCTCT GCATTATAAGT
 TACTAAGGAA TCACTGCCAT TATTAAATG CCAGTGCTTC TACATCAGGC CCAAATTTTC TGTCCCTACTA
 55 ACTGTGAATC AAGACTTGTAT TCAACCTCTA CTTGAGTATC TGCGCAATG AGAAATCACT TACCTCCACT
 AACCACACAT TTAATTGTTA ACAACAGATT GTTAGTAAGT CCTTTCTTAT ACATACTCAA CAGCTGCTTC
 CCAAGATGCT GTACGATTAT GTCTAGAGTC AACTAGGCCA GAAGCAATGT CCAAATACA CCATAACACT
 GTGCAGCAAA GGTCTACTA CCACTTGTGTT GGCCCAAACA TTCTAGGAG CACTGGATAT CTGAATCATC
 AATTATTTCC ACAACACTG ACCCCCTCTAC CAGTCACCC CACTAGAAGA ATTAATTCCA CATGATAATA
 60 GCTCCCTCAT GTTACTCCCT TCTAAGTCAA ATTGTACACC CCTTTATCTG ATTAACAGAG TCTAAGTCAC
 ATGACCTAAA TGCAAGAGAA CTGGGAATGG ACGTTTGTGG ATTCTACCT AGTAAGGCAA AGTTATCATT

	GGGAATTCCT	CTAATACAGG	AAGGGTGTTC	CAGAGACATT	AAGGAGCCAT	ATAAATGGAA	AATGTCCACT
	ACAATCCATC	ACTIGGTGC	CCCACATCAA	CATTCATTCT	TTTGCCACAC	TTAAAGTTTC	CAAGAACAAA
	AATTATCCA	CTGPAACATAA	TCTTTACTAT	CTTTTATATA	AAGGAAAATT	AGACTTGACT	CAGCAGAACT
	GAAATAACCC	AGC'CTAACAA	GTTACTGCTT	TTAACATTCAA	GTACTGTGTC	TCTAGGTGAT	ACCTGCTCCA
5	ACAATAGTT	GGTCACATT	TCATTTGAT	ATTCTCTAGT	CTCCCAACTT	GATAACTGTA	CCCTAAACCA
	TAAAGTTCAC	TACCAACATG	CTATATATAA	AATAACAAA	GGGGGAAGAA	GAAAGAGAAA	AAGGAAATCT
	CTTAAAATAC	ACAC GTATAC	ATATGACAAA	GCAAGAAGG	AAATGTGAGC	AGATAGTGCA	GTCCTCGTT
	CTGAAATTGG	TCCC CTGACT	GGGGCTATAC	CTATTCCATT	TCCTCACCT	CAGCAGGCA	GGTGGAGCAA
	AAACTTAAGT	CTTC GTGGAT	CTGAATCTG	ATGCTGTGGA	GCTGTCTAC	TAGCCCCAGA	CTACCTGCCT
10	CTCAATTCT	AATTATATCA	GTGAAAGCAA	ACAGCTTGA	TTTGTITAAG	CCTCTGATTT	TTTGGTCTAA
	CTGATGTAAG	ACCACAAGGA	CAAGAGTCT	CCAGCTCCGG	ATTCTCTCT	GTTCTGTTAA	TGGTAAAATG
	CCCGAGAGAA	GAG' TGCCAA	CTTGGCAAA	TAACAAATAC	AGGATTCCAG	TTAAATTCAA	ATTTAGATAA
	ACAACAATT	TTAGTATTA	GTGTGTCCCA	TTCAATATT	GGACATACTT	AACTAAAAAA	TGATTTGTG
	TTCATCTGAA	ATACAAATT	AACTGGGCAT	TCTGAATATT	CTCTGGCA	CCCCGAGAGA	GTGAAGAAAG
15	TGGTACAAGG	ACACTTAAGA	AGACCAGATT	TGAAAAGACA	TTACGGATGT	GTTAAATGT	CTTATTCTAG
	AGAGAGTTAG	AGCT' TAGGT	AGAACTTGGG	AAATTAAGTT	AAAAGCAGAC	ACAGAGACCT	GGCCAATATA
	TACTAAGGAG	TGGATCACTC	TGGTCACAAG	CCCAACCTGA	GACCAAGGGC	ATAGTGAGAT	GATTTGGGAA
	AGGCACTTAT	ACACTACTCA	TCCCCGTCTT	TGAACAAAT	GCCTTATAAA	TCTCCAAGAG	AAATGACAGT
	CCACCATGTG	GAC' GCTTT	TGTAAGTCCA	GGGAAAATAA	AAGCTATGT	CTTGAACACC	ACTTCTGATA
20	TTATAAGGTG	TGTC ATCTTT	GTCATGTTAA	TGGGCTGAG	TATCAATTCT	ACAATTGTA	AGTGACAGTA
	ATGGTGTGTC	CCCA GGTGT	TGTGAAAGC	TTGATTCTTA	ATGCAACAGT	AGGAAACCCC	AGCCTCTCTG
	GAGCAAACAC	CCT' CTACAT	CTTACTTCC	CCTGCACATT	GGCAGGACTC	TATTCCTCTA	TTTCTCTCTA
	GTGCTAGAGC	AGA AGGGAC	CTTGATTGA	TATCAGGAAA	ATCTATTCT	GAACCATAAG	CTATGATAGC
	TGATTAAAAA	AAT' GACTAT	CATGACATGA	TAATGATCAT	AATGGTAATA	CATATTGATA	GGGTTGCCGT
25	GAAAGTAATA	ATA ATCTAA	GAGTTGTGAC	AATATATGAT	ACGCCTAGAC	TCTCAGAAAA	TGCTAATTCC
	AATCCAATT	GCTTTTGCA	TAAAGTCTG	TCCTAGGGTC	TGTTCTTT	CCACATCTAC	CCTCCTTGA
	TCTCTCTTCT	GTCTTTCA	TGTGGTTCAG	AGGAGGAGAG	AGATCCAGGT	CAATGTTTT	CAAATTACAA
	GGAATTATCA	TTTAAATGGG	GAAGAACGTC	AAAGTTTGAC	GTGTAGTGG	ATTGGAGTGG	AGTGGAGTGG
	AATGGAAACT	AACAGGAAGA	CACTGCACAT	GGTTAAGATA	AAGATTGTTT	CCTGAAACCT	TTAATTGTG
30	CTTACATACT	CAC CATACA	TATGTGCATG	CACTGGACT	CTGCAATATG	CATTCTGAC	TATGGAACAT
	AGCCATAAAA	GTC TTGCA	TGAACGTTCA	GTGGGCTTT	CACAAGCTG	CCTAATTGGG	AAAGAAAAC
	ATGGTCCTC	CATT CCTGC	CCCCAACTCC	AGAAAAGTC	CCATAGTTGA	GGGTACATCT	GAGAAGCCAG
	CACTGGGAG	TTCA GGGCTC	AAGTCCCTT	CTAGAAAAC	ACTGGGTGAT	TCTAGGGAA	CTTCCGATCA
	GAAACAGCCA	ATT' AGAGTG	AGAGAAGAAA	ACGTGACCAT	GCAGTTCTG	TGGTACCAAG	CCTTGCCTCT
35	CTCTTGCTT	CTGG GAGTTA	TTAAACCCAA	GACTGGAAAG	AAAAACCAGC	ATTGCTCAG	GCAGCCTCTC
	TGGGAAGATG	CTG CTTCTC	CTCTCCCCCT	GCTGCTCTT	CTCTTGTGCT	CCAGAGCTGA	AGCTGGTGAG
	TATCAGGGTT	CTTC CCTCTG	AAATCTGAG	TATCAGCTCC	TGAAACAAAG	ATGTTAGTC	TGAAATAGCT
	GACTCTAAA	CAGG GTTCCA	AGATCTCT	TCAAGAGTCC	CACAGAGGAA	ATTCCACTT	GGGATGTGTG
	CCACCCACC	CCC CCCCA	CCC ACTGCCA	TTCTCTACAG	CCTAGGACAC	CCCCAGGAAC	AAGGAATTTC
40	ACCTCAATTG	TAG AAAAGCC	CAGAGCAAGT	GGAAGGAAAA	GGGGTATCCC	CAGGAAAACA	GACATGTCT
	CTTAATCTTC	TGAC CATCG	GGCTACCCAT	TACTTTGTGA	CTTCTCACT	CTGTGACCAT	GCTCAAGAGC
	TATGGAGAAA	TCTA AAACAG	GAACCTGGAC	AGTGGGTCTT	ACACAGAGAC	AGAGGAGAGT	GGGCCAGGGC
	AAGGTGGGAG	TGGGAGAAAGT	CTGAGATGAA	AAACATCAGAA	TGGAGCAGAG	GCAAGAATGA	GATTCACCT
	GGGAGGTTAT	GGG TGGGAA	AGATACGAA	TACAGGAGAC	AGGAGAGGGA	AGATGGGCAG	AACACAGGGT
45	GAGAATGAGA	TTCCAGGGAA	GCCTAGCTA	GCTTAAACCC	AATTGTCCA	TTCATTGGAG	AGAGTATCTA
	TGGCCGTGTT	CAA CCTTGG	GGT GCTCTGT	TCCAGGGGAG	ATCATCGGG	GCACAGAAATG	CAAGCCACAT
	TCCTGCCCT	ACAT' GGCCTA	CCTGGAAATT	GTAACCTCCA	ACGGTCCCTC	AAAATTGT	GGTGGTTTC
	TTATAAGACG	GAAC TTTGTG	CTGACGGCTG	CTCATTTGTG	AGGAAGGTGA	GACAACAGGG	TCTATTTATC
	TCCAAATGGG	AGAT' GAACAA	CCAGAGTAGC	ATCCAGGAAT	ACACCTGCAC	TGGGGACTGA	AGAGGGGTC
50	CTGGGTCTT	TCA A CTTCA	GGAGAGGGAA	GACTTTGGG	TGAAAGACTT	TAGTCTGTGT	TTGAATAGTT
	CCTTGAGCCT	CAGI CACTGA	GCTAAGCTCC	CTTCGGAGGA	AAAGGAGGTC	CTGCGAAG	GTCCTCTTG
	TTGCAGTAGC	ACCC CTCACC	CCTACCCAA	TCAAGACACA	CGGCTCACTT	TTCAGGGCCC	CACCCAGTCT
	CAGGGCCACT	TCTC' CTATGG	CCTTTCAAG	AAACACTGGCT	CTAGTTCTCA	GGGTCTGAA	CCCATCATT
	TATGGGAGCA	GAG AACAGGT	CTACATAAGA	CCCCCACTTT	CCC GTTTAA	CTGATATCTC	CTGCTTCAGG
55	GGCTGGCCCT	CATC CAGGGT	TCCCTGAATT	AGGAAGTGTG	AACCCGTCC	CCTGAGTCCT	CCCTGGCCCTG
	TTCAGTCCC	AGCA ATTCAA	GGGGTCGTAG	AAATTGTGTC	TGTTCTG	GAAAGCTTT	TCATGAGTTA
	AGCCTGAGCC	CTCA AATGCC	ACAAGTGGCC	CATGAAAAGG	GAGATGGTA	GAGTCCGGCN	ACCCAGTGAC
	AGAGTTTAGT	CCTC' TTTCT	CAGAATGAGC	TCACCTCAGA	AGAAACCCCA	AGCCATCACT	GTCGCTCTCT
	TTTCTCTCCT	TCTC CTCAC	AGCAGGTCTA	TAACAGTCAC	CCTTGGAGCC	CATAACATAA	CAGAGGAAGA
60	AGACACATGG	CAG AGCTTG	AGGTTATAAA	GCAATTCCGT	CATCCAAAAT	ATAACACTTC	TACTCTTCAC
	CACGATATCA	TGT ACTAAA	GGTGACAAAC	CCTCTCTTCT	CCCTTTCCAC	TTCCCATTCT	CCTAAGCTTC
	TCCTCAGGT	CCTC ATTGCC	CTGAATT	CTTAGGACTT	GGCTATAACA	TGAAGCTACT	CACCCGTGTC

	CTCCCTGATC	ACCTCCAAT	GTCCAGAGCC	CATTTCGAGG	ACTGACAGTC	CTTCATTCCC	TTCACAGTTG
	AAGGAGAAAG	CCAGCCTGAC	CCTGGCTGTG	GGGACACTCC	CCTTCCCAC	ACAATTCAAC	TTTGTCCCCAC
5	CTGGGAGAAT	GTGCCGGGTG	GCTGGCTGGG	GAAGAACAGG	TGTGTTGAAG	CCGGGCTCAG	ACACTCTGCA
	AGAGGTGAAG	CTGAGACTCA	TGGATCCCCA	GGCCTGCAGC	CACTTCAGAG	ACTTGACCA	CAATCTTCAG
10	CTGTGTGTTG	GCAATTCCCAG	GAAGACAAAAA	TCTGCATTTA	AGGTGATCCT	CCAATAGGT	TTCCCTCTCCA
	AAACTCACTG	TTCAAGGGACC	TGAATGCTCT	TAGAAGGAGA	TGGGGTCAGC	AGGTGTCAG	TCAGGTGACA
	GGGTGAGCAT	CACAGGAATT	GCTGTCCTCC	CGTGGTCCAA	GACAGCCTCT	GACCATCCAT	TCCAGTCTAC
	TGCACTGGGG	GCA1GGGGTG	ACTGTGGAGA	ATGTGGATGA	CGGTCCCAAG	AAAGGAAGAA	GGGGCATCAG
15	AACTAGATGT	ATAA GTGAGG	AGCTCACCT	CCTGGGTCTG	ACTTTAGGTC	TCACTGTGAC	TCCAAGCTGG
	CTGGCAGACA	GGAGTGGAGG	ACTTCCCGG	CTCACCTCT	TCTCTCTC	CTCCCCCTAC	AGGGAGACTC
	TGGGGGCCCT	CTTCTGTGTG	CTGGGGTGGC	CCAGGGCATC	GTATCCTATG	GACGGTCGGA	TGCAAAGCCC
	CCTGCTGTCT	TCACCCGAAT	CTCCCATTAC	CGGCCCTGGA	TCAACCAGAT	CCTGCAGGCA	AATTAATCCT
20	GGATCCTGAG	CCAC CCTGAA	GGGAAGCTGG	AACTGGACCT	TAGCAGCAA	GTGTGTGCAA	CTCATTCTGG
	TTCTACCCCT	GGTT CCTCTA	GCCACAAACC	TAAGCCTCA	AGAGGTCTCC	TACAGGTAAC	AGAAACTTCA
25	ATAAACTTCA	GTGAAGACAC	AGCTTCTAGT	CGTGAGTGTG	TGTCCCTCTC	TGCTGCTCTC	TTCTCCTGCA
	CATGTGACCT	GATTC CCAGC	CCAAGCACCAGG	ATCATGGGGG	GCACAGAACATC	CAAGCCACAT	TCCC GCCCCCT
	ACATGGCCTA	CCTCGAAATT	GTAACCTTCA	ACGGTCCCTC	AAAATTGTTGT	GGTGGTTCC	TTATAAGACG
	GAACCTTGTG	CTGACGGCTG	CTCATTGTGC	AGGAAGGTCT	ATAACAGTCA	CCCTTGGAGC	CCATAACATA
	ACAGAGGAAG	AAGACACATG	GCAGAACCTT	GAGGTTATAA	AGCAATTCCG	TCATCCAAA	TATAACACTT
30	CTACTCTTCA	CCACGATATC	ATGTTACTAA	AGTTGAAGGA	GAAAGCCAGC	CTGACCCCTGG	CTGTGGGAC
	ACTCCCCCTC	CCATCACAAT	TCAACTTTGT	CCCACCTGGG	AGAATGTGCC	GGGTGGCTGG	CTGGGAAGA
	ACAGGTGTG	TGAAGCCGGG	CTCAGACACT	CTGCAAGAGG	TGAAGCTGAG	ACTCATGGAT	CCCCAGGCT
	GCAGCCACTT	CAGAGACTTT	GACCACAATC	TTCAAGTGTG	TGTGGGCAAT	CCCAGGAAGA	CAAATCTGC
35	ATTTAAGGGA	GACTCTGGGG	GCCCTCTCT	GTGTGCTGGG	GTGGCCAGG	GCATCGTATC	CTATGGACGG
	TCGGATGCAA	AGCCTCCCTG	TGTCTCAC	CGAATCTCCC	ATTACCGGCC	CTGGATCAAC	CAGATCCTGC
	AGGCAAATTA	A-3' (FRAG. NO:1887) (SEQ. ID NO:3015)					
	5'-ATCATCGGGG	GCACAGAACATC	CAAGCCACAT	TCCCGCCCCCT	ACATGGCCTA	CCTGGAAATT	GTAACCTCCA
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40	AGGAAGGTCT	ATAA CAGTCA	CCCTTGGAGC	CCATAACATA	ACAGAGGAAG	AAGACACATG	GCAGAAAGCTT
	GAGGTATAA	AGCAATTCCG	TCATCCAAA	TATAACACTT	CTACTCTTCA	CCACGATATC	ATGTTACTAA
	AGTTGAAGGA	GAAAGCCAGC	CTGACCCCTGG	CTGTGGGAGC	ACTCCCCCTC	CCATCACAAT	TCAACTTTGT
	CCCACCTGGG	AGAA TGTGCC	GGGTGGCTGG	CTGGGGAGA	ACAGGTGTG	TGAAGCCGGG	CTCAGACACT
45	CTGCAAGAGG	TGAAGCTGAG	ACTCATGGAT	CCCCAGGCC	GCAGCCACTT	CAGAGACTTT	GACCACAATC
	TTCAGCTGTG	TGTGGGCAAT	CCCAGGAAGA	CAAATCTGC	ATTTAAGGGA	GACTCTGGG	GCCCTCTTCT
50	GTGTGCTGGG	GTGGCCCGAGG	GCATCGTATC	CTATGGACGG	TCGGATGCAA	AGCCCCCTGC	TGTCTTCACC
	CGAATCTCCC	ATTACCGGCC	CTGGATCAAC	CAGATCCTGC	AGGCAAATTA	A-3'(FRAG.NO:)(SEQ.ID NO:2468)	
	5'-TCCCAGTTAA	TA CATAATCA	ATATGCAATT	TATTAATACA	TCTCTCCATG	TCCACTCCCC	CTGTATCTG
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55	GCATTTCCA	GAAA AAAAAG	TGAAGGGCTG	GGAGCTGTCC	GTTGCTCTGA	TTTGTCTCCCT	CTGCCCTTGC
	TTCCAATATG	GGTIGGAAAG	AAGCACTATT	AAAAAAATCCC	TAAACGCACC	CCTGCAGGGT	TGGCTCTACC
	CTGTAGCCAT	GGACACATGC	TGTTGATACC	ACCTGCCTCA	TGAGTCTCAC	ATAATTGCCC	CTTTCACACT
	ATCTACCCCA	TCAC CTTAC	AAAACCATA	CCTGCATCCT	GGGCAGCATC	TGCCCTCAA	GAGACTAAGG
	AATCTCTTG	CAAC CAAGAA	TGACTAGACC	AATGAGACAC	CCTTTAAGGC	CCCAGCACAA	TATAGAAATC
60	CCACAATATG	GTAATCCCGAG	TAAGGAGCTA	TCAAGCCATT	GCAGGACCAT	CTAGAATACA	ACTAGAGTAT
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	ATCAGGGCTG	AGCCTGTGAG	CACCACTGCC	ACCACTGACA	CCAACCACAG	ATTAACACAAG	CATCTTGTTG
	ACCCCTGGG	TGGAAAGAAT	AGTTGTTGCC	TTATCAACCT	CCCCCACAGC	CCACACAGAA	AAGATAAAAT
	CATCATGGCT	ACACTGTTAC	AGAAGATGAT	GACCAAGGA	GTAGGCCTGC	CTGAGTGAAT	GCTGAGAGTG
	ATAATGGGAG	CAGAGCATC	TCAGAGACTA	CAGCAGAAAC	CATCCACATA	AAGAGTTTG	CCCAAACCTA
65	TGATAAAGGG	CACCCCTCAGA	GAECTCCCT	ACTTTAATAT	TAGCCCATTG	CAGAAATGGT	GAGTGGAAAG
	AGAAAATCTTA	GGAAGAACCC	CTTAAAAAAG	CAAAATGCTT	TTTAGGTTTG	TGCTGAAGAG	CCTGGAAAAG
	AAATAAGGAC	ACA CACGCTG	AGAAATCTTC	CTCCTGCC	AAACACTGGGA	TAATCTCAA	GGATCTCTCC
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70	TTTATAGATG	TTTAATGTAA	GCCAGCAGCT	ATTAACACGAT	AAACCTTAA	TTCGAGAAAA	ACTTGGTCAT
	TCAGAAACTA	TAGAACAGG	CAGGACTTAT	TGCGAGGGCA	AACACAGAGT	GAGCTCCAGC	CTGCTTCAGG
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	ATACCTGCCA	ACTC GAGGGT	AAAACAAGT	TGCA TAGAAA	TGCTCAATCA	AGAAAGACAC	AGTCATTACT
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	AACCAAATT	CATACAGAT	GTTAATCTGT	AATGTGTTTA	GGAGAATT	GAGGAAGTAT	AAGATTATT
75	CTTCATCAA	AAAATTATA	GCCAATGAGG	ATATATCTAT	CAATTATCCA	TCAAGTGGTG	ATATGGCAGC

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5	CCCATCTAAC	TGCAGAGCAA	ACTGCATGCC	TTAAATGTCA	AAGTGAATAC	TAGCACAGTT	AATACAATGT
	TTGGAAACTC	AGAGAAGGAA	TGATCCCTCT	GCATTATAGT	TACTAAGGAA	TCATTGCCAT	TATTTAAATG
	CCAGTGCTTC	TACPTCAGGC	CCAAATTTC	TGTCTACTA	ACTGTGAATC	AAGACCTGAT	TCAACCTCTA
	CTTGAGTATC	TGCCGCAATG	AGAAAATCACT	TACCTCCACT	AACCACACAT	TTATTTATA	ACAACAGATT
	GTTAGTAAGT	CCTITCTTAT	ACATACTCAA	CAGCTGCTTC	CCAAGATGCT	GTAGGATTAT	GTCTAGAGTC
10	AAACTAGCCA	GAAGCAATGT	CCAAATACAA	CCATAACACT	GTGCAGCAA	GGTCTACTA	CCACTTGTTC
	GGCCAAACAA	TTCTAGGCAG	CACTGGATAT	CTGAATCATC	AATTATTC	ACAAACACTG	ACCCCTCTAC
	CAGTCACCCCT	CACTAGAAGA	ATTAATTCCA	CATGATAATA	GCTCCCTCAT	GTТАCTCCCT	TCTAAGTCAA
	ATTGTACACC	CCTTATCTG	ATTAACAGAG	TCTAAGTCAC	ATGACCTAA	TGCAAGAGAA	CTGGGAATGG
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15	CAGAGACATT	AAGGAGCCAT	ATAAAATGAA	AATGTCACACT	ACAATCCATC	ACTTGGTGC	CCCACATCAA
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	TTAACTTCAA	GTACTGTGTC	TCTAGGTGAT	ACCTGCTCCA	ACAATAGTT	GGTCACATTT	TCAATTGTAT
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20	AAATAACAAA	GGGGGAAGAA	GAAGAGAAA	AAGGAAATCT	CTTAAAATAC	ACAGGTATAC	ATATGACAAA
	GCAAGAAGG	AAA'TGTGAGC	AGATAGTGC	GTCTCGTTT	CTGAAATTGG	TCCCCGTACT	GGGGCTATAC
	CTATTCATT	TCCTCACCCCT	CAGCCAGGCA	GGTGGAGCAA	AAACTTAAGT	CTTGGTGGAT	CTGAATCTTG
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25	CCAGCTCCGG	ATTCTCTTCT	GTTCGTAA	TGGTGAATG	CCCGAGAGAA	GAGTTGCCAA	CTTTGGCAA
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30	AAATTAAGTT	AAA'GCAGAC	ACAGAGACCT	GGCCAATATA	TACTAAGGAG	TGGATCACTC	TGGTCACAAG
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	TGGGTCTGAG	TATCAATTCT	ACAATTGTAA	AGTACAGTA	ATGGTGTGTC	CCCAGGTTGT	TGTGGAAAGC
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	CCTGCACATT	GGC'GGACTC	TATTCTCTA	TTTCTCTA	GTGCTAGAGC	AGAAAGGGAC	CTTGATTGAA
	TATCAGGAAA	ATC'ATTCT	GAACCATAAG	CTATGATAGC	TGATTTAAA	AATTGACTAT	CATGACATGA
	TAATGATCAT	AATCTGAATA	CATATTGATA	GGGTTGCCGT	GAAAGTAATA	ATATATCTAA	GAGTTGTGAC
	AATATATGAT	ACGGCTAGAC	TCTCAGAAAA	TGCTAATTCC	AATCCAATT	GCTCTTGCA	TAAAGTTCTG
40	TCCTAGGGTC	TGTCTTTTC	CCACATCTAC	CCTCCTTGG	TCTCTCTT	GTCTTTTCA	TGTGGTTCA
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	AAGTTTGAC	GTGTAGTGG	ATTGGAGTGG	AGTGGAGTGG	AATGGAAACT	AACAGGAAGA	CACTGCACAT
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45	GTGGGCTTT	CACAAGCTGC	CCTAATTGGG	AAAGAAAAAC	ATGGTCCCTC	CATTCCCTGC	CCCCAACTCC
	AGAAAAGTC	CCA'AGTTGA	GGGTACATCT	GAGAAGCCAG	CACTTGGGAG	TTCAGGGCTC	AAGTTCTTT
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	ACGTGACCAT	GCAGTTCCCTG	TGGTTACCG	CCTTCCCCCT	CTCTTGCCTT	CTGGGAGTTA	TAAAACCCAA
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	TATCAGCTCC	TGAAACAAAG	ATGTTAGTC	TGAAATAGCT	GACTCTAAA	CAGGGTTCCA	AGATCTCTT
	TCAAGAGTCC	CACAGAGGA	ATTCACCTT	GGGATGTGTG	CCACCCCA	CCCACCCCCA	CCCACTGCCA
	TTCTCTACAG	CCTA3GACAC	CCCCAGGAAC	AAGGAATTTC	ACCTCAATTG	TAGAAAAGCC	CAGAGCAAGT
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55	AGTGGGTCC	ACACAGAGAC	AGAGGAGAGT	GGGCCAGGGC	AAGGTGGAG	TGGGAGAAGT	CTGAGATGAA
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60	TCCAGGGAG	ATCATCGGGG	GCACAGAATG	CAAGCCACAT	TCCC GCCCT	ACATGGCTA	CCTGGAAATT
	GTAACCTCCA	ACGCTCCCTC	AAAATTGTTGT	GGTGGTTTCC	TTATAAGACG	GAACCTTGTG	CTGACGGCTG
	CTCATTGTGC	AGGAAGGTGA	GACAACAGGG	TCTATTATC	TCCAAATGGG	AGATGAACAA	CCAGAGTAGC
	ATCCAGGAAT	ACAC'CTGCAC	TGGGGACTGA	AGAGGGGGTC	CTGGGTCTG	TCAACTTCA	GGAGAGGGAA

GACTTTGGC TGAAGAGACTT TAGTCTGTGT TTGAATAGTT CCTTGAGCCT CAGTCACTGA GCTAAGCTCC
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 15 CATTCTGAGG ACTC ACAGTC CTTCATTCCTC TTCACTGGT AAGGAGAAAG CCAGCCTGAC CCTGGCTGTG
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 25 CCAGGGCATC GTATCCTATG GACGGTCGGA TGCAAAGCCC CCTGCTGTCT TCACCCGAAT CTCCCATTAAC
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 CGTAGTGTG TGTCCTCTC TGCTGCTCTC TTCTCCTGCA CATGTGACCT GATTCCCAGC CCAAGCACCA AGGA-3'
 (FRAG. NO:) (SEQ. ID NO:2467)
 30 5'-GGBGCBGBG-3' (FRAG. NO:1888) (SEQ. ID NO:1901)
 5'-GBBGBGCG-3' (FRAG. NO:1889) (SEQ. ID NO:1902)
 5'-GGGGCBBGG CG-3' (FRAG. NO:1890) (SEQ. ID NO:1903)
 5'-CGTTTCTTCTCTC-3' (FRAG. NO:1369)(SEQ. ID NO:1378)
 5'-GCTGGTTTCTTCTC-3' (FRAG. NO:1370)(SEQ. ID NO:1379)
 35 5'-TGGCAGTGGGTGGGGTGGGGTGGC-3' (FRAG. NO:1371)(SEQ. ID NO:1380)
 5'-TTCCTGTTCTGGGGTGTCTC-3' (FRAG. NO:1372)(SEQ. ID NO:1381)
 5'-CTTGCCTGGGCTTTCT-3' (FRAG. NO:1373)(SEQ. ID NO:1382)
 5'-CCCCTTTCTTC-3' (FRAG. NO:1374)(SEQ. ID NO:1383) [
 5'-TGTCTGTTCTGGGG-3' (FRAG. NO:1375)(SEQ. ID NO:1384)
 40 5'-CTCTCCTCTGTCTGTGT-3' (FRAG. NO:1376)(SEQ. ID NO:1385)
 5'-CCTGCCCTGGCCC-3' (FRAG. NO:1377)(SEQ. ID NO:1386)
 5'-TCTTCCCTCTCTGTCTCTGT-3' (FRAG. NO:1378)(SEQ. ID NO:1387)
 5'-CCCTGTGTTCCGCC-3' (FRAG. NO:1379)(SEQ. ID NO:1388)
 5'-GTCTTCCCTCTCTG-3' (FRAG. NO:1380)(SEQ. ID NO:1389)
 45 5'-ACCTCCTTTCTCCCG-3' (FRAG. NO:1381)(SEQ. ID NO:1390)
 5'-CTGGGTGGGGCCCTG-3' (FRAG. NO:1382)(SEQ. ID NO:1391)
 5'-CCTGTTCTCTGCTCCC-3' (FRAG. NO:1383)(SEQ. ID NO:1392)
 5'-TGGCTGGGGTTCTCTG-3' (FRAG. NO:1384)(SEQ. ID NO:1393)
 5'-TGTGTCCTCTTCTCTGTT-3' (FRAG. NO:1385)(SEQ. ID NO:1394)
 50 5'-GGCTGGCTTCTCCCTTC-3' (FRAG. NO:1386)(SEQ. ID NO:1395)
 5'-TTTGTCTTCTGGG-3' (FRAG. NO:1387)(SEQ. ID NO:1396) [1397]
 5'-TGCCCCCTCTTCTCTTCTGGG-3' (FRAG. NO:1388)(SEQ. ID NO:1397)
 5'-TCCTTGGTGCTTGC GCTGGG-3' (FRAG. NO:1389)(SEQ. ID NO:1398)
 5'-GGBGCTGBTB CTGCBGATT CBGBGGBBG BBCCCTGBTB CTCBCCBGCT TCBGCTCTGG BGBCBGBG
 55 BBBGBGCBGC BGGCGBGBG GBBGBGCBG CBTCTCCCB GBGBGGCTGC CTGBGCBBT GCTGGTTTC
 CTTCCBGTC TTGGGTTTB TBBCCTCCBG BBGGCBBGBG BGGGCBGBG BGGGCBGBG-3' (FRAG.NO:1891) (SEQ.ID NO:1904)

Endothelial Nitric Oxide Synthase Nucleic Acids and Antisense Oligonucleotide Fragments

5'-GCGCTTGGG GTGCBGGGCC CBTCCTGCTG CGCCTGGCG CTGCTGTGCG TCCGCTGCT GGGGGGCCGG
 GGTGGCTGGG CCCCTGCTTGC CGCACGACCC CGGGCCGACC CGAGGCTCGG GGGGCTGTGT TCTGGCGCTG
 60 GTGGGCTTGG GCCCTCTCTGG GGGCTGGGTT TCCCTGCTGCG CCTGGGCCT GGCCTCTTGG GGTGCGGGGC
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GCCGTCTGC TGCCGGTCGT TGGCTGGTC CCCCCGCCG TTTCTGGGG TCCCGTGGG GTGCTCCGGT
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 10 CGGGTCTCTCC GGGCTGCCCT TCTCCGCCGG GGGTCCCAGC CTCCCTGCTGT CCTCTGGGCT CTTCTGCCTC
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 25 TGTCTGGGC GGCC GCCTTG GCGCTCCGTT TGGGGCTGCC TCTGGCGCTT CGGCCCTCG GCCTGGCGC
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 CGCGCTCTG CTGTCCTCG GGCTCTCTG CCTCTCTCCT GGGTGGGTGC TGGGTGCCGG GGTCTCCGGG
 CTTGCCCCGC GCTCTGGGC GTTCTGGGT CTTGGGGTTG TCTGTGGGCC CGCTCGTGTG GCCCTCCGTC
 GCCCGTCGCC GGCCI CGTCC CCTCCTGGGT GCGCGGGGG CTGGCTCTGG CGTTTGCTC CTTCTGG-3' (FRAG.
 NO:1892) (SEQ. ID NO 1905)
 5'-GCAGGGGCGC-3' (FRAG. NO:1893) (SEQ. ID NO: 1906)
 5'-CGGGGGGC-3' (FRAG. NO:1894) (SEQ. ID NO: 1907)
 5'-GCGCGGGGGC-3' (FRAG. NO:1895) (SEQ. ID NO: 1908)
 30 5'-CTGTGCGTCCGTCGCTGG (FRAG. NO:1390)(SEQ. ID NO:1399)
 GGGGCGGGGGTGGCTGGGCCCTGCTTGC (FRAG. NO:1391)(SEQ. ID NO:1400)
 ACGACCCCGGGGCCACCGAG (FRAG. NO:1392)(SEQ. ID NO:1401)
 GCTCGGGGGGCTGTG ITCTGGCGCTGGTGGG (FRAG. NO:1393)(SEQ. ID NO:1402)
 CTTGGGGCCCTCTGGGGCTGGGTT (FRAG. NO:1394)(SEQ. ID NO:1403)
 35 TCCCTGCTGCGCCTGGCGCTG (FRAG. NO:1395)(SEQ. ID NO:1404)
 GCGCTTGGGGTGC (FRAG. NO:1396)(SEQ. ID NO:1405)
 GGGGCGGGGGGCC GGGG (FRAG. NO:1397)(SEQ. ID NO:1406)
 GCCGCTTCTCGTGGG CCTGGG (FRAG. NO:1398)(SEQ. ID NO:1407)
 GGTGCCTGTGGCTGCC (FRAG. NO:1399)(SEQ. ID NO:1408)
 40 GGTGCCCCGGTTGGTGGC (FRAG. NO:1400)(SEQ. ID NO:1409)
 GCCGCTCTGCTGCCGT (FRAG. NO:1401)(SEQ. ID NO:1410)
 CGTTGGCTGGTCCCCCGC (FRAG. NO:1402)(SEQ. ID NO:1411)
 CCGTTCTGGGGTCC (FRAG. NO:1403)(SEQ. ID NO:1412)
 GCGTGGGGTGCCTCC (FRAG. NO:1404)(SEQ. ID NO:1413)
 45 GGTTCCTCGTGCCTG (FRAG. NO:1405)(SEQ. ID NO:1414)
 CTGCTGCCCTGTCTTIC (FRAG. NO:1406)(SEQ. ID NO:1415)
 GGCCTGGCGGGCGTGGTCC (FRAG. NO:1407)(SEQ. ID NO:1416)
 GCCCCCCTGGCCTCTGCTC (FRAG. NO:1408)(SEQ. ID NO:1417)
 GGGGTCTGGCTGGT (FRAG. NO:1409)(SEQ. ID NO:1418)
 50 TGCCTGGTGCCTTGGCG (FRAG. NO:1410)(SEQ. ID NO:1419)
 GGTCTTCTCTGGT (FRAG. NO:1411)(SEQ. ID NO:1420)
 GCTCTGGGCCCGGCCG (FRAG. NO:1412)(SEQ. ID NO:1421)
 GCGTCTCGTGTTCG (FRAG. NO:1413)(SEQ. ID NO:1422)
 CTCTTGCTGTCTTCCC (FRAG. NO:1414)(SEQ. ID NO:1423)
 55 CTCCCTCTCTCCGCC (FRAG. NO:1415)(SEQ. ID NO:1424)
 GCCGCTCCCCGCC (FRAG. NO:1416)(SEQ. ID NO:1425)
 GCTCGTCGCCCTGGGCC (FRAG. NO:1417)(SEQ. ID NO:1426)
 GGCCTCCCTGGGCCGC (FRAG. NO:1418)(SEQ. ID NO:1427)
 TGTCTGGGGCGGCCG CCTTGGC (FRAG. NO:1419)(SEQ. ID NO:1428)
 60 GCTCCGTTGGGGCTG (FRAG. NO:1420)(SEQ. ID NO:1429)
 CCTCTGGCGCTTCC (FRAG. NO:1421)(SEQ. ID NO:1430)
 GGCCTCGGCCCTGG CGCTC (FRAG. NO:1422)(SEQ. ID NO:1431)

TCTTCCGCCCTGTGC (FRAG. NO:1423)(SEQ. ID NO:1432)
 TGGTGGCCCTCGTGG (FRAG. NO:1424)(SEQ. ID NO:1433)
 GCCCCTCCTGGCCTCCGGTGTCC (FRAG. NO:1425)(SEQ. ID NO:1434)
 TGTGGTCCCCCGGCTGGT (FRAG. NO:1426)(SEQ. ID NO:1435)
 5 GGCGGGGCCGGTTGGGCAGGGC (FRAG. NO:1427)(SEQ. ID NO:1436)
 GTGGGCGCCGGCGGGTCCTCC (FRAG. NO:1428)(SEQ. ID NO:1437)
 GGGCTGCCCTCTCC (FRAG. NO:1429)(SEQ. ID NO:1438)
 GCCGGGGGTCCCAGC (FRAG. NO:1430)(SEQ. ID NO:1439)
 GCTCTGCTGTTCTCTGGGCTCTGCC (FRAG. NO:1431)(SEQ. ID NO:1440)
 10 TCTCTCTGGGTGGGCTGGG (FRAG. NO:1432)(SEQ. ID NO:1441)
 GGGTCTCCGGGCTTG (FRAG. NO:1433)(SEQ. ID NO:1442)
 CCCCGCGCTGCTGGCGTCTGCC (FRAG. NO:1434)(SEQ. ID NO:1443)
 GGTCTTGGGTGTGTC (FRAG. NO:1435)(SEQ. ID NO:1444)
 TGTGGCCCCGCTCG (FRAG. NO:1436)(SEQ. ID NO:1445)
 15 TGTGCCCTCCGTCGCC (FRAG. NO:1437)(SEQ. ID NO:1446)
 CGTCGCCGGCCTCGTCC (FRAG. NO:1438)(SEQ. ID NO:1447)
 CCTCTGGGTGCGC (FRAG. NO:1439)(SEQ. ID NO:1448)
 GGCGGGCTGGTCCT (FRAG. NO:1440)(SEQ. ID NO:1449)
 GGCCTTTGCTCCTCTGG (FRAG. NO:1441)(SEQ. ID NO:1450)
 20 5'-GCGTCTGGGTGCBGGGCCBCTCTGCGCTGGCGCTG-3' (FRAG. NO:1896) (SEQ. ID NO: 1909)

Inducible Nitric Oxide Synthase Nucleic Acids and Antisense Oligonucleotide Fragments

5'-CTGCCCGCBGT TT TGBTCCCT CBCBTGCCGT GGGGBGGBCB BTGGCTGCCCT CCCCCGGGTT TCTGCTGCTT
 GCTGCTTCTT TCCCGTCTCC CTTCTTCCC GTCTCCTTT TGCCCTCTTG GGTTCTCTGTT GTTTCTGGCC
 25 TGCTTGGTGG CGCGCTTGTGC GTTCTCTCTC TCTTCTCTG GGTCTCCGCT TCTCGTCTG CCTTTTCTG
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 GGTGCTCCC CCGGGGGCCG GCTGGTTGCC TGGGCCTGTC TGGTGGGTG TGGGGCCGCT GGGTTGGGG
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 CCTCCCTGTG GCTGGGTGCG GCCTCCCCGC CCCCTCTG GGCGGGTGGC CTGGCTCTT GTGGCGCTT
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 CAGTTCTAGA CAGICCCGAA GTTCTCAAGG CACAGGTCTC TTCTGGTT GACTGTCCTT ACCCCGGGA
 5 GGCAGTGCAG CCAGCTGCAA GGTGAGTGC C-3' (FRAG. NO.:) (SEQ. ID NO: 3016)
 5'-CTGCTTAAA ATCTCTCGC CACCTTTGAT GAGGGACTG GGCAGTTCTA GACAGTCCCC AAGTTCTCAA
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 10 CAACAATGTG GAGAACGCC CCTGTGCCAC CTCCAGTCCA GTGACACAGG ATGACCTTCA GTATCACAA
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 15 AAGCTATCGA ATTIGTCAAC CAATATTACG GCTCTTCAA AGAGGCAAAA ATAGAGGAAC ATCTGGCCAG
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5	CATTTTACTT	TAATC	GAATTCCCAC	TCTGCTGCCT	GCTCCAGCAG	ACGGACGCAC	AGTAACATGG
	GAGCGTGGCC	CAGCAGCTG	GGCCACCCCTG	CGGCCCTGGGG	CTGGGGCTGG	GCCTTGGGCT	GTGCGGCAAG
	CAGGGCCCAG	CCAC'CCCAGC	CCCTGAGCCC	AGCCGGGCC	CAGCATCCCT	ACTCCCACCA	GCGCCAGAAC
	ACAGCCCCC	GAGC TCCCCG	CTAACCCAGC	CCCCAGAGGG	GCCCAAGTTC	CCTCGTGTGA	AGAACTGGGA
	GGTGGGGAGC	ATCA.CCTATG	ACACCCCTCAG	CGCCCAAGGG	CAGCAGGATG	GGCCCTGCAC	CCCAAGACGC
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10	AGCTGCTGAG	TCAC GCCCG	GACTTCATCA	ACCAGTACTA	CAGCTCCATT	AAGAGGAGCG	GCTCCCAGGC
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20	CTGGTACATG	AGCA CTGAGA	TCGGCACGAG	GAACCTGTGT	GACCCCTCACC	GCTACAACAT	CCTGGAGGAT
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	CTCTTTCATG	AAGC ACCTGG	AGAATGAGCA	GAAGGCCAGG	GGGGGCTGCC	CTGCAGACTG	GGCCTGGATC
	GTGCCCCCCTA	TCTCGGGCAG	CCTCACTCT	GTTTTCCATC	AGGAGATGGT	CAACTATTTC	CTGTCCCCGG
25	CCTTCGGCTA	CCAG CCAGAC	CCCTGGAAGG	GGAGTGCCTG	CAAGGGCACC	GGCATCACCA	GGAAGAAGAC
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	GCTTCAACAG	CATCTCTGC	TCAGACCCAC	TGGTGTCTC	TTGGCGCGG	AAGAGGAAGG	AGTCCAGTAA
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40	CGCCCACTGA	GCCCCGTGGCA	GTAGAGCAGC	TGGAGAAGGG	CAGCCCTGGT	GGCCCTCCCC	CCGGCTGGGT
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55	GCATACGCAC	CCAGAGCTT	TCCTTGCA	AGCGTCAGT	CGGGGGCGCA	GTGCCCTGGG	CGTTCGACCC
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60	GCCACCCGCT	TCCGTGTTCT	TAGTCCGAAT	GTTAGATTCC	TCTTGCTCT	CTCAGGAGTA	TCTTACCTGT
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5	GCAGAGATCG	TGCC ACTCCG	CTCCAGTCTT	GGTGACAGAA	TGAGACTCCA	TCTCAAAAAT	AAATAAATAA
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	CCATGTGGCT	TGGCCAAATA	AAACCTGGCT	CCGTGGTGC	TCTGTCTTAG	CAGCCACCC	GCTGATGAAC
	TGCCACCTTG	GACTGGGAC	CAGAAAGAGG	TGGGTTGGGT	GAAGAGGCAC	CACACAGAGT	GATGTAACAG
	CAAGATCAGG	TCACCCACAG	GCCCTGGCAG	TCACAGTCAT	AAATTAGCTA	ACTGTACACA	AGCTGGGAC
15	ACTCCCTTG	GAAA CCAAAA	AAAAAAAAAA	AAAAAAAGAGA	CCTTATGCA	AAAACAAC	TCTGGATGGC
	ATGGGTGAG	TATAAATACT	TCTTGGCTGC	CAGTGTGTC	ATAACTTGT	AGCGAGTCGA	AAACTGAGGC
	TCCGGCCGCA	GAGACTCAG	CCTCATTCCT	GCTTAAAT	CTCTGGCCA	CCTTGTGTA	GGGGACTGGG
	CAGTTCTAGA	CAGICCCGAA	GTTCTCAAGG	CACAGGTCTC	TTCTGGTTT	GACTGTCTT	ACCCCGGGGA
	GGCAGTGCAG	CCAGCTGCAA	GGTGAGTTGC C-3'	(FRAG. NO:) (SEQ. ID NO: 2506)			
20	5'-CTGCTTAA	ATCTCTCGGC	CACCTTGAT	GAGGGACTG	GGCAGTTCTA	GACAGTCCC	AAGTTCTCAA
	GGCACAGGTC	TCTCCTGGT	TTGACTGTCC	TTACCCGGG	GAGGCAGTGC	AGCCAGCTG	AAGCCCCACA
	GTGAAGAAC	TCTC AGCTCA	AATCCAGATA	AGTACATAA	GTGACCTGCT	TTGTAAGGCC	ATAGAGATGG
	CCTGTCTTG	GAAATTCTG	TTCAAGACCA	AATCCACCA	GTATGCAATG	AATGGGAAA	AAGACATCAA
	CAACAATGTG	GAGAAGCCC	CCTGTGCCAC	CTCCAGTCCA	GTGACACAGG	ATGACCTTCA	GTATCACAAAC
25	CTCAGCAAGC	AGCA GAATGA	GTCCCCGCG	CCCCCTGTGG	AGACGGGAAA	GAAGTCTCCA	GAATCTCTGG
	TCAAGCTGGA	TGCA ACCCCA	TTGTCTCTCC	CACGGCATGT	GAGGATCAA	AACTGGGCA	GCGGGATGAC
	TTTCAAGAC	ACACTTCACC	ATAAGGCCA	AGGGATTAA	ACTTGCAGGT	CCAAATCTT	CCTGGGTTCC
	ATTATGACTC	CCAAAAGTTT	GACCAGAGGA	CCCAGGGACA	AGCCTACCC	TCCAGATGAG	CTTCTACCTC
	AAGCTATCGA	ATTITGTCAC	CAATATTACG	GCTCTTCAA	AGAGGCAAA	ATAGAGGAAC	ATCTGGCCAG
30	GGTGGAAAGCG	GTA.CAAAGG	AGATAGAAC	AACAGGAACC	TACCAACTGA	CGGGAGATGA	GCTCATCTTC
	GCCACCAAGC	AGGCCTGGCG	CAATGCCCA	CGCTGCATTG	GGAGGATCCA	GTGGTCAAC	CTGCAGGTCT
	TCGATGCCCG	CAGCTGTTCC	ACTGCCCGGG	AAATGTTGA	ACACATCTG	AGACACGTG	GTTACTCCAC
	CAACAATGGC	AAACATCAGG	CGGCCATCAC	CGTGTCCCC	CAGCGGAGTG	ATGCAAGCA	CGACTTCCGG
	GTGTGGATG	CTCAGCTCAT	CCGCTATGCT	GGCTACCGA	TGCCAGATGG	CAGCATCAGA	GGGGACCCCTG
35	CCAACGTGGA	ATTCACTCAG	CTGTGCATCG	ACCTGGGCTG	GAAGCCCAAG	TACGGCCGCT	TCGATGTGGT
	CCCCCTGGTC	CTGCAGGCCA	ATGGCCGTGA	CCCTGAGCTC	TTCGAAATCC	CACCTGACCT	TGTGCTTGAG
	GTGGCCATGG	AAACATCCCAA	ATACGAGTGG	TTTCGGGAAC	TGGAGCTAA	GTGGTACGCC	CTGCTCGCAG
	TGGCCAACAT	GCTCCTTGAG	GTGGCGGGC	TGGAGTTCCC	AGGGTGC	TTCAATGGCT	GGTACATGGG
	CACAGAGATC	GGAGTCCGGG	ACTTCTGTGA	CGTCCAGCGC	TACAACATCC	TGGAGGAAGT	GGGCAGGAGA
40	ATGGGCCTGG	AAACCGACAA	GCTGGCCTCG	CTCTGGAAAG	ACCAGGCTGT	CGTTGAGATC	AACATTGCTG
	TGATCCATAG	TTTCAGAAG	CAGAATGTGA	CCATCATGGA	CCACCACTCG	GCTGCAGAAT	CCTTCATGAA
	GTACATGCAG	AATGAATACC	GGTCCCGTGG	GGGCTGCCCG	GCAGACTGGA	TTTGGCTGGT	CCCTCCCCATG
	TCTGGGAGCA	TCACCCCCGT	GTTCACCAG	GAGATGCTGA	ACTACGTCCT	GTCCCCTTTC	TACTACTATC
	AGGTAGAGGC	CTGGAAAACC	CATGTCTGGC	AGGACGAGAA	GCGGAGACCC	AAGAGAAGAG	AGATTCCATT
45	GAAAGTCTTG	GTCA AAGCTG	TGCTCTTGC	CTGTATGCTG	ATGCGCAAGA	CAATGGCGTC	CCGAGTCAGA
	GTCACCATCC	TCTTIGCGAC	AGAGACAGGA	AAATCAGAGG	CGCTGGCTG	GGACCTGGGG	GCCTTATTCA
	GCTGTGCCCT	CAACCCCAAG	GTGTCCTGCA	TGGATAAGTA	CAGGCTGAGC	TGCCTGGAGG	AGGAACGGCT
	GCTGTGGTG	GTGACCAAGT	CGTTTGGCAA	TGGAGACTGC	CCTGGCAATG	GAGAGAAACT	GAAGAAATCG
	CTCTTCATGC	TGAAAGAGCT	CAACAACAA	TTCAGGTACG	CTGTGTTGG	CCTCGGCTCC	AGCATGTACC
50	CTCGGTTCTG	CGCC TTGCT	CATGACATTG	ATCAGAAGCT	GTCCCACCTG	GGGGCCTCTC	AGCTCACCCC
	GATGGGAGAA	GGGGATGAGC	TCAGTGGGCA	GGAGGACGCC	TTCCGCAGCT	GGGGCGTGCA	AACCTTCAAG
	GCAGCCTGTG	AGACGTTGA	TGTCCGAGGC	AAACAGCACA	TTCAGATCCC	CAAGCTCTAC	ACCTCCAATG
	TGACCTGGGA	CCCCCACCCAC	TACAGGCTCG	TGCAGGACTC	ACAGCCTTG	GACCTCAGCA	AAGCCCTCAG
	CAGCATGCAT	GCCAGAGAACG	TGTTCACCAT	GAGGCTAAA	TCTCGGCAGA	ATCTACAAAG	TCCGACATCC
55	AGCCGTGCCA	CCATCCTGGT	GGAACTCTCC	TGTGAGGATG	GCCAAGGCT	GAACCTACCTG	CCGGGGGAGC
	ACCTTGGGTT	TTGCCAGGGC	AACCAGCCGG	CCCTGGTCCA	AGGCATCTG	GAGGGAGTGG	TGGATGGCCC
	CACACCCAC	CAGAAGTGC	GCCTGGAGGA	CCTGGATGAG	AGTGGCAGCT	ACTGGGTCA	TGACAAGAGG
	CTGCCCCCT	GCTCACTCAG	CCAGGCCCTC	ACCTACTCCC	CGGACATCAC	CACACCCCA	ACCCAGCTGC
	TGCTCCAAA	GCTC GCCCAG	GTGGCCACAG	AAGAGCCTGA	GAGACAGAGG	CTGGAGGCC	TGTGCCAGCC
60	CTCAGAGTAC	AGCAAGTGG	AGTTCACCAA	CAGCCCCACA	TTCTGGAGG	TGCTAGAGGA	GTTCCCCTGCC
	CTGCGGGTGT	CTGCTGGCTT	CCTGCTTCC	CAGCTCCCCA	TTCTGAAGCC	CAGGTTCTAC	TCCATCAGCT
	CCTCCGGGGA	TCACACGCC	ACGGAGATCC	ACCTGACTGT	GGCCGTGGTC	ACCTACCA	CCGGAGATGG
	CCAGGGTCCC	CTGCACCACG	GTGTCTGCC	CACATGGCTC	AACAGCCTGA	AGCCCCAAGA	CCCAGTGCC

	TGCTTGTGC	GGAATGCCAG	CGCCCTCCAC	CTCCCCGAGG	ATCCCTCCCA	TCCTTGATC	CTCATCGGGC
	CTGGCACAGG	CATGTGCCC	TTCCGCGAGT	TCTGGCAGCA	ACGGCTCCAT	GACTCCCAGC	ACAAGGGAGT
	GCGGGGAGGC	CGCATGACCT	TGGTGTGTTG	GTGCCGCCG	CCAGATGAGG	ACCACATCTA	CCAGGAGGAG
	ATGCTGGAGA	TGGGCCAGAA	GGGGGTGCTG	CATGCGGTGC	ACACAGCCTA	TTCCCGCTG	CCTGGCAAGG
5	CCAAGGTCTA	TGTICAGGAC	ATCTCGCGC	AGCAGCTGGC	CAGCGAGGTG	CTCCGTGTC	TCCACAAGG
	GCCAGGCCAC	CTCTATGTT	GCGGGGATGT	GCGCATGCC	CGGGACGTGG	CCCACACCTT	GAAGCAGCTG
	GTGGCTGCA	AGCTGAAATT	GAATGAGGAG	CAGGTCGAGG	ACTATTCTT	TCAGCTCAAG	AGCCAGAACG
	GCTATCACGA	AGATATCTC	GGTGCTGTAT	TTCCCTACGA	GGCGAAGAAG	GACAGGGTGG	CGGTGCAAGCC
	'CAGCAGCCTG	GAGATGTCAG	CGCTCTGAGG	GCCTACAGGA	GGGGTTAAAG	CTGCCGGCAC	AGAACTTAAG
10	GATGGAGCCA	GCTCTGCATT	ATCTGAGGTC	ACAGGGCTG	GGGAGATGGA	GGAAAGTGT	ATCCCCCAGC
	CTCAAGTCTT	ATTICCTCAA	CGTGCTCCC	CATCAAGCCC	TTTACTTGAC	CTCCTAACAA	GTAGCACCC
	GGATTGATCG	GAGCTCTCTC	TCTCAAACGT	GGGCCTCCCT	GGTCCCTTGG	AGACAAAATC	TTAAATGCCA
	GGCCTGGCGA	GTGGGTGAAA	GATGGAACCT	GCTGCTGAGT	GCACCACTTC	AAGTGACCCAC	CAGGAGGGTGC
	TATCGCACCA	CTGTGTATTT	AACTGCTCTG	TGTACAGTTA	TTTATGCTC	TGTATTTAAA	AAACTAACAC
15	CCAGTCTGTT	CCCCATGGCC	ACTTGGGTCT	TCCCTGTATG	ATTCCCTGAT	GGAGATATT	ACATGAATTG
	CATTTTACTT	TAATC 3' (FRAG. NO:) (SEQ. ID NO:2507)					
	5'-GAATTCCCAC	TCTGCTGCCT	GCTCCAGCAG	ACGGACGCAC	AGTAACATGG	GCAACTGAA	GAGCGTGGCC
	CAGGAGCCTG	GGCCACCCCTG	CGGCCTGGGG	CTGGGGCTGG	GCCTGGGCT	GTGCGGCAAG	CAGGGCCAG
	CCACCCCCGGC	CCCTGAGCCC	AGCCGGGCC	CAGCATCCCT	ACTCCCACCA	GCGCCAGAAC	ACAGCCCCCC
20	GAGCTCCCCG	CTAACCCAGC	CCCCAGAGGG	GCCAAGTTC	CCTCGTGTGA	AGAACTGGGA	GGTGGGGAGC
	ATCACCTATG	ACACCCCTAG	CGCCCAGGCG	CAGCAGGATG	GGCCCTGAC	CCAAGAGAC	TGCTGGGCT
	CCCTGGTATT	TCCA CGGAAA	CTACAGGGCC	GGCCCTCCCT	CGGCCCTCCCG	GCCCCCTGAGC	AGCTGCTGAG
	TCAGGCCCGG	GACITCATCA	ACCAGTACTA	CAGCTCCATT	AAGAGGAGCG	GCTCCCAGGC	CCACGAACAG
	CGGCTTCAAG	AGGTGGAAGC	CGAGGTGGCA	GCCACAGC	CCTACCAAGCT	TAGGGAGAGC	GAGCTGGTGT
25	TCGGGGCTAA	GCACGCCTGG	CGCAACGCTC	CCCGCTGCGT	GGGCCGGATC	CAGTGGGGA	AGCTGAGGT
	GTTCGATGCC	CGGGACTGCA	GGTCTGCACA	GGAAATGTT	ACCTACATCT	GCAACCACAT	CAAGTATGCC
	ACCAACCGGG	GCAACCTTCG	CTCGGCCATC	ACAGTGTCC	CGCAGCGCTG	CCCTGGCCGA	GGAGACTTCC
	GAATCTGGAA	CAGCCAGCTG	GTGCGCTACG	CGGGCTACCG	GCAGCAGGAC	GGCTCTGTG	GGGGGGACCC
	AGCCAACGTG	GAGATCACCG	AGCTCTGCAT	TCAGCACGGC	TGGACCCAG	GAAACGGTC	CTTCGACGTTG
30	CTGCCCCCTGC	TGCTGCAGGC	CCCAGATGAG	CCCCCAGAAC	TCTTCCTCT	GCCCCCCCAG	CTGGTCCITG
	AGGTGCCCCCT	GGAGCACCCC	ACGCTGGAGT	GGTTTGCGAC	CCTGGGCTG	CGCTGGTACG	CCCTCCCGGC
	AGTGTCCAAC	ATGCTGCTGG	AAATTGGGGG	CCTGGAGTT	CCCAGCAGCCC	CCTTCAGTGG	CTGGTACATG
	AGCACTGAGA	TCGGCACGAG	GAACCTGTGT	GACCCCTCACC	GCTACAACAT	CCTGGAGGAT	GTGGTGTCT
	GCATGGACCT	GGATACCCGG	ACCACCTCGT	CCCTGTGGAA	AGACAAGGCA	GCAGTGGAAA	TCAACGTGGC
35	CGTGTGCAAC	AGTTACCAAGC	TAGCCAAAGT	CACCATCGT	GACCACCA	CCGCCACGGC	CTCTTCATG
	AAGCACCTGG	AGAATGAGCA	GAAGGCCAGG	GGGGGCTGCC	CTGCAGACTG	GGCCTGGATC	GTGCCCCC
	TCTGGGCAG	CCTCACTCT	GTTTTCCATC	AGGAGATGGT	CAACTATTTC	CTGTCCCCGG	CCTTCGCTA
	CCAGCCAGAC	CCCTGGAAGG	GGAGTGCCTG	CAAGGGCACC	GGCATCACCA	GGAAGAAGAC	CTTTAAAGAA
	GTGGCCAACG	CCGTGAAGAT	CTCCGCTCG	CTCATGGGCA	CGGTGATGGC	GAAGCGAGT	AAGGGACAA
40	TCCTGTATGG	CTCCGAGACC	GGCCGGGCC	AGAGCTACGC	ACAGCAGCTG	GGGAGACTCT	TCCGGAAGGG
	TTTGATCCC	CGGGTCTGT	GTATGGATGA	GTATGACGTG	GTGTCCTCG	AAACAGAGAC	GCTGGTCTG
	GTGGTAACCA	GCACATTGG	GAATGGGGAT	CCCCCGGAGA	ATGGAGAGAG	CTTTCGAGCT	GCCCTGTATGG
	AGATGTCGG	CCCCATACAAC	AGCTCCCTC	GGCCGGAACAA	GCACAAGAGT	TATAAGATCC	GCTTCACAG
	CATCTCTGCA	TCAGACCCAC	TGGTGTCTC	TTGGCGGCC	AAGAGGAAGG	AGTCCAGTAA	CACAGACAGT
45	GCAGGGGCC	TGGCACCC	CAGGTTCTGT	GTGTTCGGGC	TCGGCTCCCG	GGCATACCC	CACTTCCTG
	CCTTGTCTG	TGCCCTGGAC	ACACGGCTG	AGGAACCTGG	CGGGGAGCGG	CTGCTGAGC	TGGGCCAGGG
	CGACGAGCTG	TGCG3CCAGG	AGGAGGCC	CCGAGGCTG	GCCCAGGCTG	CCTTCAGG	CGCTGTGAG
	ACCTTCTGTG	TGGGAAGGA	TGCCAAGGCC	GCCGCCAG	ACATCTTCAG	CCCCAAACGG	AGCTGGAAGC
	GCCAGAGGTA	CCGGCTGAGC	GCCCAGGCC	AGGGCCTGCA	GTTGCTGCCA	GGTCTGATCC	ACGTGACAG
50	GCGGAAGATG	TTCCAGGCTA	CAATCCGTC	AGTGGAAAAC	CTGCAAAGCA	GCAAGTCCAC	GAGGGCCACC
	ATCCCTGGTC	GCCTGGACAC	CGGAGGCCAG	GAGGGGCTG	AGTACCAGCC	GGGGGACCA	ATAGGTGTCT
	GCCCCCCAA	CCGGCCCGGC	CTTGTGGAGG	CGCTGCTGAG	CCGCGTGGAG	GACCCGCC	CGCCCCACTGA
	GCCCGTGGCA	GTAGAGCAGC	TGGAGAAGGG	CAGCCCTGGT	GGCCCTCCCC	CCGGCTGGGT	GCAGGACCCCC
	CGGCTGCCCC	CGTGACCGCT	GCGCCAGGCT	CTCACCTTCT	TCCTGGACAT	CACCTCCCCA	CCCAGCCCTC
55	AGCTCTTGC	GCTGCTCAGC	ACCTTGGCAG	AAGAGCCCAG	GGAACAGCAG	GAGCTGGAGG	CCCTCAGCCA
	GGATCCCCGA	CGCTACGAGG	AGTGGAAAGTG	GTTCCGCTGC	CCCACGCTG	TGGAGGTGCT	GGAGCAGTT
	CCGTCGGTGG	CGCTGCTGC	CCCACTGCTC	CTCACCCAGC	TGCCTCTGCT	CCAGCCCCGG	TACTACTCAG
	TCAGCTCGGC	ACCCAGCACC	CACCCAGGAG	AGATCCACCT	CACTGTAGCT	GTGCTGGCAT	ACAGGACTCA
	GGATGGGCTG	GGCCCTCTGC	ACTATGGAGT	CTGCTCCACG	TGGCTAAGCC	AGCTCAAGCC	CGGAGACCC
60	GTGCCCTGCT	TCATCCGGGG	GGCTCCCTCC	TTCCGGCTGC	CACCCGATCC	CAGCTTGCCC	TGCATCCTGG
	TGGGTCCAGG	CACTGGCATT	GGCCCTTCC	GGGGATTCTG	GCAGGAGCGG	CTGCTATGACA	TTGAGAGCAA
	AGGGCTGCG	CCCACTCCCA	TGACTTTGGT	GTTCGGCTGC	CGATGCTCCC	AACTTGACCA	TCTCTACCGC

GACGAGGTGC AG_nACGCCA GCAGCGCGG GTGTTGGCC GAGTCCTCAC CGCCTTCTCC CGGGAACCTG
 ACAACCCAA GACCTACGTG CAGGACATCC TGAGGACGGA GCTGGCTGCG GAGGTGCACC GCGTGTGCTG
 CCTCGAGCGG GGC'CACATGT TTGTCTGCG CGATGTTACCG ATGGCAACCA ACGTCCTGCA GACCGTGCAG
 CGCATCCTGG CGACGGAGGG CGACATGGAG CTGGACGAGG CCGGCAGCGT CATCGGCCTG CTGCAGGATC
 5 AGCAACGCTA CCACGAAGAC ATTTTCCGGC TCACGCTGCG CACCCAGGAG GTGACAAGCC GCATACGCAC
 CCAGAGCTT TCCITGCAGG AGCGTCAGTT GCGGGCGCA GTGCCCTGGG CGTTCGACCC TCCCGGCTCA
 GACACCAACA GCC'CCTGAGA GCCGCCTGGC TTTCCTTCC AGTCCGGGA GAGCGGCTGC CCGACTCAGG
 TCCGCCGAC CAGGATCAGC CCCGCTCTC CCCCCTTGAG GTGGTGCCTT CTCACATCTG TCCAGAGGCT
 GCAAGGATTG AGC'ATTATTG CTCCAGGAAG GAGCAAACAG CCTCTTTTCC CTCTCTAGGC CTGTTGCCTC
 10 10 GGGCTGGGT CGGCCTTAAT CTGGAAGGCC CCTCCCAGCA GCGGTACCCC AGGGCTACT GCCACCCGCT
 TCCTGTTCT TAG'TCCGAAT GTTAGATTCC TCTTGCCTCT CTCAGGAGTA TCTTACCTGT AAAGTCTAAT
 CTCTAAATCA AGTATTTATT ATTGAAGATT TACCATAGG GACTGTGCCA GATGTTAGGA GAACTACTAA
 AGTGCCTACC CCAGCTC-3' (FRAG. NO:_) (SEQ. ID NO:2508)
 5'-CCCCGGGG-3' (FRAG. NO:1898) (SEQ. ID NO: 1911)
 15 5'-GGGGCCGCTGGG-3' (FRAG. NO:1899) (SEQ. ID NO:1912)
 5'-GGGGGTGTGG-3' (FRAG. NO:1900) (SEQ. ID NO: 1913)
 5'-CTGCCTCCCCGGGG-3' (FRAG. NO:1442)(SEQ. ID NO:1451)
 5'-TTCTGCTGCTGCTG-3' (FRAG. NO:1443)(SEQ. ID NO:1452)
 20 5'-CTTCTTCCCGTC'CC-3' (FRAG. NO:1444)(SEQ. ID NO:1453)
 5'-TTTTGCTCTTC-3' (FRAG. NO:1446)(SEQ. ID NO:1455)
 5'-GGTTCCTGTTGTTCT-3' (FRAG. NO:1447)(SEQ. ID NO:1456)
 5'-GGCCTGCTGGTGGCG-3' (FRAG. NO:1448)(SEQ. ID NO:1457)
 5'-GCTTGTGCGTTCC-3' (FRAG. NO:1449)(SEQ. ID NO:1458)
 25 5'-TCTCTCTCTCTCTGCTCGCTCGC-3' (FRAG. NO:1450)(SEQ. ID NO:1459)
 5'-TTTCTCTGCTCTCTCGC-3' (FRAG. NO:1451)(SEQ. ID NO:1460)
 5'-GCCGTTCTCCTCC-3' (FRAG. NO:1452)(SEQ. ID NO:1461)
 5'-GGCGTCCTCCTGCC-3' (FRAG. NO:1453)(SEQ. ID NO:1462)
 5'-TGTGCTGTTGCTCGG-3' (FRAG. NO:1454)(SEQ. ID NO:1463)
 30 30 5'-GTGGTGCAGGGTCCC-3' (FRAG. NO:1455)(SEQ. ID NO:1464)
 5'-GGTGCCTCCCCGGC-3' (FRAG. NO:1456)(SEQ. ID NO:1465)
 5'-GGGCCGGCTGGTTCGCTGGG-3' (FRAG. NO:1457)(SEQ. ID NO:1466)
 5'-CTGCTCTGGTGGGGTGTGGGG-3' (FRAG. NO:1458)(SEQ. ID NO:1467)
 5'-GCTGGGTTGGGGTGTGGT-3' (FRAG. NO:1459)(SEQ. ID NO:1468)
 35 35 5'-GGCTCTCTGTGCC-3' (FRAG. NO:1460)(SEQ. ID NO:1469)
 5'-TGTGGGGCTGTTGTTG-3' (FRAG. NO:1461)(SEQ. ID NO:1470)
 5'-TCTCTGTGGCGTGTG-3' (FRAG. NO:1462)(SEQ. ID NO:1471)
 5'-CTGGGTCTGGGGCTTC-3' (FRAG. NO:1463)(SEQ. ID NO:1472)
 5'-CTCCCTGTGCTGG-3' (FRAG. NO:1464)(SEQ. ID NO:1473)
 40 40 5'-TGCGCCCTCCCG-3' (FRAG. NO:1465)(SEQ. ID NO:1474)
 5'-CCCCCTCTGGGCC-3' (FRAG. NO:1466)(SEQ. ID NO:1475)
 5'-GGTGCCTGGCTCTTGTGG-3' (FRAG. NO:1467)(SEQ. ID NO:1476)
 5'-GCGCTTCTGGCTCTG-3' (FRAG. NO:1468)(SEQ. ID NO:1477)
 5'-CCCTGTCCTCTTCGCTCGT-3' (FRAG. NO:1469)(SEQ. ID NO:1478)
 45 45 5'-GGCTGCTGGCTG-3' (FRAG. NO:1470)(SEQ. ID NO:1479)
 5'-CTGCCCBGTTTGBTCCTCBCBTGCCGTGGGBGGBCBTGG-3'(FRAG. NO:1901) (SEQ. ID NO: 1914)

NF-κB Nucleic Acids and Antisense Oligonucleotide Fragments

5'-CGGCCCTTCT CACTGGAGGC ACCGGGCAGT CCTCCATGGG AGGGTTGGGC TTGGCCGGGG CTGCCCGGTG
 CCTCCTTGTG GCTGGTCCCT CGTTGCTCTT GGGCCCCGC TCCCGCTGCT CGGCCTCCGT GTTCTTGGC
 50 50 CTCTTGTCTCC GCC'TGCTGTC TTGTCCCGTC CCCTCCTCGC TTGCGTTTCC CTCTCCTTG TCTTCCAGGC
 CTTCTCCGC TTCCGCTGCT GGGGCCCGC CGGGGGGGGC GCTCGGCTCC GCGGCTTCCCT CCCCAGGCTGG
 GGGGTCTGG TCTC'GGGGC CTGCGGCTCG CGGGCTCGGG GCTCGTGC CGCGCGCGGG CGTCCGCGGT
 GGGTGGCGCT GTCC'CGCCGT GGTGTGTC CGTTCTCGTC CTGCGCCGTC CTGGTCTGCC CGTGGGGTCC
 TGGGCGTGGT GGGGGCGTC TGGTGCCTCG TCTGCCCGT GGGGCTTCGG GCTCGGGGCT GTTCGTCCCC
 55 55 CCTGCCGCTC TGTCGCCCTCC GGGGCTCCTC GTTTTCGCTG CTTCGGGTGT CTTCTCGGC GTGTGGCCCC
 GGGTCCCGGC CCTGCTGGC TGGGCGGGGT CGCTGCCCTG GGCTTCTGGC CCGTCTGGTT GTCTGTCGGT
 GCTTGTCTCG GGT'TCTGGC CTCTGTGCTG GGCCTCTC TGCCCTCTG TCCGCCCTCC TGGTGGCTCG
 GCTGGGGGTG CCCG'GCGGG GGTGGGTGTG GGGTGTTC GGGGCTCTCC CCTTCCC-3' (FRAG. NO:1902) (SEQ.
 ID NO:1915)
 60 60 5'-GGGCGGGGTCGC-3' (FRAG. NO:1903) (SEQ. ID NO:1916)
 5'-GCGCCGTCC-3' (FRAG. NO:1904) (SEQ. ID NO:1917)

5'-GGGCGTGGTGG-3' (FRAG. NO:1905) (SEQ. ID NO:1918)
 5'-GTTGGGCTTGGCCGGGG-3' (FRAG. NO:1471)(SEQ. ID NO:1480)
 5'-CTGCCCGGTGCCTCC-3' (FRAG. NO:1472)(SEQ. ID NO:1481)
 5'-TCTGGCTGGTCCCTCGT-3' (FRAG. NO:1473)(SEQ. ID NO:1482)
 5'-TGTCTTGGGCC-3' (FRAG. NO:1474)(SEQ. ID NO:1483)
 5'-GCTCCCGCTGCTC^GGCCTCCGT-3' (FRAG. NO:1475)(SEQ. ID NO:1484)
 5'-GTTCTTGGCCTCTGCTCC-3' (FRAG. NO:1476)(SEQ. ID NO:1485)
 5'-GCCTGCTGTCTTG^TCC-3' (FRAG. NO:1477)(SEQ. ID NO:1486)
 5'-CGTCCCCTCCTCG^CTTGCGTTTC-3' (FRAG. NO:1478)(SEQ. ID NO:1487)
 10 5'-CCTCTTCCTTGTCTCCA-3' (FRAG. NO:1479)(SEQ. ID NO:1488)
 5'-GGCCTTCCTCCGC^TTCCGCTGC-3' (FRAG. NO:1480)(SEQ. ID NO:1489)
 5'-TGGGGCCCGGCCGG-3' (FRAG. NO:1481)(SEQ. ID NO:1490)
 5'-GGGGGCGCTCGG^GTCCGCGCTTCCTCCCCGG-3' (FRAG. NO:1482)(SEQ. ID NO:1491)
 5'-CTGGGGGGTCTTGG-3' (FRAG. NO:1483)(SEQ. ID NO:1492)
 15 5'-TCTCCGGGGCCTG^CGGCTCGC-3' (FRAG. NO:1484)(SEQ. ID NO:1493)
 5'-GGGCTCGGGGCTG^TGTGCGCC-3' (FRAG. NO:1485)(SEQ. ID NO:1494)
 5'-GCGCGCGGCGTCC^GCGGTG-3' (FRAG. NO:1486)(SEQ. ID NO:1495)
 5'-GGTGGCGCTGTCCC^GCC-3' (FRAG. NO:1487)(SEQ. ID NO:1496)
 20 5'-GTGGTGTGTCTCC^TTTCTCGCTCGGCCGTC-3' (FRAG. NO:1488)(SEQ. ID NO:1497)
 5'-CTGGTCTGCCGTGG-3' (FRAG. NO:1489)(SEQ. ID NO:1498)
 5'-GGTCTGGGCGTGGTGC-3' (FRAG. NO:1490)(SEQ. ID NO:1499)
 5'-GGGGCGTCTGGTGC-3' (FRAG. NO:1491)(SEQ. ID NO:1500)
 5'-CTCGTCTGCCCG^TG-3' (FRAG. NO:1492)(SEQ. ID NO:1501)
 25 5'-GGGCTTCGGGCTC^GG-3' (FRAG. NO:1493)(SEQ. ID NO:1502)
 5'-GGCTGTTCGTCCC^CCCTGCCGCTCTGTGCCCTCC-3' (FRAG. NO:1494)(SEQ. ID NO:1503)
 5'-GGGGCTCCTCGTT^TTC-3' (FRAG. NO:1495)(SEQ. ID NO:1504)
 5'-GCTGCTCGGGT^GTCTTCCTC-3' (FRAG. NO:1496)(SEQ. ID NO:1505)
 5'-GGCGTGTGGCCCC^GG-3' (FRAG. NO:1497)(SEQ. ID NO:1506)
 30 5'-GTC^CGGCCGCCCC^GT^GGGGCTGGGCGGGGTC-3' (FRAG. NO:1498)(SEQ. ID NO:1507)
 5'-GCTGCCCTGGGCT^TCTGGCCGTCT-3' (FRAG. NO:1499)(SEQ. ID NO:1508)
 5'-GGTTGTCTGTCGG^T-3' (FRAG. NO:1500)(SEQ. ID NO:1509)
 5'-GCTTGCTCTGGGT^TTCTGG-3' (FRAG. NO:1501)(SEQ. ID NO:1510)
 5'-CCTCTGTGCTGGGC-3' (FRAG. NO:1502)(SEQ. ID NO:1511)
 35 5'-GCTTCTCTGCCCTC^TGCTCC-3' (FRAG. NO:1503)(SEQ. ID NO:1512)
 5'-GCCCTCTGGTG^CTC-3' (FRAG. NO:1504)(SEQ. ID NO:1513)
 5'-GGCTGGGGGTGCC^CGTGCG-3' (FRAG. NO:1505)(SEQ. ID NO:1514)
 5'-GGGGTGGGTGTGG^GGTGTT-3' (FRAG. NO:1506)(SEQ. ID NO:1515)
 5'-TTCGGGGTCCTCCC^TTTCCC-3' (FRAG. NO:1507)(SEQ. ID NO:1516)
 5'-CGGCCCTCTCACT^TGGAGGCACCGGGCAGTCCTCCATGGAGG-3' (FRAG.NO:1906)(SEQ.ID NO:1919)

Human Major Basic Protein Nucleic Acids and Antisense Oligonucleotide Fragments

40 5'-GTT TCA TCT TGG CTT TAT CCTCT CCC CTT GTT CCT CCC CTCT CCT GCT CTG GRG TCT CCT C TTC CCT
 CCC TCC CCT GCC G^TG TTG TCT GTG GGT GTC^T GTT TCG CTC TTG TTG CCC TGG GCC CTT CCC TGC TGG GGG
 GGA GTT TCA TCT TGG CTT TCB TCT TGG CTT TBT CCTCT CCC CTT GTT CCT CCC CTCT CCT GCT CTG GRG
 TCT CCT C TTC CCT CCC TCC CCT GCC GTG TTG TCT GTG GGT GTC^T GTT TCG CTC TTG TTG CCC TGG GCC CTT
 CCC TGC TGG GGG G^BB GTT TCB TCT TGG-3' (FRAG. ID:1907) (SEQ. ID NO:1920)
 5'-GGG GGA GTT-3' (FRAG. ID:1908) (SEQ. ID NO:1921)
 5'-G CCC TGG GCC C-3' (FRAG. ID:1909) (SEQ. ID NO:1922)
 5'-GTT TCA TCT TGG CTT TAT CC-3' (FRAG. NO:1508) (SEQ. ID NO:1517)
 5'-TCT CCC CTT GTT CCT CCC C-3' (FRAG. NO:1509)(SEQ. ID NO:1518)
 50 5'-TCT CCT GCT CTG GRG TCT CCT C-3' (FRAG. NO:1510)(SEQ. ID NO:1519)
 5'-TTC CCT CCC TCC CCT GCC-3' (FRAG. NO:1511)(SEQ. ID NO:1520)
 5'-GTG TTG TCT GTG GGT GTC C-3' (FRAG. NO:1512)(SEQ. ID NO:1521)
 5'-GTT TCG CTC TTG TTG CCC^TCC-3' (FRAG. NO:1513)(SEQ. ID NO:1522)
 5'-TGG GCC CTT CCC TGC TGG-3' (FRAG. NO:1514)(SEQ. ID NO:1523)
 55 5'-GGG GGA GTT TCA TCT TGG-3' (FRAG. NO:1515)(SEQ. ID NO:1524)
 5'-GTT TCA TCT TGG CTT TAT CCTCT CCC CTT GTT CCT CCC CTCT CCT GCT CTG GRG TCT CCT C TTC CCT
 CCC TCC CCT GCC G^TG TTG TCT GTG GGT GTC^T GTT TCG CTC TTG TTG CCC TGG GCC CTT CCC TGC TGG GGG
 GGA GTT TCA TCT TCG-3' (FRAG. ID:1910) (SEQ. ID NO:1923)
 60 5'-GTT TCB TCT TGG CTT TBT CCTCT CCC CTT GTT CCT CCC CTCT CCT GCT CTG GRG TCT CCT C TTC CCT CCC
 TCC CCT GCC GTG T^TG TCT GTG GGT GTC^T GTT TCG CTC TTG TTG CCC TGG GCC CTT CCC TGC TGG GGG G^BB
 GTT TCB TCT TGG-3' (FRAG. ID:1911) (SEQ. ID NO:1924)

Human Eosinophil Major Basic Protein Nucleic Acids and Antisense Oligonucleotide Fragments

5'-GGG GGB GTT TCB TCT TGG CTT T-3' (FRAG. NO:1516)(SEQ. ID NO:1525)
 5'-GGG GGB GTT TCB TCT TGG CTT-3' (FRAG. NO:1517)(SEQ. ID NO: 1526)
 5'-GGG GGB GTT TCB TCT TGG CT-3' (FRAG. NO:1518)(SEQ. ID NO:1527)
 5 5'-GGG GGB GTT TCB TCT TGG C-3' (FRAG. NO:1519)(SEQ. ID NO: 1528)
 5'-GGG GGB GTT TCB TCT TGG-3' (FRAG. NO:1520)(SEQ. ID NO: 1529)
 5'-GGG GGB GTT TCB TCT TG-3' (FRAG. NO:1521)(SEQ. ID NO: 1530)
 5'-GGG GGB GTT TCB TCT T-3' (FRAG. NO:1522)(SEQ. ID NO: 1531)
 5'-GGG GGB GTT TCB TCT-3' (FRAG. NO:1523)(SEQ. ID NO: 1532)
 10 5'-GGG GGB GTT TCB TC-3' (FRAG. NO:1524)(SEQ. ID NO: 1533)
 5'-GGG GGB GTT TCB T-3' (FRAG. NO:1525)(SEQ. ID NO: 1534)
 5'-GGG GGB GTT TCB-3' (FRAG. NO:1526)(SEQ. ID NO: 1535)
 5'-GG GGB GTT TCB TCT TGG CTT T-3' (FRAG. NO:1527)(SEQ. ID NO: 1536)
 5'-GG GGB GTT TCB TCT TGG CTT-3' (FRAG. NO:1528)(SEQ. ID NO: 1537)
 15 5'-GG GGB GTT TCB TCT TGG CT-3' (FRAG. NO:1529)(SEQ. ID NO: 1538)
 5'-GG GGB GTT TCB TCT TGG C-3' (FRAG. NO:1530)(SEQ. ID NO: 1539)
 5'-GG GGB GTT TCB TCT TGG-3' (FRAG. NO:1531)(SEQ. ID NO: 1540)
 5'-GG GGB GTT TCB TCT TG-3' (FRAG. NO:1532)(SEQ. ID NO: 1541)
 5'-GG GGB GTT TCB TCT T-3' (FRAG. NO:1533)(SEQ. ID NO: 1542)
 20 5'-GG GGB GTT TCB TCT C-3' (FRAG. NO:1534)(SEQ. ID NO: 1543)
 5'-GG GGB GTT TCB TCT-3' (FRAG. NO:1535)(SEQ. ID NO: 1544)
 5'-GG GGB GTT TCB T-3' (FRAG. NO:1536)(SEQ. ID NO: 1545)
 5'-G GGB GTT TCB TCT TGG CTT T-3' (FRAG. NO:1537)(SEQ. ID NO: 1546)
 5'-G GGB GTT TCB TCT TGG CTT-3' (FRAG. NO:1538)(SEQ. ID NO: 1547)
 25 5'-G GGB GTT TCB TCT TGG CT-3' (FRAG. NO:1539)(SEQ. ID NO: 1548)
 5'-G GGB GTT TCB TCT TGG C-3' (FRAG. NO:1540)(SEQ. ID NO: 1549)
 5'-G GGB GTT TCB TCT TGG-3' (FRAG. NO:1541)(SEQ. ID NO: 1550)
 5'-G GGB GTT TCB TCT TG-3' (FRAG. NO:1542)(SEQ. ID NO: 1551)
 5'-G GGB GTT TCB TCT T-3' (FRAG. NO:1543)(SEQ. ID NO: 1552)
 30 5'-G GGB GTT TCB TCT C-3' (FRAG. NO:1544)(SEQ. ID NO: 1553)
 5'-G GGB GTT TCB TCT-3' (FRAG. NO:1545)(SEQ. ID NO: 1554)
 5'-GGB GTT TCB TCT TGG CTT T-3' (FRAG. NO:1546)(SEQ. ID NO: 1555)
 5'-GGB GTT TCB TCT TGG CTT-3' (FRAG. NO:1547)(SEQ. ID NO: 1556)
 5'-GGB GTT TCB TCT TGG CT-3' (FRAG. NO:1548)(SEQ. ID NO: 1557)
 35 5'-GGB GTT TCB TCT TGG C-3' (FRAG. NO:1549)(SEQ. ID NO: 1558)
 5'-GGB GTT TCB TCT TGG-3' (FRAG. NO:1550)(SEQ. ID NO: 1559)
 5'-GGB GTT TCB TCT TG-3' (FRAG. NO:1551)(SEQ. ID NO: 1560)
 5'-GGB GTT TCB TCT T-3' (FRAG. NO:1552)(SEQ. ID NO: 1561)
 5'-GGB GTT TCB TCT-3' (FRAG. NO:1553)(SEQ. ID NO: 1562)
 40 5'-GB GTT TCB TCT TGG CTT T-3' (FRAG. NO:1554)(SEQ. ID NO: 1563)
 5'-GB GTT TCB TCT TGG CTT-3' (FRAG. NO:1555)(SEQ. ID NO: 1564)
 5'-GB GTT TCB TCT TGG CT-3' (FRAG. NO:1556)(SEQ. ID NO: 1565)
 5'-GB GTT TCB TCT TGG C-3' (FRAG. NO:1557)(SEQ. ID NO: 1566)
 45 5'-GB GTT TCB TCT TGG-3' (FRAG. NO:1558)(SEQ. ID NO: 1567)
 5'-GB GTT TCB TCT TG-3' (FRAG. NO:1559)(SEQ. ID NO: 1568)
 5'-GB GTT TCB TCT T-3' (FRAG. NO:1560)(SEQ. ID NO: 1569)
 5'-B GTT TCB TCT TGG CTT T-3' (FRAG. NO:1561)(SEQ. ID NO: 1570)
 5'-B GTT TCB TCT TGG CTT-3' (FRAG. NO:1562)(SEQ. ID NO: 1571)
 50 5'-B GTT TCB TCT TGG CTT-3' (FRAG. NO:1563)(SEQ. ID NO: 1572)
 5'-B GTT TCB TCT TGG CT-3' (FRAG. NO:1564)(SEQ. ID NO: 1573)
 5'-B GTT TCB TCT TGG C-3' (FRAG. NO:1565)(SEQ. ID NO: 1574)
 5'-B GTT TCB TCT TGG-3' (FRAG. NO:1565)(SEQ. ID NO: 1575)
 5'-B GTT TCB TCT TG-3' (FRAG. NO:1567)(SEQ. ID NO: 1576)
 5'-GTT TCB TCT TGG CTT T-3' (FRAG. NO:1568)(SEQ. ID NO: 1577)
 55 5'-GTT TCB TCT TGG CTT-3' (FRAG. NO:1569)(SEQ. ID NO: 1578)
 5'-GTT TCB TCT TGG CT-3' (FRAG. NO:1570)(SEQ. ID NO: 1579)
 5'-GTT TCB TCT TGG C-3' (FRAG. NO:1571)(SEQ. ID NO: 1580)
 5'-GTT TCB TCT TGG-3' (FRAG. NO:1572)(SEQ. ID NO: 1581)
 60 5'-TT TCB TCT TGG CTT T-3' (FRAG. NO:1573)(SEQ. ID NO: 1582)
 5'-TT TCB TCT TGG CTT-3' (FRAG. NO:1574)(SEQ. ID NO: 1583)
 5'-TT TCB TCT TGG CT-3' (FRAG. NO:1575)(SEQ. ID NO: 1584)

5'-TT TCB TCT TGG C-3' (FRAG. NO:1576)(SEQ. ID NO: 1585)
5'-T TCB TCT TGG C' T T-3' (FRAG. NO:1577)(SEQ. ID NO: 1586)
5'-T TCB TCT TGG C' T-3' (FRAG. NO:1578)(SEQ. ID NO: 1587)
5'-T TCB TCT TGG C'-3' (FRAG. NO:1579)(SEQ. ID NO: 1588)
5 5'-TCB TCT TGG CTT T-3' (FRAG. NO:1580)(SEQ. ID NO: 1589)
5'-TCB TCT TGG CTT-3' (FRAG. NO:1581)(SEQ. ID NO: 1590)
5'-GGG GGB GTT TCB TCT TGG CTT T-3' (FRAG. NO:1582)(SEQ. ID NO:1591)
5'-GG GGB GTT TCB TCT TGG CTT T-3' (FRAG. NO:1583)(SEQ. ID NO: 1592)
5'-G GGB GTT TCB TCT TGG CTT T-3' (FRAG. NO:1584)(SEQ. ID NO: 1593)
10 5'-GGG GTT TCB TCT TGG CTT T-3' (FRAG. NO:1585)(SEQ. ID NO: 1594)
5'-GB GTT TCB TCT TGG CTT T-3' (FRAG. NO:1586)(SEQ. ID NO: 1595)
5'-B GTT TCB TCT TC G CTT T-3' (FRAG. NO:1587)(SEQ. ID NO: 1596)
5'-GTT TCB TCT TGG CTT T-3' (FRAG. NO:1588)(SEQ. ID NO: 1597)
5'-TT TCB TCT TGG CTT T-3' (FRAG. NO:1589)(SEQ. ID NO: 1598)
15 5'-T TCB TCT TGG C' T T-3' (FRAG. NO:1590)(SEQ. ID NO: 1599)
5'-TCB TCT TGG CTT T-3' (FRAG. NO:1591)(SEQ. ID NO: 1600)
5'-CB TCT TGG CTT T-3' (FRAG. NO:1592)(SEQ. ID NO: 1601)
5'-GGG GGB GTT TCE TCT TGG CTT-3' (FRAG. NO:1593)(SEQ. ID NO: 1602)
5'-GG GGB GTT TCB TCT TGG CTT-3' (FRAG. NO:1594)(SEQ. ID NO: 1603)
20 5'-G GGB GTT TCB TCT TGG CTT-3' (FRAG. NO:1595)(SEQ. ID NO: 1604)
5'-GGB GTT TCB TCT TGG CTT-3' (FRAG. NO:1596)(SEQ. ID NO: 1605)
5'-GB GTT TCB TCT TGG CTT-3' (FRAG. NO:1597)(SEQ. ID NO: 1606)
5'-B GTT TCB TCT TGG CTT-3' (FRAG. NO:1598)(SEQ. ID NO: 1607)
5'-GTT TCB TCT TGG CTT-3' (FRAG. NO:1599)(SEQ. ID NO: 1608)
25 5'-TT TCB TCT TGG CTT-3' (FRAG. NO:1600)(SEQ. ID NO: 1609)
5'-T TCB TCT TGG C' T-3' (FRAG. NO:1601)(SEQ. ID NO: 1610)
5'-TCB TCT TGG CTT 3' (FRAG. NO:1602)(SEQ. ID NO: 1611)
5'-GGG GGB GTT TCB TCT TGG CT-3' (FRAG. NO:1603)(SEQ. ID NO: 1612)
5'-GG GGB GTT TCB TCT TGG CT-3' (FRAG. NO:1604)(SEQ. ID NO: 1613)
30 5'-G GGB GTT TCB TCT TGG CT-3' (FRAG. NO:1605)(SEQ. ID NO: 1614)
5'-GGB GTT TCB TCT TGG CT-3' (FRAG. NO:1606)(SEQ. ID NO: 1615)
5'-GB GTT TCB TCT TGG CT-3' (FRAG. NO:1607)(SEQ. ID NO: 1616)
5'-B GTT TCB TCT TGG CT-3' (FRAG. NO:1608)(SEQ. ID NO: 1617)
5'-GTT TCB TCT TGG CT-3' (FRAG. NO:1609)(SEQ. ID NO: 1618)
35 5'-TT TCB TCT TGG CT-3' (FRAG. NO:1610)(SEQ. ID NO: 1619)
5'-T TCB TCT TGG CT-3' (FRAG. NO:1611)(SEQ. ID NO: 1620)
5'-GGG GGB GTT TCB TCT TGG C-3' (FRAG. NO:1612)(SEQ. ID NO: 1621)
5'-GG GGB GTT TCB TCT TGG C-3' (FRAG. NO:1613)(SEQ. ID NO: 1622)
40 5'-G GGB GTT TCB TCT TGG C-3' (FRAG. NO:1614)(SEQ. ID NO: 1623)
5'-GGB GTT TCB TCT TGG C-3' (FRAG. NO:1615)(SEQ. ID NO: 1624)
5'-GB GTT TCB TCT TGG C-3' (FRAG. NO:1616)(SEQ. ID NO: 1625)
5'-B GTT TCB TCT TG 3 C-3' (FRAG. NO:1617)(SEQ. ID NO: 1626)
5'-GTT TCB TCT TGG C-3' (FRAG. NO:1618)(SEQ. ID NO: 1627)
45 5'-TT TCB TCT TGG C-3' (FRAG. NO:1619)(SEQ. ID NO: 1628)
5'-GGG GGB GTT TCB TCT TGG-3' (FRAG. NO:1620)(SEQ. ID NO: 1629)
5'-GG GGB GTT TCB TCT TGG-3' (FRAG. NO:1621)(SEQ. ID NO: 1630)
5'-G GGB GTT TCB TCT TGG-3' (FRAG. NO:1622)(SEQ. ID NO: 1631)
5'-GGB GTT TCB TCT TGG-3' (FRAG. NO:1623)(SEQ. ID NO: 1632)
50 5'-GB GTT TCB TCT TGG-3' (FRAG. NO:1624)(SEQ. ID NO: 1633)
5'-B GTT TCB TCT TG 3 C-3' (FRAG. NO:1625)(SEQ. ID NO: 1634)
5'-GTT TCB TCT TGG-3' (FRAG. NO:1626)(SEQ. ID NO: 1635)
5'-GGG GGB GTT TCB TCT TG-3' (FRAG. NO:1627)(SEQ. ID NO: 1636)
5'-GG GGB GTT TCB TCT TG-3' (FRAG. NO:1628)(SEQ. ID NO: 1637)
5'-G GGB GTT TCB TCT TG-3' (FRAG. NO:1629)(SEQ. ID NO: 1638)
55 5'-GGB GTT TCB TCT TG-3' (FRAG. NO:1630)(SEQ. ID NO: 1639)
5'-GB GTT TCB TCT TG-3' (FRAG. NO:1631)(SEQ. ID NO: 1640)
5'-B GTT TCB TCT TG-3' (FRAG. NO:1632)(SEQ. ID NO: 1641)
5'-GGG GGB GTT TCB TCT T-3' (FRAG. NO:1633)(SEQ. ID NO: 1642)
5'-GG GGB GTT TCB TCT T-3' (FRAG. NO:1634)(SEQ. ID NO: 1643)
60 5'-G GGB GTT TCB TCT T-3' (FRAG. NO:1635)(SEQ. ID NO: 1644)
5'-G GGB GTT TCB TCT T-3' (FRAG. NO:1636)(SEQ. ID NO: 1645)
5'-GGB GTT TCB TCT T-3' (FRAG. NO:1637)(SEQ. ID NO: 1646)

5'-GB GTT TCB TCT T-3' (FRAG. NO:1638)(SEQ. ID NO: 1647)
 5'-GGG GGB GTT TCE TCT-3' (FRAG. NO:1639)(SEQ. ID NO: 1648)
 5'-GG GGB GTT TCB ``CT-3' (FRAG. NO:1640)(SEQ. ID NO: 1649)
 5'-G GGB GTT TCB TCT-3' (FRAG. NO:1641)(SEQ. ID NO: 1650)
 5'-GGB GTT TCB TCT 3' (FRAG. NO:1642)(SEQ. ID NO: 1651)
 5'-GGG GGB GTT TCE TC-3' (FRAG. NO:1643)(SEQ. ID NO: 1652)
 5'-GG GGB GTT TCB T'C-3' (FRAG. NO:1644)(SEQ. ID NO: 1653)
 5'-G GGB GTT TCB TC-3' (FRAG. NO:1645)(SEQ. ID NO: 1654)
 5'-GGG GGB GTT TCB T-3' (FRAG. NO:1646)(SEQ. ID NO: 1655)
 10 5'-GG GGB GTT TCB T'-3' (FRAG. NO:1647)(SEQ. ID NO: 1656)
 5'-GGG GGB GTT TCB-3' (FRAG. NO:1648)(SEQ. ID NO: 1657)
 5'-TCT CCC CTT GTT CCT CCC C-3' (FRAG. NO:1649)(SEQ. ID NO: 1658)
 5'-TCT CCT GCT CTG GTG TCT CCT C-3' (FRAG. NO:1650)(SEQ. ID NO: 1659)
 15 5'-TTC CCT CCC TCC CCT GCC-3' (FRAG. NO:1651)(SEQ. ID NO:1660)
 5'-GTG TTG TCT GTG GGT GTC C-3' (FRAG. NO:1652)(SEQ. ID NO: 1661)
 5'-GTT TCG CTC TTG CCC-3' -3' (FRAG. NO:1653)(SEQ. ID NO: 1661)
 5'-TGG GCC CTT CCC TGC TGG-3' (FRAG. NO:1654)(SEQ. ID NO: 1663)
 5'-GGG GGB G-3' (FRAG. NO:1912)(SEQ. ID NO:1925)
 5'-GTG GGT GTC C-3' (FRAG. NO:1913) (SEQ. ID NO: 1926)

BP-1 Nucleic Acids and Antisense Oligonucleotide Fragments

20 5'-CCGTGTTGTC BGTGGTGCTG CCCGTTGBG GTBTGGCGCT CCBCCBTTTC CCTTTCTCC TTGTTTCCG
 TTTCTCTGC CGTCTGTGGT T-3' (FRAG. NO:1914) (SEQ. ID NO: 1927)
 5'-CCCGTTGBGGTB1GGC-3'(FRAG. NO:1915) (SEQ. ID NO: 1928)
 5'-GCTCCBCCBTTCCCTTTCTCC-3'(FRAG. NO:1916) (SEQ. ID NO: 1929)
 25 5'-TTGTTTCCGTTTC ``CTTG-3'(FRAG. NO:1917) (SEQ. ID NO: 1930)
 5'-CCGTCTGTGGTT-3'(FRAG. NO:1918) (SEQ. ID NO: 1931)
 5'-CCCGTTGAGGTA1GGC-3'(FRAG. NO:1919) (SEQ. ID NO: 1932)
 5'-GCTCCBCCAATTCC CTTTCTCC-3'(FRAG. NO:1920) (SEQ. ID NO: 1933)

C/EBP Nucleic Acids and Antisense Oligonucleotide Antisense Oligonucleotide Fragments

30 5'-GGGCCBGCCCCGCGCCTTTCTBGC CCC GGCC-3' (FRAG. NO:1921) (SEQ. ID NO: 1934)
 5'-GGGCCBGCCCCGCGCCTTTCTBGC CCC GGC-3' (FRAG. NO:1922) (SEQ. ID NO: 1935)
 5'-GGGCCBGCCCCGCCGCTTTCTBGC CCCGG-3' (FRAG. NO:1923) (SEQ. ID NO: 1936)
 5'-GGGCCBGCCCCGCGCCTTTCTBGC CCCCG-3' (FRAG. NO:1924) (SEQ. ID NO: 1937)
 5'-GGGCCBGCCCCGCGCCTTTCTBGC CCC-3' (FRAG. NO:1925) (SEQ. ID NO: 1938)
 35 5'-GGGCCBGCCCCGCGCCTTTCTBGC CCC-3' (FRAG. NO:1926) (SEQ. ID NO: 1939)
 5'-GGGCCBGCCCCGCGCCTTTCTBGC CCC-3' (FRAG. NO:1927) (SEQ. ID NO: 1940)
 5'-GGGCCBGCCCCGCGCCTTTCTBGC CCC-3' (FRAG. NO:1928) (SEQ. ID NO: 1941)
 5'-GGGCCBGCCCCGCGCCTTTCTBGC CCC-3' (FRAG. NO:1929) (SEQ. ID NO: 1942)
 5'-GGGCCBGCCCCGCGCCTTTCTBGC CCC-3' (FRAG. NO:1930) (SEQ. ID NO: 1943)
 40 5'-GGGCCBGCCCCGCGCCTTTCTBGC CCC-3' (FRAG. NO:1931) (SEQ. ID NO:1942) 1944)
 5'-GGGCCBGCCCCGCGCCTTTCTBGC CCC-3' (FRAG. NO:1932) (SEQ. ID NO: 1945)
 5'-GGGCCBGCCCCGCGCCTTTCTBGC CCC-3' (FRAG. NO:1933) (SEQ. ID NO: 1946)
 5'-GGGCCBGCCCCGCGCCTTTCTBGC CCC-3' (FRAG. NO:1934) (SEQ. ID NO: 1947) [1945]
 5'-GGGCCBGCCCCGCGCCTTTCTBGC CCC-3' (FRAG. NO:1935) (SEQ. ID NO: 1948)
 45 5'-GGGCCBGCCCCGCGCCTTTCTBGC CCC-3' (FRAG. NO:1936) (SEQ. ID NO: 1949)
 5'-GGGCCBGCCCCGCGCCTTTCTBGC CCC-3' (FRAG. NO:1937) (SEQ. ID NO: 1950)
 5'-GGGCCBGCCCCGCGCCTTTCTBGC CCC-3' (FRAG. NO:1938) (SEQ. ID NO: 1951)
 5'-GGGCCBGCCCCGCGCCTTTCTBGC CCC-3' (FRAG. NO:1939) (SEQ. ID NO: 1952)
 5'-GGGCCBGCCCCGCGCCTTTCTBGC CCC-3' (FRAG. NO:1940) (SEQ. ID NO: 1953)
 50 5'-GGGCCBGCCCCGCGCCTTTCTBGC CCC-3' (FRAG. NO:1941) (SEQ. ID NO: 1954)
 5'-GGGCCBGCCCCGCGCCTTTCTBGC CCC-3' (FRAG. NO:1942) (SEQ. ID NO: 1955)
 5'-GGGCCBGCCCCGCGCCTTTCTBGC CCC-3' (FRAG. NO:1943) (SEQ. ID NO: 1956)
 5'-GGGCCBGCCCCGCGCCTTTCTBGC CCC-3' (FRAG. NO:1944) (SEQ. ID NO: 1957)
 5'-GGGCCBGCCCCGCGCCTTTCTBGC CCC-3' (FRAG. NO:1945) (SEQ. ID NO: 1958)
 55 5'-GCCCBGCCCCGCCGCCTTTCTBGC CCCGGC-3' (FRAG. NO:1946) (SEQ. ID NO: 1959)
 5'-CCCBGCCCCGCCGCCTTTCTBGC CCCGGC-3' (FRAG. NO:1947) (SEQ. ID NO: 1960)
 5'-CCBGCCCCGCCGCCTTTCTBGC CCCGGC-3' (FRAG. NO:1948) (SEQ. ID NO: 1961)
 5'-CBGCCCCGCCGCCTTTCTBGC CCCGGC-3' (FRAG. NO:1948) (SEQ. ID NO: 1962)
 5'-BGCCCCGCCGCCTTTCTBGC CCCGGC-3' (FRAG. NO:1950) (SEQ. ID NO: 1963)
 60 5'-GCCCGCCGCCCTTCTBGC CCCGGC-3' (FRAG. NO:1951) (SEQ. ID NO: 1964)

5'-CCCCGCCGCCCTTCTBGGCCCGGC-3' (FRAG. NO:1952) (SEQ. ID NO: 1965)
 5'-CCCGCCGCCCTTTCTBGGCCCGGC-3' (FRAG. NO:1953) (SEQ. ID NO: 1966)
 5'-CCGCCGCCCTTTCTBGGCCCGGC-3' (FRAG. NO:1954) (SEQ. ID NO: 1967)
 5'-CGGCCGCCCTTTCTBGGCCCGGC-3' (FRAG. NO:1955) (SEQ. ID NO: 1968)

5 5'-GCCGCCCTTTCTBGGCCCGGC-3' (FRAG. NO:1956) (SEQ. ID NO: 1969)
 5'-CCGCCCTTTCTBGGCCCGGC-3' (FRAG. NO:1957) (SEQ. ID NO: 1970)
 5'-CGCCCTTTCTBGGCCCGGC-3' (FRAG. NO:1958) (SEQ. ID NO: 1971)
 5'-GCCTTTCTBGGCCCGGC-3' (FRAG. NO:1959) (SEQ. ID NO: 1972)
 5'-CCTTTCTBGGCCCGGC-3' (FRAG. NO:1960) (SEQ. ID NO: 1973)

10 10 5'-CTTTCTBGGCCCGGC-3' (FRAG. NO:1961) (SEQ. ID NO: 1974)
 5'-TTTCTBGGCCCGGC-3' (FRAG. NO:1962) (SEQ. ID NO: 1975)
 5'-TTTCTBGGCCCGGC-3' (FRAG. NO:1963) (SEQ. ID NO: 1976)
 5'-TTCTBGGCCCGGC-3' (FRAG. NO:1964) (SEQ. ID NO: 1977)
 5'-TCTBGGCCCGGC-3' (FRAG. NO:1965) (SEQ. ID NO: 1978)

15 15 5'-CTBGGCCCGGC-3' (FRAG. NO:1966) (SEQ. ID NO: 1979)
 5'-GCGBGGCTTCBCCTCGCTGGGCC-3' (FRAG. NO:1967) (SEQ. ID NO: 1980)
 5'-GCGBGGCTTCBCCTCGCTGGGCC-3' (FRAG. NO:1968) (SEQ. ID NO: 1981)
 5'-GCGBGGCTTCBCCTCGCTGGGCC-3' (FRAG. NO:1969) (SEQ. ID NO: 1982)
 5'-GCGBGGCTTCBCCTCGCTGGGCC-3' (FRAG. NO:1970) (SEQ. ID NO: 1983)

20 20 5'-GCGBGGCTTCBCCTCGCTGG-3' (FRAG. NO:1971) (SEQ. ID NO:1984)
 5'-GCGBGGCTTCBCCTCGCTG-3' (FRAG. NO:1972) (SEQ. ID NO:1985)
 5'-GCGBGGCTTCBCCTCGCT-3' (FRAG. NO:1973) (SEQ. ID NO:1986)
 5'-GCGBGGCTTCBCCTCGC-3' (FRAG. NO:1974) (SEQ. ID NO:1987)
 5'-GCGBGGCTTCBCCTCG-3' (FRAG. NO:1975) (SEQ. ID NO:1988)

25 25 5'-GCGBGGCTTCBCCTC-3' (FRAG. NO:1976) (SEQ. ID NO:1989)
 5'-GCGBGGCTTCBCCT-3' (FRAG. NO:1977) (SEQ. ID NO:1990)
 5'-GCGBGGCTTCBC-3' (FRAG. NO:1978) (SEQ. ID NO:1991)
 5'-GCGBGGCTTCBC-3' (FRAG. NO:1979) (SEQ. ID NO:1992)
 5'-GCGBGGCTTCBC-3' (FRAG. NO:1980) (SEQ. ID NO:1993)

30 30 5'-GCGBGGCTGTGTC-3' (FRAG. NO:1981) (SEQ. ID NO:1994)
 5'-GCGBGGCTGTG-3' (FRAG. NO:1982) (SEQ. ID NO:1995)
 5'-CGBGGCTTCBCCTCGCTGGGCC-3' (FRAG. NO:1983) (SEQ. ID NO:1996)
 5'-GBGGCTTCBCCTCGCTGGGCC-3' (FRAG. NO:1984) (SEQ. ID NO:1997)
 5'-BGGCTTCBCCTCGCTGGGCC-3' (FRAG. NO:1985) (SEQ. ID NO:1998)

35 35 5'-GGCTTCBCCTCGCTGGGCC-3' (FRAG. NO:1986) (SEQ. ID NO:1999)
 5'-GCTTCBCCTCGCTGGGCC-3' (FRAG. NO:1987) (SEQ. ID NO:2000)
 5'-CTGTCBCCTCGCTGGGCC-3' (FRAG. NO:1988) (SEQ. ID NO:2001)
 5'-TGTBCBCCTCGCTGCC-3' (FRAG. NO:1989) (SEQ. ID NO:2002)
 5'-GTCBCBCCTCGCTGCC-3' (FRAG. NO:1990) (SEQ. ID NO:2003)

40 40 5'-TCBCCTCGCTGGGCC-3' (FRAG. NO:1991) (SEQ. ID NO:2004)
 5'-CBCCTCGCTGGGCC-3' (FRAG. NO:1992) (SEQ. ID NO:2005)
 5'-BCCTCGCTGGGCC-3' (FRAG. NO:1993) (SEQ. ID NO:2006)
 5'-CCTCGCTGGGCC-3' (FRAG. NO:1994) (SEQ. ID NO:2007)
 5'-CTCGCTGGGCC-3' (FRAG. NO:1995) (SEQ. ID NO:2008)

45 45 5'-TCGCTGGGCC-3' (FRAG. NO:1996) (SEQ. ID NO:2009)
 5'-CGCTGGGCC-3' (FRAG. NO:1997) (SEQ. ID NO:2010)
 5'-GCGCGGCCGTCBTGCGCGCTCGGGCCGGG-3' (FRAG. NO:1998) (SEQ. ID NO:2011)
 5'-GCGCGGCCGTCBTGCGCGCTCGGGCCGG-3' (FRAG. NO:1999) (SEQ. ID NO:2012)

50 50 5'-GCGCGGCCGTCBTGCGCGCTCGGGCCGG-3' (FRAG. NO:2000) (SEQ. ID NO:2013)
 5'-GCGCGGCCGTCBTGCGCGCTCGGGCCGG-3' (FRAG. NO:2001) (SEQ. ID NO:2014)
 5'-GCGCGGCCGTCBTGCGCGCTCGGGCC-3' (FRAG. NO:2002) (SEQ. ID NO:2015)
 5'-GCGCGGCCGTCBTGCGCGCTCGGG-3' (FRAG. NO:2003) (SEQ. ID NO:2016)
 5'-GCGCGGCCGTCBTGCGCGCTCGGG-3' (FRAG. NO:2004) (SEQ. ID NO:2017)
 5'-GCGCGGCCGTCBTGCGCGCTCGGG-3' (FRAG. NO:2005) (SEQ. ID NO:2018)

55 55 5'-GCGCGGCCGTCBTGCGCGCTCG-3' (FRAG. NO:2006) (SEQ. ID NO:2019)
 5'-GCGCGGCCGTCBTGCGCGCTCG-3' (FRAG. NO:2007) (SEQ. ID NO:2020)
 5'-GCGCGGCCGTCBTGCGCGCTCG-3' (FRAG. NO:2008) (SEQ. ID NO:2021)
 5'-GCGCGGCCGTCBTGCGCGCTCG-3' (FRAG. NO:2009) (SEQ. ID NO:2022)
 5'-GCGCGGCCGTCBTGCGCGCTCG-3' (FRAG. NO:2010) (SEQ. ID NO:2023)

60 60 5'-GCGCGGCCGTCBTGCGCGCTCG-3' (FRAG. NO:2011) (SEQ. ID NO:2024)
 5'-GCGCGGCCGTCBTGCGCGCTCG-3' (FRAG. NO:2012) (SEQ. ID NO:2025)
 5'-GCGCGGCCGTCBTGCGCGCTCG-3' (FRAG. NO:2013) (SEQ. ID NO:2026)

5'-GCGCGGCCGTCTGG-3' (FRAG. NO:2014) (SEQ. ID NO:2027)
 5'-GCGCGGCCGTCTGG-3' (FRAG. NO:2015) (SEQ. ID NO:2028)
 5'-GCGCGGCCGTCTGG-3' (FRAG. NO:2016) (SEQ. ID NO:2029)
 5'-GCGCGGCCGTCTGG-3' (FRAG. NO:2017) (SEQ. ID NO:2030)
 5'-GCGCGGCCGTCTGG-3' (FRAG. NO:2018) (SEQ. ID NO:2031)
 5'-GCGCGGCCGT-3' (FRAG. NO:2019) (SEQ. ID NO:2032)
 5'-CGCGGCCGTCTBTGCGCGCCGGCCGGC-3' (FRAG. NO:2020) (SEQ. ID NO:2033)
 5'-GCGGCCGTCTBTGGCGCGCCGGCCGGC-3' (FRAG. NO:2021) (SEQ. ID NO:2034)
 5'-CGGCCGTCTBTGGCGCGCCGGCCGGC-3' (FRAG. NO:2022) (SEQ. ID NO:2035)
 10 5'-GGCGCTCTBTGGCGCGCCGGCCGGC-3' (FRAG. NO:2023) (SEQ. ID NO:2036)
 5'-GCCGTCTBTGGCGCGCCGGCCGGC-3' (FRAG. NO:2024) (SEQ. ID NO:2037)
 5'-CCGTCBTGGCGGCCTCGGGCCGGC-3' (FRAG. NO:2025) (SEQ. ID NO:2038)
 5'-CGTCBTGGCGGCCTCGGGCCGGC-3' (FRAG. NO:2026) (SEQ. ID NO:2039)
 5'-GTCBTGGCGGCCTCGGGCCGGC-3' (FRAG. NO:2027) (SEQ. ID NO:2040)
 15 5'-TCBTGGCGGCCTCGGGCCGGC-3' (FRAG. NO:2028) (SEQ. ID NO:2041)
 5'-CBTGGCGGCCTCGGGCCGGC-3' (FRAG. NO:2029) (SEQ. ID NO:2042)
 5'-BTGGCGGCCTCGGGCCGGC-3' (FRAG. NO:2030) (SEQ. ID NO:2043)
 5'-TGGCGGCCTCGGGCCGGC-3' (FRAG. NO:2031) (SEQ. ID NO:2044)
 20 5'-GGCGCGCTCGGGCCGGC-3' (FRAG. NO:2032) (SEQ. ID NO:2045)
 5'-GCGCGCTCGGGCCGGC-3' (FRAG. NO:2033) (SEQ. ID NO:2046)
 5'-CGGCGCTCGGGCCGGC-3' (FRAG. NO:2034) (SEQ. ID NO:2047)
 5'-GGCGCTCGGGCCGGC-3' (FRAG. NO:2035) (SEQ. ID NO:2048)
 5'-GCGTCGGGCCGGC-3' (FRAG. NO:2036) (SEQ. ID NO:2049)
 25 5'-CGTCGGGCCGGC-3' (FRAG. NO:2037) (SEQ. ID NO:2050)
 5'-GTCGGGCCGGC-3' (FRAG. NO:2038) (SEQ. ID NO:2051)
 5'-TCGGGCCGGC-3' (FRAG. NO:2039) (SEQ. ID NO:2052)
 5'-CGGGCCGGC-3' (FRAG. NO:2040) (SEQ. ID NO:2053)
 5'-CCGCBGGCCBGGCGCGCCGGCCGGC-3' (FRAG. NO:2041) (SEQ. ID NO:2054)
 30 5'-CCGCBGGCCBGGCGCGCCGGCCGGC-3' (FRAG. NO:2042) (SEQ. ID NO:2055)
 5'-CCGCBGGCCBGGCGCGCCGGCCGGC-3' (FRAG. NO:2043) (SEQ. ID NO:2056)
 5'-CCGCBGGCCBGGCGCGCCGGCCGGC-3' (FRAG. NO:2044) (SEQ. ID NO:2057)
 5'-CCGCBGGCCBGGCGCGCCGGCCGGC-3' (FRAG. NO:2045) (SEQ. ID NO:2058)
 5'-CCGCBGGCCBGGCGCGCCGGCCGGC-3' (FRAG. NO:2046) (SEQ. ID NO:2059)
 35 5'-CCGCBGGCCBGGCGCGCCGGCCGGC-3' (FRAG. NO:2047) (SEQ. ID NO:2060)
 5'-CCGCBGGCCBGGCGCGCCGGC-3' (FRAG. NO:2048) (SEQ. ID NO:2061)
 5'-CCGCBGGCCBGGCGCGCCGGC-3' (FRAG. NO:2049) (SEQ. ID NO:2062)
 5'-CCGCBGGCCBGGCGCGCCGGC-3' (FRAG. NO:2050) (SEQ. ID NO:2063)
 5'-CCGCBGGCCBGGCGCGCCGGC-3' (FRAG. NO:2051) (SEQ. ID NO:2064)
 40 5'-CCGCBGGCCBGGCGCGCCGGC-3' (FRAG. NO:2052) (SEQ. ID NO:2065)
 5'-CCGCBGGCCBGGCGCGCCGGC-3' (FRAG. NO:2053) (SEQ. ID NO:2066)
 5'-CCGCBGGCCBGGCGCGCCGGC-3' (FRAG. NO:2054) (SEQ. ID NO:2067)
 5'-CCGCBGGCCBGGCGCGCCGGC-3' (FRAG. NO:2055) (SEQ. ID NO:2068)
 5'-CCGCBGGCCBGGCGCG-3' (FRAG. NO:2056) (SEQ. ID NO:2069)
 45 5'-CCGCBGGCCBGGCGCG-3' (FRAG. NO:2057) (SEQ. ID NO:2070)
 5'-CCGCBGGCCBGGCGCG-3' (FRAG. NO:2058) (SEQ. ID NO:2071)
 5'-CCGCBGGCCBGGCGCG-3' (FRAG. NO:2059) (SEQ. ID NO:2072)
 5'-CCGCBGGCCBGGCGCG-3' (FRAG. NO:2060) (SEQ. ID NO:2073)
 5'-CCGCBGGCCBGGCGCG-3' (FRAG. NO:2061) (SEQ. ID NO:2074)
 50 5'-CCGCBGGCCBGGCGCG-3' (FRAG. NO:2062) (SEQ. ID NO:2075)
 5'-CCGCBGGCCB-3' (FRAG. NO:2063) (SEQ. ID NO:2076)
 5'-CCGCBGGCCB-3' (FRAG. NO:2064) (SEQ. ID NO:2077)
 5'-CGCBGGCCBGGCGCGCCGGCCGGCCGGC-3' (FRAG. NO:2065) (SEQ. ID NO:2078)
 5'-GCBGGCCBGGCGCGCCGGCCGGCCGGC-3' (FRAG. NO:2066) (SEQ. ID NO:2079)
 55 5'-CBGGCCBGGCGCGCCGGCCGGCCGGC-3' (FRAG. NO:2067) (SEQ. ID NO:2080)
 5'-BGGCCBGGCGCGCCGGCCGGCCGGC-3' (FRAG. NO:2068) (SEQ. ID NO:2081)
 5'-GCCCBGGCGCGCCGGCCGGCCGGC-3' (FRAG. NO:2069) (SEQ. ID NO:2082)
 5'-GCCBGCCGCGCCGGCCGGCCGGC-3' (FRAG. NO:2070) (SEQ. ID NO:2083)
 5'-CCBGGCGCGCCGGCCGGCCGGC-3' (FRAG. NO:2071) (SEQ. ID NO:2084)
 60 5'-CBGGCGCGCCGGCCGGCCGGC-3' (FRAG. NO:2072) (SEQ. ID NO:2085)
 5'-BGGGCGCGCCGGCCGGCCGGC-3' (FRAG. NO:2073) (SEQ. ID NO:2086)
 5'-GGGCGCGCCGGCCGGC-3' (FRAG. NO:2074) (SEQ. ID NO:2087)
 5'-GGCGCGCCGGCCGGC-3' (FRAG. NO:2075) (SEQ. ID NO:2088)

5'-CCCGCGGCCGGCTTGCCGCCGGGG-3' (FRAG. NO:2138) (SEQ. ID NO:2151)
 5'-CCGCGGCCGGCTTGCCGCCGGGG-3' (FRAG. NO:2139) (SEQ. ID NO:2152)
 5'-CGCGGCCGGCTTGCCGCCGGGG-3' (FRAG. NO:2140) (SEQ. ID NO:2153)
 5'-GCAGGCCGGCTTGCCGCCGGGG-3' (FRAG. NO:2141) (SEQ. ID NO:2154)
 5'-CGGCCGGCTTGCCGCCGGGG-3' (FRAG. NO:2142) (SEQ. ID NO:2155)
 5'-GGCCCGGCCGGCTTGCCGCCGGGG-3' (FRAG. NO:2143) (SEQ. ID NO:2156)
 5'-GCCCGGCCGGCTTGCCGCCGGGG-3' (FRAG. NO:2144) (SEQ. ID NO:2157)
 5'-CCCGGCCGGCTTGCCGCCGGGG-3' (FRAG. NO:2145) (SEQ. ID NO:2158)
 5'-CCGGCTTGCCGCCGGGG-3' (FRAG. NO:2146) (SEQ. ID NO:2159)
 10 5'-CGGCTTGCCGCCGGGG-3' (FRAG. NO:2147) (SEQ. ID NO:2160)
 5'-GGCTTGCCGCCGGGG-3' (FRAG. NO:2148) (SEQ. ID NO:2161)
 5'-GCTTGCCGCCGGGG-3' (FRAG. NO:2149) (SEQ. ID NO:2162)
 5'-CTTGGCCGCCGGGG-3' (FRAG. NO:2150) (SEQ. ID NO:2163)
 5'-TTGGCCGCCGGGG-3' (FRAG. NO:2151) (SEQ. ID NO:2164)
 15 5'-TGGCCGCCGGGG-3' (FRAG. NO:2152) (SEQ. ID NO:2165)
 5'-GCCGCCGCCGGGG-3' (FRAG. NO:2153) (SEQ. ID NO:2166)
 5'-CCGCCGCCGGGG-3' (FRAG. NO:2154) (SEQ. ID NO:2167)
 5'-CCGCCGCCGGGG-3' (FRAG. NO:2155) (SEQ. ID NO:2168)
 5'-CGCCGCCGGGG-3' (FRAG. NO:2156) (SEQ. ID NO:2169)
 20 5'-GCCGCCGCCGGGG-3' (FRAG. NO:2157) (SEQ. ID NO:2170)
 5'-GGCGGGGGCGGCCGGCTGGCTCGCCTBGGGGCCC-3' (FRAG. NO:2158) (SEQ. ID NO:2171)
 5'-GGCGGGGGCGGCCGGCTGGCTCGCCTBGGGGCCC-3' (FRAG. NO:2159) (SEQ. ID NO:2172)
 5'-GGCGGGGGCGGCCGGCTGGCTCGCCTBGGGCC-3' (FRAG. NO:2160) (SEQ. ID NO:2173)
 5'-GGCGGGGGCGGCCGGCTGGCTCGCCTBGGGC-3' (FRAG. NO:2161) (SEQ. ID NO:2174)
 25 5'-GGCGGGGGCGGCCGGCTGGCTCGCCTBGG-3' (FRAG. NO:2162) (SEQ. ID NO:2175)
 5'-GGCGGGGGCGGCCGGCTGGCTCGCCTBGG-3' (FRAG. NO:2163) (SEQ. ID NO:2176)
 5'-GGCGGGGGCGGCCGGCTGGCTCGCTBG-3' (FRAG. NO:2164) (SEQ. ID NO:2177)
 5'-GGCGGGGGCGGCCGGCTGGCTCGCTB-3' (FRAG. NO:2165) (SEQ. ID NO:2178)
 5'-GGCGGGGGCGGCCGGCTGGCTCGCT-3' (FRAG. NO:2166) (SEQ. ID NO:2179)
 30 5'-GGCGGGGGCGGCCGGCTGGCTCGCC-3' (FRAG. NO:2167) (SEQ. ID NO:2180)
 5'-GGCGGGGGCGGCCGGCTGGCTCGC-3' (FRAG. NO:2168) (SEQ. ID NO:2181)
 5'-GGCGGGGGCGGCCGGCTGGCTCGC-3' (FRAG. NO:2169) (SEQ. ID NO:2182)
 5'-GGCGGGGGCGGCCGGCTGGCTCGC-3' (FRAG. NO:2170) (SEQ. ID NO:2183)
 5'-GGCGGGGGCGGCCGGCTGGCT-3' (FRAG. NO:2171) (SEQ. ID NO:2184)
 35 5'-GGCGGGGGCGGCCGGCTGGC-3' (FRAG. NO:2172) (SEQ. ID NO:2185)
 5'-GGCGGGGGCGGCCGGCTGG-3' (FRAG. NO:2173) (SEQ. ID NO:2186)
 5'-GGCGGGGGCGGCCGGCTG-3' (FRAG. NO:2174) (SEQ. ID NO:2187)
 5'-GGCGGGGGCGGCC-3' (FRAG. NO:2175) (SEQ. ID NO:2188)
 5'-GGCGGGGGCGGCC-3' (FRAG. NO:2176) (SEQ. ID NO:2189)
 40 5'-GGCGGGGGCGGCC-3' (FRAG. NO:2177) (SEQ. ID NO:2190)
 5'-GGCGGGGGCGGCC-3' (FRAG. NO:2178) (SEQ. ID NO:2191)
 5'-GGCGGGGGCGGCC-3' (FRAG. NO:2179) (SEQ. ID NO:2192)
 5'-GGCGGGGGCGGCC-3' (FRAG. NO:2180) (SEQ. ID NO:2193)
 5'-GGCGGGGGCGGCC-3' (FRAG. NO:2181) (SEQ. ID NO:2194)
 45 5'-GGCGGGGGCGGC-3' (FRAG. NO:2182) (SEQ. ID NO:2195)
 5'-GGCGGGGGCGG-3' (FRAG. NO:2183) (SEQ. ID NO:2196)
 5'-GGGGGGCGGCCGGCTGGCTCGCCTBGGGGCCC-3' (FRAG. NO:2184) (SEQ. ID NO:2197)
 5'-GGGGGGCGGCCGGCTGGCTCGCCTBGGGGCCC-3' (FRAG. NO:2185) (SEQ. ID NO:2198)
 5'-GGGGGGCGGCCGGCTGGCTCGCCTBGGGGCCC-3' (FRAG. NO:2186) (SEQ. ID NO:2199)
 50 5'-GGGGGGCGGCCGGCTGGCTCGCCTBGGGGCCC-3' (FRAG. NO:2187) (SEQ. ID NO:2200)
 5'-GGGGGGCGGCCGGCTGGCTCGCCTBGGGGCCC-3' (FRAG. NO:2188) (SEQ. ID NO:2201)
 5'-GGCGGGCGGCCCTGGCTCGCCTBGGGGCCC-3' (FRAG. NO:2189) (SEQ. ID NO:2202)
 5'-GGCGGGCGGCCCTGGCTCGCCTBGGGGCCC-3' (FRAG. NO:2190) (SEQ. ID NO:2203)
 5'-GGCGGGCGGCCCTGGCTCGCCTBGGGGCCC-3' (FRAG. NO:2191) (SEQ. ID NO:2204)
 55 5'-GGCGGGCGGCCCTGGCTCGCCTBGGGGCCC-3' (FRAG. NO:2192) (SEQ. ID NO:2205)
 5'-GGCGGGCGGCCCTGGCTCGCCTBGGGGCCC-3' (FRAG. NO:2193) (SEQ. ID NO:2206)
 5'-GGCGGGCGGCCCTGGCTCGCCTBGGGGCCC-3' (FRAG. NO:2194) (SEQ. ID NO:2207)
 5'-GGCGGGCGGCCCTGGCTCGCCTBGGGGCCC-3' (FRAG. NO:2195) (SEQ. ID NO:2208)
 60 5'-GGCGGGCGGCCCTGGCTCGCCTBGGGGCCC-3' (FRAG. NO:2196) (SEQ. ID NO:2209)
 5'-GGCGGGCGGCCCTGGCTCGCCTBGGGGCCC-3' (FRAG. NO:2197) (SEQ. ID NO:2210)
 5'-GGCGGGCGGCCCTGGCTCGCCTBGGGGCCC-3' (FRAG. NO:2198) (SEQ. ID NO:2211)
 5'-GGCGGGCGGCCCTGGCTCGCCTBGGGGCCC-3' (FRAG. NO:2199) (SEQ. ID NO:2212)

5'-CTGGCTCGCCTBGGGCC-3' (FRAG. NO:2200) (SEQ. ID NO:2213)
 5'-TGGCTCGCCTBGGGCC-3' (FRAG. NO:2201) (SEQ. ID NO:2214)
 5'-GGCTCGCCTBGGGCC-3' (FRAG. NO:2202) (SEQ. ID NO:2215)
 5'-GCTCGCCTBGGGCC-3' (FRAG. NO:2203) (SEQ. ID NO:2216)
 5 5'-CTCGCCTBGGGCC-3' (FRAG. NO:2204) (SEQ. ID NO:2217)
 5'-TCGCTBGGGCC-3' (FRAG. NO:2205) (SEQ. ID NO:2218)
 5'-CGCCTBGGGCC-3' (FRAG. NO:2206) (SEQ. ID NO:2219)
 5'-GCCTBGGGCC-3' (FRAG. NO:2207) (SEQ. ID NO:2220)
 5'-CCTBGGGCC-3' (FRAG. NO:2208) (SEQ. ID NO:2221)
 10 10 5'-CTBGGGCC-3' (FRAG. NO:2209) (SEQ. ID NO:2222)
 5'-GGGTGGGCBGGCGCC-3' (FRAG. NO:2210) (SEQ. ID NO:2223)
 5'-GGTCGGCGBBGBGCTCGTCGTGGC-3' (FRAG. NO:2211) (SEQ. ID NO:2224)
 5'-GGTCGGCGBBGBGCTCGTCGTGG-3' (FRAG. NO:2212) (SEQ. ID NO:2225)
 5'-GGTCGGCGBBGBGCTCGTCGTG-3' (FRAG. NO:2213) (SEQ. ID NO:2226)
 15 15 5'-GGTCGGCGBBGBGCTCGTCGT-3' (FRAG. NO:2214) (SEQ. ID NO:2227)
 5'-GGTCGGCGBBGBGCTCGTCG-3' (FRAG. NO:2215) (SEQ. ID NO:2228)
 5'-GGTCGGCGBBGBGCTCGTC-3' (FRAG. NO:2216) (SEQ. ID NO:2229)
 5'-GGTCGGCGBBGBGCTCGT-3' (FRAG. NO:2217) (SEQ. ID NO:2230)
 5'-GGTCGGCGBBGBGCTCG-3' (FRAG. NO:2218) (SEQ. ID NO:2231)
 20 20 5'-GGTCGGCGBBGBGCTC-3' (FRAG. NO:2219) (SEQ. ID NO:2232)
 5'-GGTCGGCGBBGBGCT-3' (FRAG. NO:2220) (SEQ. ID NO:2233)
 5'-GGTCGGCGBBGBGCT-3' (FRAG. NO:2221) (SEQ. ID NO:2234)
 5'-GGTCGGCGBBGBGCT-3' (FRAG. NO:2222) (SEQ. ID NO:2235)
 5'-GGTCGGCGBBGBGCT-3' (FRAG. NO:2223) (SEQ. ID NO:2236)
 25 25 5'-GGTCGGCGBBGBGCT-3' (FRAG. NO:2224) (SEQ. ID NO:2237)
 5'-GTCGGCGBBGBGCTCGTCGTGGC-3' (FRAG. NO:2225) (SEQ. ID NO:2238)
 5'-TCGGCGBBGBGCTCGTCGTGGC-3' (FRAG. NO:2226) (SEQ. ID NO:2239)
 5'-CGGCGBBGBGCTCGTCGTGGC-3' (FRAG. NO:2227) (SEQ. ID NO:2240)
 5'-GGCGBBGBGCTCGTCGTGGC-3' (FRAG. NO:2228) (SEQ. ID NO:2241)
 30 30 5'-GCGBBGBGCTCGTCGTGGC-3' (FRAG. NO:2229) (SEQ. ID NO:2242)
 5'-CGBBGBGCTCGTCGTGGC-3' (FRAG. NO:2230) (SEQ. ID NO:2243)
 5'-GBBGBGCTCGTCGTGGC-3' (FRAG. NO:2231) (SEQ. ID NO:2244)
 5'-BBGBGCTCGTCGTGGC-3' (FRAG. NO:2232) (SEQ. ID NO:2245)
 5'-BGBGCTCGTCGTGGC-3' (FRAG. NO:2233) (SEQ. ID NO:2246)
 35 35 5'-GBGCTCGTCGTGGC-3' (FRAG. NO:2234) (SEQ. ID NO:2247)
 5'-BGCTCGTCGTGGC-3' (FRAG. NO:2235) (SEQ. ID NO:2248)
 5'-GCTCGTCGTGGC-3' (FRAG. NO:2236) (SEQ. ID NO:2249)
 5'-CTCGTCGTGGC-3' (FRAG. NO:2237) (SEQ. ID NO:2250)
 5'-TCGTCGTGGC-3' (FRAG. NO:2238) (SEQ. ID NO:2251)
 40 40 5'-GGGGCCCCCGGCCGCCGCC-3' (FRAG. NO:2239) (SEQ. ID NO:2252)
 5'-GGGGCCCCCGGCCGCCGCC-3' (FRAG. NO:2240) (SEQ. ID NO:2253)
 5'-GGGGCCCCCGGCCGCCGCC-3' (FRAG. NO:2241) (SEQ. ID NO:2254)
 5'-GGGGCCCCCGGCCGCCGCC-3' (FRAG. NO:2242) (SEQ. ID NO:2255)
 5'-GGGGCCCCCGGCCGCC-3' (FRAG. NO:2243) (SEQ. ID NO:2256)
 45 45 5'-GGGGCCCCCGGCCGCC-3' (FRAG. NO:2244) (SEQ. ID NO:2257)
 5'-GGGGCCCCCGGCCGCC-3' (FRAG. NO:2245) (SEQ. ID NO:2258)
 5'-GGGGCCCCCGGCC-3' (FRAG. NO:2246) (SEQ. ID NO:2259)
 5'-GGGGCCCCCGGCC-3' (FRAG. NO:2247) (SEQ. ID NO:2260)
 5'-GGGGCCCCCGGCCGCC-3' (FRAG. NO:2248) (SEQ. ID NO:2261)
 50 50 5'-GGCCCCCGGCCGCCGCC-3' (FRAG. NO:2249) (SEQ. ID NO:2262)
 5'-GCCCGCGCCGCCGCCGCC-3' (FRAG. NO:2250) (SEQ. ID NO:2263)
 5'-CCCCCGCGCCGCCGCC-3' (FRAG. NO:2251) (SEQ. ID NO:2264)
 5'-CCCGCGCCGCCGCC-3' (FRAG. NO:2252) (SEQ. ID NO:2265)
 5'-CCCGCGCCGCCGCC-3' (FRAG. NO:2253) (SEQ. ID NO:2266)
 55 55 5'-CGCGCCGCCGCC-3' (FRAG. NO:2254) (SEQ. ID NO:2267)
 5'-GCGCCGCCGCC-3' (FRAG. NO:2255) (SEQ. ID NO:2268)
 5'-CGCCGCCGCC-3' (FRAG. NO:2256) (SEQ. ID NO:2269)
 5'-GCCGCCGCC-3' (FRAG. NO:2257) (SEQ. ID NO:2270)
 5'-GGGGCGCGGGGGCGCCGGG-3' (FRAG. NO:2258) (SEQ. ID NO:2271)
 60 60 5'-GGCGGGGBGC GGCGCCGGG-3' (FRAG. NO:2259) (SEQ. ID NO:2272)
 5'-GGCGCGTCGCCGTGCCGCCGCCGCC-3' (FRAG. NO:2260) (SEQ. ID NO:2273)
 5'-GCGCGGGCBBCBGCGBGCCGGCGCG-3' (FRAG. NO:2261) (SEQ. ID NO:2274)

5' GCGCAGGGCCGCTGGCTGGGC-3' (FRAG. NO:2262) (SEQ. ID NO:2275)
5' GGGCGGGGTGGCTGCCCTGCGGGCC-3' (FRAG. NO:2263) (SEQ. ID NO:2276)
5' GGGCTGCTGCGCG CGGGCTCCGGCGA-3' (FRAG. NO:2264) (SEQ. ID NO:2277)
5' CTCGGGGGGGGGG CGGGCGCGGGG-3' (FRAG. NO:2265) (SEQ. ID NO:2278)
5 5' GGGCTGCCGCGGT CGGGCCCCCTTGCAGGG-3' (FRAG. NO:2266) (SEQ. ID NO:2279)
5' GCGCTCGCGCCGCTGGG-3' (FRAG. NO:2267) (SEQ. ID NO:2280)
5' GCGCCGCTTGGCC TGTGCGGC-3' (FRAG. NO:2268) (SEQ. ID NO:2281)
5' GCTGCTCCBCGCGCTGG-3' (FRAG. NO:2269) (SEQ. ID NO:2282)
5' GCCGGBGGCCGGC BGGTCCCGCG-3' (FRAG. NO:2270) (SEQ. ID NO:2283)
10 5' CCCGGCGGCCGGC 3GBBBGGCGGGCTGGGC-3' (FRAG. NO:2271) (SEQ. ID NO:2284)
5' GTCTCTCCCGCCCCGGCGCG-3' (FRAG. NO:2272) (SEQ. ID NO:2285)
5' GGGCGTCCGCTCCGGCCGTGGG-3' (FRAG. NO:2273) (SEQ. ID NO:2286)
5' GCGGGCACCGCGGC 3GCTCTGGCGTCGGC-3' (FRAG. NO:2274) (SEQ. ID NO:2287)

Bradykinin Receptor Nucleic Acids and Antisense Oligonucleotide Fragments

15	5'-GGTGCBCITG	BGCBTGTCGG	CGCGGTCCCG	TTBBGBGTGG	GCCCCGCCAGC	CCAGCCACTC	CACTGGGGC
	CGGGTGGCCA	GCACGAACAG	CACCCAGAGG	AAAGGGGGCG	GCCCCAGAAGG	GCAGCCCGCA	GGCCAGGATC
	AGGTCTGCTG	CGGC CGGAGA	TAATGGCATT	CACCACGCGG	CGGCCCGAGCG	CACGCCGCGC	ATCCGGCCCG
	GGTTCTGACC	TGCAGCCCCC	GTCTCCTTGG	CATTCTGGG	CCCCAGTCAC	TCCTCTCCCT	GCCCCCCCCTG
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	TCAGAGGGGG	CTCTGTAAGA	CCCAGGGGAG	TCAGGTGCAC	TGGAGCGCGG	GCTGCAGAAA	ACAGCCTGAG
	CTCCACCTCG	GCTCTCCCTT	GCCCTGGCTG	GTTGTCCTTA	ACCCCTGTCT	CCTCTGGAC	CAGTTTTGT
	CCTCCCTTG	TGACCTGAGG	GGTAACAGCC	TCTTTCCAC	TTTCTTTCA	CGCCGACATG	CTCAATGTCA
60	CCTTGCAAGG	GCCCACCTT	AACGGGACCT	TTGCCAGAG	CAAATGCC	CAAGTGGAGT	GGCTGGGCTG
	GCTCAACACC	ATCCAGCCCC	CCTTCCTCTG	GGTGTGTT	GTGCTGGCCA	CCCTAGAGAA	CATCTTTGTC
	CTCAGCGTCT	TCTGCTGCA	CAAGAGCAGC	TGCACTGG	CAGAGATCTA	CCTGGGGAAC	CTGGCCGCG

	CAGACCTGAT	CCTC GCCTGC	GGGCTGCCCT	TCTGGCCAT	CACCATCTCC	AACAACCTCG	ACTGGCTCTT
	TGGGGAGACG	CTC'GCCGCG	TGGTGAATGC	CATTATCTCC	ATGAACCTGT	ACAGCAGCAT	CTGTTTCTG
5	ATGCTGGTGA	GCA1 CGACCG	CTACCTGGCC	CTGGTAAAAA	CCATGTCCAT	GGGCCGGATG	CGCGGCGTGC
	GCTGGGCCAA	GCT'CATACGC	TTGGTGTACT	GGGGGTGTAC	GCTGCTCTG	AGCTCACCCA	TGCTGGTGT
	CCGGACCATG	AAGGAGTACA	GCGATGAGGG	CCACAACGTC	ACCGCTTG	TCATCAGCTA	CCCACCCCTC
	ATCTGGGAAG	TGT'CACCAA	CATGCTCTG	AATGCTGTGG	GCTTCCTGCT	GCCCCCTGAGT	GTCATCACCT
	TCTGCACGAT	GCAGATCATG	CAGGTGCTG	GGAAACAACGA	GATGCAGAAG	TTCAAGGAGA	TCCAGACGGA
10	GAGGAGGGCC	ACG'GTGCTAG	TCTGGTTGT	GCTGCTGCTA	TTCATCATCT	GCTGGCTGCC	CTTCCAGATC
	AGCACCTTCC	TGGATACGCT	GCATGCCCT	GGCATCCTCT	CCAGCTGCCA	GGACGAGCGC	ATCATCGATG
	TAATCACACA	GATC GCCTCC	TTCATGGCC	ACAGCAACAG	CTGCTCAAC	CCACTGGTGT	ACGTGATCGT
	GGGCAAGCGC	TTCCGAAAGA	AGTCTGGGA	GGTGTACCG	GGAGTGTGCC	AGAAAGGGGG	CTGCAGGTCA
15	GAACCCATTG	AGATGGAGAA	CTCCATGGGC	ACACTGCGGA	CCTCCATCTC	CGTGGAACGC	CAGATTACA
	AACTGCAGGA	CTGC GCAGGG	AGCAGACAGT	GAGCAAACGC	CAGCAGGGCT	GCTGTGAATT	TGTGTAAGGA
	TTGAGGGACA	GTG CTTTTC	AGCATGGCC	CAGGAATGCC	AAGGAGACAT	CTATGCACGA	CCTTGGGAAA
20	TGAGTGTGTA	TGTC TCCGGT	AAAACACCGG	AGACTAATT	CTGCCCTGCC	CAATTTCGA	GGGAGCATGG
	CTGTGAGGAT	GGGC'TGAACT	CACGCACAGC	CAAGGACTCC	AAAATCACAA	CAGCATTACT	GTTCTTATTT
	GCTGCCACAC	CTGAGGCCAGC	CTGCTCTTC	CCAGGAGTGG	AGGAGGCCTG	GGGGAGGGAG	AGGAGTGA
	GAGCTTCCCT	CCCGTGTGTT	CTCCGTCCCT	GCCCCAGCAA	GACAACCTAG	ATCTCAGGA	GAACATGCCAT
25	CCACGTTGG	TGCAATGGCT	GAGTGCACAA	GTGAGTTGTT	GCCCTGGGTT	TCTTAATCT	ATCAGCTAGA
	ACTTTGAAGG	ACA A TTTCIT	GCATTAATAA	AGGTTAACG	CTGAGGGGTC	CCTTGATAAC	AACCTGGAGA
	CCAGGATTTT	ATGGCTCCCC	TCACTGATGG	ACAAGGAGGT	CTGTGCCAA	GAAGAATCAA	TAAGCACATA
	TGAGCACTTC	TGT' TATCAG	TATTGAGCAC	TGTAGGCA	ATGTTCTCTC	CCTGGAAGAT	ATCAATGTT
	CTGTCTGTT	GTGA GGA	CGTCCCACC	ACGGCCTTT	TCAGCGCCGA	CATGCTCAAT	GTCACCTTGC
30	AAGGGCCCAC	TCTTAACGGG	ACCTTTGCC	AGAGCAAATG	CCCCAAGTG	GAGTGGCTGG	GCTGGCTCAA
	CACCATCCAG	CCCC CCTTCC	TCTGGGTCT	GTTCGTGCT	GCCACCTAG	GAACACATCTT	TGTCCCTCAGC
	GTCTTCTGCC	TGCA CAAGAG	CAGCTCACG	GTGGCAGAGA	TCTACCTGGG	GAACCTGGCC	GCAGCAGACC
	TGATCCTGGC	CTGCGGGCTG	CCCTTCTGGG	CCATCACCAT	CTCCAACAAAC	TTCGACTGGC	TCTTGGGGA
35	GACGCTCTG	CGCGTGTGTA	ATGCCATTAT	CTCCATGAAC	CTGTACAGCA	GCATCTGTTT	CCTGATGCTG
	GTGAGCATCG	ACCG CTACCT	GGCCCTGGT	AAAACCATGT	CCATGGGCCG	GATGCGCGGC	GTGCGCTGGG
	CCAAGCTCTA	CAGCTGGTG	ATCTGGGGT	GTACGCTGCT	CCTGAGCTCA	CCCATGCTGG	TGTTCCGGAC
	CATGAAGGAG	TACAGCGATG	AGGGCCACAA	CGTCACCGCT	TGTGTATCA	GCTACCCATC	CCTCATCTGG
40	GAAGTGTCA	CCAA CATGCT	CCTGAATGT	GTGGGCTCC	TGCTGCCCT	GAGTGTATCA	ACCTTCTGCA
	CGATGCAGAT	CATG CAGGTG	CTGCGGAACA	ACGAGATGCA	GAAGTTCAG	GAGATCCAGA	CGGAGAGGAG
	GGCCACGGTG	CTAC TCCCTG	TTGTGCTGCT	GCTATTCTC	ATCTGCTGCC	TGCCCTTCCA	GATCAGCAC
45	TTCCCTGGATA	CGCT GCATCG	CCTCGGCATC	CTCTCCAGCT	GCCAGGACGA	GCGCATCATC	GATGTAATCA
	CACAGATCGC	CTCC ITCATG	GCCTACAGCA	ACAGCTGCC	CAACCCACTG	GTGTACGTGA	TCGTGGCAA
	GCGCTTCCGA	AAGA AGTCTT	GGGAGGTGTA	CCAGGGAGTG	TGCCAGAAAG	GGGGCTGCA	GTCAGAACCC
	ATTCA GATGG	AGAA CTCCAT	GGGCACACTG	CGGACCTCCA	TCTCCGTGGA	ACGCCAGATT	CACAAACTGC
50	AGGACTGGC	AGGC AGCAGA	CAGTGAGCAA	ACGCCAGCAG	GGCTGCTGTG	AATTGTTGTA	AGGATTGAGG
	GACAGTTGCT	T AT GTTCTCTC	CCTGGAAAGAT	ATCAATGTTT	CTGTCTGTT	GTGAGGACTC	CGTGCCCACC
	ACGGCCTCTT	TCAG CGCCGA	CATGCTCAAT	GTCACCTTGC	AAGGGCCAC	TCTTAACGGG	ACCTTCTGCC
	AGAGCAAATG	CCCC CAAGTG	GAGTGGCTGG	GCTGGCTCAA	CACCATCCAG	CCCCCTTCTCC	TCTGGGTGCT
55	GTTCGTGCTG	GCC ACCCTAG	AGAACATCTT	TGTCCCTCAGC	GTCTTCTGCC	TGCACAAGAG	CAGCTGCACG
	GTGGCAGAGA	TCTACCTGGG	GAACCTGGCC	GCAGCAGACC	TGATCCTGGC	CTGCGGGCTG	CCCTTCTGGG
	CCATCACCAT	CTCC ACAAC	TTCGACTGGC	TCTTGGGGAA	GACGCTCTGC	CGCGTGGTGA	ATGCCATTAT
	CTCCATGAAC	CTGT ACAGCA	GCATCTGTTT	CCTGATGCTG	GTGAGCATCG	ACCGCTACCT	GGCCCTGGTG
60	AAAACCATGT	CCAT GGGCCG	GATGCGCGGC	GTGCGCTGGG	CCAAGCTCTA	CAGCTGGTG	ATCTGGGGGT
	GTACGCTGCT	CCTG AGCTCA	CCCATGCTGG	TGTTCCGGAC	CATGAAGGAG	TACAGCGATG	AGGGCCACAA
	CGTCACCGCT	TGTG TCATCA	GCTACCCATC	CCTCATCTGG	GAAGTGTCA	CCAACATGCT	CCTGAATGTC
	GTGGGCTTCC	TGCT GCCCC	GAGTGTATCA	ACCTCTGCA	CGATGCAGAT	CATGCAGGTG	CTGCGGAACA
	ACGAGATGCA	GAAC TTCAAG	GAGATCCAGA	CGGAGAGGGAG	GGCCACGGTG	CTAGTCCCTGG	TTGTGCTGCT
	GCTATTCTATC	ATCT GCTGGC	TGCCCTTCCA	GATCAGCACC	TTCCTGGATA	CGCTGCATCG	CCTCGGCATC
	CTCTCCAGCT	GCCA GAGCGA	GCGCATCATC	GATGTAATCA	CACAGATCGC	CTCCTTCATG	GCCTACAGCA
	ACAGCTGCC	CAACCCACTG	GTGTACGTGA	TCGTGGGCAA	GCGCTTCCGA	AAGAAGTCTT	GGGAGGTGTA
65	CCAGGGAGTG	TGCCAGAAAG	GGGGCTGCCAG	GTCAGAACCC	ATTCA GATGG	AGAAACTCCAT	GGGCACACTG
	CGGACCTCCA	TCTCGTGG	ACGCCAGATT	CACAAACTGC	AGGACTGGC	AGGGAGCAGA	CAGTGAGCAA
	ACGCCAGCAG	GGCT GCTGTG	AATTGTTGTA	AGGATTGAGG	GACAGTTGCT	T GCCCTTCAA	GATGAGCTGT
	TCCCGCCGCC	ACTCCAGCTC	TGGCTCTGG	GCTCCGAGGA	GGGGTGGGGAA	CGGTGGGGAC	ATCAGGCTGC
	CCCGCAGTAC	CAGG GAGCGA	CTGAAGTGCC	CATGCCGCTT	GCTCCGGAGA	AGGTGGGTGC	CGGGCAGGGG
70	CTGCTCCAGC	CGCC CACCT	CTGCTGGGAG	GACAAACTGT	CCCAGCACAG	AGGGAGGGAG	GGAGGGCAGG
	CAGCGGGAG	AAGTTCCCT	GTGGTGTGTT	GGAGTT	GCCCTTCAA	GATGAGCTGT	TCCCAGCCGCC
	ACTCCAGCTC	TGGC TCTGG	GCTCCGAGGA	GGGGTGGGGAA	CGGTGGTGAC	GGTGGGGAC	TCAGGCTGCC

CCGCAGTACC AGGGAGCGAC TGAAGTGCCC ATGCCGCTTG CTCCGGAGAA GGTGGGTGCC GGGCAGGGC
 TGCTCCAGCC GCCTCACCTC TGCTGGGAGG ACAAACTGTC CCAGCACAGA GGGAGGGAGG GAGGGCAGGC
 AGCGGGGAGA AGTTCCCTG TGGTCGTGGG GAGTT GAGCTCTCA ATATTTAGT GAAAGCTATA GATGAGGCTC
 5 CATAGGGGAT AAAGCACAGA CACACCTTT CAGAGGGCTT GTGGACTCTG GGCAGCCTGT CCATAGACCT
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 AGATGAGTCA ACCAACACAGC CAGGCCAGGG AGGGCCTTC CTCAGAGCC TACAGCCAGT TCACAGGCAA
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 TCAGGCTTGA TTGCTGGTT GTAGGCTTGT TATGAATCAA GTCACAGGGAGA AGAGGAGCTG ATGGGCTGGG
 10 GGGACGTCCT CTGGCCCTCC TGTCTCTTCC CCAGATCCAC TGGGCCACT CTTATCTGTT CTCTTCTGAA
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 CCGTACCCAG GAAACAGGAC AGCTTCTGCC ACTGTCGCC TTGGGAGCC TACGTGGCAT GACAAAGAAA
 15 TCCCAGGACT CGGCCTGCC ACCTGGCCAC CCTCTGTTA CACCTCCGC GTAAACGCC ACTGTTTACA
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 CAAATTATT CACATGGGGC TTCCCAGGCC ACTTGTGGT CAGCCGGAG GGACGTTTTT GCGGTCCCAC
 GACTCCAACG GGCAAGCGGG CCTACGCAA CATGGAATAC TTCCAAGAGC CTCCTGGCC CCCAGGGCTC
 AGAGGGTGGC AGAGCGGAGA GCGAAGGTGG CCCAGCCTT CCCAGGCCCA CAGCCAGCCT GGCTCCAGCT
 20 GGGCAGGAGT GCACAGCTCA GCTGGAGGCG AGGGGAAAGT GCCCAGGAGG CTGATGACAT CACTACCCAG
 CCCTCAAAG ATGAGCTGTT CCCGCCGCCA CTCCAGCTCT GGCTCTGGG CTCCAGGAGG GGGTGGGAC
 GGTGGTACG GTGCGGACAT CAGGCTGCC CGCAGTACCA GGGAGCGACT GAAGTGCCA TGCGCTTGC
 TCCGGAGAAG GTGCGTGCAG GGCAGGGCT GCTCAGGCC CTCACCTCT GCTGGGAGGA CAAACTGTCC
 CAGCACAGAG GGAACGGAGGG AGGGCAGGCA GCAGGGAGAA GTTCCCTGT GGTGTGGGG AGTTGGGAAA
 AGTTCCCTTC CTTCCGGAGG GAGG -3' (FRAG. NO:2275) (SEQ. ID NO:3018)
 25 5'- GAGCTCTTCA ATATTTAGT GAAAGCTATA GATGAGGCTC CATAGGGGAT AAAGCACAGA CACACCTTT
 CAGAGGGCTT GTGC ACTCTG GGCAGCCTGT CCATAGACCT CTGCCCCAA CTGGCAAGTC AGGAAACTCC
 AGATTAAGGA GCCCAATGT GGTTGAACAG CCAGGTGCAC AGATGAGTCA ACCACACAGC CAGGCCAGGG
 AGGGCCTTCA CTCAAGAGCC TACAGCCAGT TCACAGCCAA GCCAGGGCTA GCGCCAGGCC ACCCATAAAC
 TGATCTGAGA CTCTGTTTCC CTGTCTCCAT GATGATGGGA TCAGGTTGA TTGCTGGTTT GTAGGCTTGT
 30 TATGAATCAA GTCA CAGGGA AGAGGAAGCTG ATGGGCTGGG GGGACGTCCT CTGGCCCTCC TGTCTCTTCC
 CCAGATCCAC TGGC CCCACT CTTATCTGTT CTCTCTGAA GGAAGGGTTT TAAGGCTTCA AAAAAAAATG
 TTTGAAAGT CCCTGCCCT TCCAGCTCT ACCGCTCTAG CCCTGGGAGT GTAAAGTGT GCAGATAGTT
 AGTAAGTCTT TGAGCAAACAC TGAGAAAGCC AGCTTGAGCC TTGACATGGG AGAAACCTCC GCCATACATC
 TCCGAAGAAA CGGCCGCGT TCTCAGGGGA GCGCAAACAC CCGTACCCAG GAAACAGGAC AGCTTCTGCC
 35 ACTGTCGCC TTGGGAGCC TACGTGGCAT GACAAAGAAA TCCAGGACT CCGCCCTGCC ACCTGGCAC
 CCTCTGTTA CACCCTCCGC GTAAACGCC ACTGTTACA TCCAAAACCTC AGACACAAAAA TAACCACCTC
 AAGAAGATAA ATAATGATAA GAAATAAATG TTACGCGAGG CAAATTATT CACATGGGGC TTCCAGGGCC
 ACTTTGTGGT CAGCCGGGAG GGACGTTTTT GCCGCTCCAC GACTCCAACG GGCAGCCGGG CCTACGCAA
 CATGGAAATC TTCAAGAGC CTCCCTGCC CCCAGGGCTC AGAGGGTGGC AGAGCGGAGA GCGAAGGTGG
 40 CCGCAGCCTT CCGGCCCCA CAGCCAGCCT GGCTCCAGCT GGGCAGGAGT GCAGAGCTCA GCTGGAGGG
 AGGGGAAGT GCCCAGGAGG CTGATGACAT CACTACCCAG CCCTCAAAG ATGAGCTGTT CCCGCCCA
 CTCCAGCTCT GGCTCTGGG CTCCAGGGAG GGGTGGGGAC GGTGGTACG GTGGGGACAT CAGGCTGCC
 CGCAGTACCA GGGAGCGACT GAAGTGCCA TGCCGCTTGC TCCGGAGAAG GTGGGGCCG GGCAGGGGCT
 GCTCCAGCCG CCTCACCTCT GCTGGGAGGA CAAACTGTCC CAGCACAGAG GGAGGGAGGG AGGGCAGGCC
 45 GCGGGAGAA GTTCCCTGT GGTGTGGGG AGTTGGGAAA AGTTCCCTC CTTCCGGAGG GAGG-3'
 (FRAG.NO:2275) (SEQ.ID NO:2461)
 5'- GCCCTTCAAA GATGAGCTGT TCCCGCCGCC ACTCCAGCTC TGGCTCTGG GCTCCGAGGA GGGGTGGGG
 CGGTGGTGAC GGTGGGGACA TCAGGCTGCC CGCAGTAC AGGGAGCGAC TGAAGTGCC ATGCCGTTG
 50 CTCCGGAGAA GGTCGGTGC GGGCAGGGGC TGCTCCAGCC GCCTCACCTC TGCTGGGAGG ACAAACTGTC
 CCAGCACAGA GGGAGGGAG GAGGGCAGGC AGCGGGGAGA AGTTCCCTG TGGTCGTGGG GAGTT -3' (FRAG.
 NO:2275) (SEQ. ID NC:2460)
 5'- GCCCTTCAAA GATGAGCTGT TCCCGCCGCC ACTCCAGCTC TGGCTCTGG GCTCCGAGGA GGGGTGGGG
 CGGTGGGAC ATCAGGCTGC CGCAGTAC CAGGGAGCGA CTGAAGTGCC CATGCCGTT GCTCCGGAGA
 AGGTGGGTGC CGGCAGGGG CTGCTCCAGC CGCTCACCT CTGCTGGGAG GACAAACTGT CCCAGCACAG
 55 AGGGAGGGAG GGAGGCAGG CAGCGGGGAG AAGTTCCCT GTGGTCGTGG GGAGTT -3' (FRAG.NO:2275)(SEQ. ID
 NO:2459)
 5'- ATGTTCTCTC CCTGGAAGAT ATCAATGTTT CTGCTCTGTC GTGAGGAAC TCGGCCACC ACGGCCTCTT
 TCAGGCCGA CATGCTCAAT GTCACCTTG C AAGGGCCAC TCTTAACGGG ACCTTGCCC AGAGCAAATG
 CCCCCAAGTG GAGIGGCTGG GCTGGCTAA CACCATCCAG CCCCCCTTCC TCTGGGTGCT GTTCGTGCTG
 60 GCCACCTAG AGAAATCTT TGTCTCTAGC GTCTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA
 TCTACCTGGG GAACCTGGCC GCAGCAGACC TGATCTGCC CTGCGGGCTG CCCTCTGGG CCATCACCAT
 CTCCAACAAAC TTGCACTGCC TCTTGGGA GACGCTCTGC CGCGTGGTGA ATGCCATTAT CTCCATGAAC

	CTGTACAGCA	GCA ^t CTGTTT	CCTGATGCTG	GTGAGCATCG	ACCGCTACCT	GGCCCTGGTG	AAAACCATGT
	CCATGGCCG	GAT ^t CGCGGC	GTGCGCTGGG	CCAAGCTCTA	CAGCTTGGTG	ATCTGGGGGT	GTACGCTGCT
5	CCTGAGCTCA	CCC ^t TGCTGG	TGTTCCGGAC	CATGAAGGAG	TACAGCGATG	AGGGCCACAA	CGTCACCGCT
	TGTGTATCA	GCT ^t CCCATC	CCTCATCTGG	GAAGTGTTC	CCAACATGCT	CCTGAATGTC	GTGGGCTTCC
10	TGCTGCCCT	GAG ^t GTCACT	ACCTTCTGCA	CGATGCAGAT	CATGCAGGTG	CTGCGGAACA	ACGAGATGCA
	GAAGTTCAG	GAG ^t ATCCAGA	CGGAGAGGAG	GGCCACGGTG	CTAGCTCTGG	TTGTGCTGCT	GCTATTCATC
	ATCTGCTGGC	TGCC ^t CTTCCA	GATCAGCACC	TTCTCGATA	CGCTGCATCG	CCTCGGCATC	CTCTCCAGCT
	GCCAGGACGA	GCG ^t CATCATC	GATGTAATCA	CACAGATCGC	CTCCTTCATG	GCCTACAGCA	ACAGCTGCT
15	CAACCCACTG	GTG ^t ACGTGA	TCGTGGGCA	GCCTTCCGA	AAGAACGTCT	GGGAGGTGTA	CCAGGGAGTG
20	TGCCAGAAAG	GGGGCTGCAG	GTCAGAACCC	ATTCAAGATGG	AGAACCTCCAT	GGGCACACTG	CGGACCTCCA
	TCTCCGTGGA	ACGCCAGATT	CACAAACTGC	AGGACTGGGC	AGGGAGCAGA	CAGTGAGCAA	ACGCCAGCGAG
	GGCTGCTGTG	AATT ^t GTGTA	AGGATTGAGG	GACAGTTGCT T -3'	(FRAG. NO:2275)	(SEQ. ID NO:2458)	
25	5'- ATGTTCTCTC	CCTGGAAGAT	ATCAATGTTT	CTGCTCTGTT	GTGAGGACTC	CGTCCCACC	ACGGCCTCTT
	TCAGGCCGA	CAT ^t CTCAAT	GTCACCTTGC	AAAGGCCAAC	TCTTAACCGG	ACCTTGCCCC	AGAGCAAATG
30	CCCCCAAGTG	GAG ^t GGCTGG	GCTGGCTCAA	CACCATCCAG	CCCCCCTTCC	TCTGGGTGCT	GTTCGTGCTG
	GCCACCTAG	AGAA ^t CATCTT	TGTCCTCAGC	GTCTCTGCC	TGACAAGAG	CAGCTGCACG	GTGGCAGAGA
	TCTACCTGGG	GAAC ^t CTGGCC	GCAGCAGACC	TGATCCTGGC	CTGCGGGCTG	CCCTCTGGG	CCATCACCAT
	CTCCAACAAAC	TTCC ACTGGC	TCTTGGGGA	GACGCTCTGC	CGCGTGTGA	ATGCCATTAT	CTCCATGAAC
35	CTGTACAGCA	GCA ^t CTGTTT	CCTGATGCTG	GTGAGCATCG	ACCGCTACCT	GGCCCTGGTG	AAAACCATGT
40	CCATGGCCG	GAT ^t CGCGGC	GTGCGCTGGG	CCAAGCTCTA	CAGCTTGGTG	ATCTGGGGGT	GTACGCTGCT
	CCTGAGCTCA	CCC ^t ATGCTGG	TGTTCCGGAC	CATGAAGGAG	TACAGCGATG	AGGGCCACAA	CGTCACCGCT
	TGTGTATCA	GCT ^t CCCATC	CCTCATCTGG	GAAGTGTTC	CCAACATGCT	CCTGAATGTC	GTGGGCTTCC
45	GAAGTTCAG	GAG ^t ATCCAGA	CGGAGAGGAG	GGCCACGGTG	CATGCAAGCA	GGGAGGTGTA	CCAGGGAGTG
50	ATCTGCTGGC	TGCC ^t CTTCCA	GATCAGCACC	TTCTCGATA	GTGAGGACTC	CGTCCCCTG	CTCTCCAGCT
	GCCAGGACGA	GCG ^t CATCATC	GATGTAATCA	CACAGATCGC	CTCCTTCATG	GCCTACAGCA	ACAGCTGCT
	CAACCCACTG	GTG ^t ACGTGA	TCGTGGGCA	GCCTTCCGA	AAGAACGTCT	GGGAGGTGTA	CCAGGGAGTG
	TGCCAGAAAG	GGGGCTGCAG	GTCAGAACCC	ATTCAAGATGG	AGAACCTCCAT	GGGCACACTG	CGGACCTCCA
55	TCTCCGTGGA	ACGCCAGATT	CACAAACTGC	AGGACTGGGC	AGGGAGCAGA	CAGTGAGCAA	ACGCCAGCGAG
60	30 GGCTGCTGTG	AATT ^t GTGTA	AGGATTGAGG	GACAGTTGCT T -3'	(FRAG. NO:2275)	(SEQ. ID NO:2457)	
5'- TGATCCTATC	AC ^t AACCTGAG	AGTAGTTTT	ACTCCATTAA	CAGGTGAGGT	CATTGTGGTT	CAAGGACGTT	
	AAGTAACCTC	CCCAGCTCAC	ACGGCTTATA	AGTAAGGCAG	CCAGGATGTG	AACCCAGTAG	GACTATCTGG
	CTGCAAAGTC	CCC ^t ACCTCC	CTCGCCATCT	GTATCCTCCA	ATCATCTTC	GTGCTTGCT	GATAGAAGGT
	ACGGAAATAC	GAT ^t CCACAG	ACTGTCCAGG	AAAGACAGAAA	CTAGGCAAGAT	GGGCTGGCCA	TGGTCTCCA
35	GCCAGACTGG	AAATCTCCAGG	TCTGGAATGA	TATCATTTTT	CTTTTTAAT	AAATAACTC	ACCCACCA
	CGGCTTGGAG	AGG ^t CTCAAAG	GTGACCAACT	CCCTTGGGAG	GGCCCCGGTT	GATAAGGAAG	GAATGTGAAT
	CCTCCCATCA	CGGA AGCTTC	AAGGAGGTCA	AGGGTCCAAC	ACTTGAGATT	GTTAGTGTG	TTGGTGGATA
	CTGCAGAATA	TCCAGTGGAG	CCTCAGATGA	AGAACATGAG	GCCCCGTTA	GATCCAAGGA	TCAGAGGGG
40	CTCTGTAAAGA	CCCAGGGGAG	TCAGGTGCA	TGGAGCGCGG	GCTGCAGAAA	ACAGCTGAG	CTCCACCTCG
	GCTTCTCCTT	GCC ^t TGGCTG	GTTGCTCTTA	ACCCCTGTCT	CCTTCTGGAC	CAGTTTTGT	CCTTCCCTTG
	TGACCTGAGG	GGT ^t ACAGCC	TCTTTCCAC	TTCTTTCAG	CGCCGACATG	CTCAATGTCA	CCTTGCAAGG
	GCCCACCTT	AAACGGGACCT	TTGCCAGAG	CAAATGCC	CAAGTGGAGT	GGCTGGGCTG	GCTCAACACC
45	ATCCAGCCCC	CCT ^t CCCTCG	GGTGCTGTT	GTGCTGGCCA	CCCTAGAGAA	CATCTTGTC	CTCAGCGCT
	TCTGCCTGCA	CAAGAGCAGC	TGCACGGTGG	CAGAGATCTA	CCTGGGGAAAC	CTGGCCGCAG	CAGACCTGAT
	GCTCTACAGC	TTGGTGTACT	GGGGGTGTAC	GCTGCTCTG	AGCTCACCCA	TGCTGGTGT	CCGGACCATG
	AAGGAGTACA	GCG ^t TGAGGG	CCACAACTGC	ACCGCTTGTG	TCATCAGCTA	CCCACCCCTC	ATCTGGGAAG
50	TGTTCACCAA	CAT ^t CTCCCTG	AATGTCGTGG	GCTTCTGCT	GCCCCCTGAGT	GTCATCACCT	TCTGCACGAT
	GCAGATCATG	CAG ^t GTGCTGC	GGAAACAACGA	GATGCAGAAG	TTCAAGGAGA	TCCAGACGGA	GAGGAGGGCC
	ACGGTGTAG	TCC ^t GGTTGT	GCTGCTGCTA	TTCATCATCT	GCTGGCTGCC	CTTCCAGATC	AGCACCTTCC
	TGGATACGCT	GCATCGCCTC	GGCATCCTCT	CCAGCTGCCA	GGACGAGCGC	ATCATCGATG	TAATCACACA
	GATGCCCTCC	TTCA ^t GGCCT	ACAGCAACAG	CTGCTCAAC	CCACTGGTGT	ACGTGATCGT	GGGCAAGCGC
55	TTCCGAAAGA	AGTC TTGGGA	GGTGTACCA	GGAGTGTGCC	AGAAAGGGGG	CTGCAGGTCA	GAACCCATTC
	AGATGGAGAA	CTCC ^t ATGGGC	ACACTGCGGA	CCTCCATCTC	CGTGGAACGC	CAGATTCA	AACTGCAGGA
	CTGGGCAGGG	AGCA ^t GACAGT	GAGCAAACGC	CAGCAGGGCT	GCTGTGAATT	TGTGTAAGGA	TTGAGGGACA
	GTTGCTTTTC	AGCA ^t GGGCC	CAGGAATGCC	AAGGAGACAT	CTATGCACGA	CCTTGGGAAA	TGAGTGTGTA
60	TGTCTCCGGT	AAAACACCAGG	AGACTAATTC	CTGCCCTGCC	CAATTTCGA	GGGAGCATGG	CTGTGAGGAT
	GGGGTGAACCT	CACC CACAGC	CAAGGACTCC	AAAATCACAA	CAGCATTACT	GTTCTTATTT	GCTGCCACAC
	CTGAGCCAGC	CTG ^t CCCTTC	CCAGGAGTGG	AGGAGGCC	GGGGAGGGAG	AGGAGTGA	GAGCTTCCCT
	CCCGTGTGTT	CTCC ^t GTCCCT	GCCCCAGCAA	GACAACCTAG	ATCTCCAGGA	GAACCTGCCAT	CCACGTTTGG

TGCAATGGCT GAG¹GCACAA GTGAGTTGTT GCCCTGGGTT TCTTAACTCT ATCAGCTAGA ACTTTGAAGG
 ACAATTCTT GCATTAATAA AGGTTAACCC CTGAGGGTC CCTTGATAAC AACCTGGAGA CCAGGATTTC
 ATGGCTCCCC TCACGTGATGG ACAAGGAGGT CTGTGCCAA GAAGAATCAA TAAGCACATA TGAGCACTTC
 TGTATATCAG TATTGAGCAC TGTAGGCA -3' (FRAG. NO:2275) (SEQ. ID NO:2456)
 5 5'- CTGCAGAAAA CAGCCTGAGC TCCACCTCGG CTTCTCCTTG CCCTGGCTGG TTGTCCTTAA CCCCTGTCTC
 CTTCTGGACC AGT¹TTTGTGTC CTTCCCTTGT GACCCCTGAGG GGTAACAGCC TCTTTCCAC TTTCTTCAG
 CGCCGACATG CTCATGTCA CTTGCAAGG GCCCACTCTT AACGGGACCT TTGCCCAGAG CAAATGCC
 CAAGTGGAGT GGC¹GGGCTG GCTCAACACC ATCCAGCCCC CTTCTCCTG GGTGCTGTTG GTGCTGGCCA
 CCCTAGAGAA CAT¹TTTGTGTC CTCAGCGTCT TCTGCCGCA CAAGAGCAGC TGACGGTGG CAGAGATCTA
 10 CCTGGGAAC CTGGCCGAG CAGACCTGAT CCTGGCCTGC GGGCTGCCCT TCTGGCCAT CACCATCTCC
 AACAACTTCG ACT¹GCTCTT TGGGGAGACG CTCTGCCGCG TGGTGAATGC CATTATCTCC ATGAACCTGT
 ACAGCAGCAT CTG¹TTCTG ATGCTGGTGA GCATCGACCG CTACCTGGCC CTGGTGAAA CCATGTCCAT
 GGGCCGGATG CGC¹CGCGTGC GCTGGCCAA GCTCTACAGC TTGGTGATCT GGGGGTGTAC GCTGCTCCTG
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DRAFT - NOT FOR CITATION

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 GGCTGCTGTG AATTGTGTA AGGATTGAGG GACAGTTGCT T -3' (FRAG. NO:2275) (SEQ. ID NO:2449)
 45 5'- ATGTTCTCTC CCTGGAAGAT ATCAATGTT CTGTCCTGTT GTGAGGACTC CGTCCCAC ACGGCCTCTT
 TCAGCGCCGA CATCCTCAAT GTCACCTGC AAGGGCCAC TCTTAACGGG ACCTTGCCT AGAGCAAATG
 CCCCCAAGTG GAGTGGCTGG GCTGGCTCAA CACCATCCAG CCCCCCTTCC TCTGGGTGCT GTTCGTGCTG
 GCCACCTAG AGAACATCTT TGTCCTCAGC GTCTCTGCC TGACACAAGAG CAGCTGCACG GTGGCAGAGA
 50 TCTACCTGGG GAAACCTGGCC GCAGCAGACC TGATCCTGGC CTGCGGGCTG CCCTCTGGG CCATCACCCT
 CTCCAACAAC TTCCACTGGC TCTTGGGG AAGCCTGTC GCGCTGGTGA ATGCCATTAT CTCCATGAAC
 CTGTACAGCA GCATCTGTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGTG AAAACCATGT
 CCATGGGCCG GATCAGCGCCG GTGCGCTGGG CCAAGCTCTA CAGCTTGGTG ATCTGGGGGT GTACGCTGCT
 CCTGAGCTCA CCCATGCTGG TGTTCCGGAC CATGAAGGAG TACAGCGATG AGGGCCACAA CGTCACCGCT
 TGTGTCATCA GCTACCATC CCTCATCTGG GAAGTGTCA CCAACATGCT CCTGAATGTC GTGGGCTTCC
 55 TGCTGCCCT GAGTGTACATC ACCTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA
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 ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCTGGATA CGTGCATCG CCTCGGCATC CTCTCCAGCT
 GCCAGGACGA GCGCATCATC GATGTAATCA CACAGATCGC CTCCCTCATG GCCTACAGCA ACAGCTGCT
 CAACCCACTG GTGTACGTGA TCGTGGGAA GCGCTCCGA AAGAAGTCTT GGGAGGTGTA CCAGGGAGTG
 60 TGCCAGAAAG GGGGCTGCAG GTCAGAACCC ATTCAAGATGG AGAAACTCCAT GGGCACACTG CGGACCTCCA
 TCTCCGTGGA ACGCCAGATT CACAAACTGC AGGACTGGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG
 GGCTGCTGTG AATTGTGTA AGGATTGAGG GACAGTTGCT T -3' (FRAG. NO:2275) (SEQ. ID NO:2448)

5'- TGATCCTATC ACAACCTGAG AGTAGTTTT ACTCCATTAA CAGGTGAGGT CATTGTGGTT CAAGGACGTT
 AAGTAACCTTC CCCAGCTCAC ACGGCTTATA AGTAAGGCAG CCAGGATGTG AACCCAGTAG GACTATCTGG
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 5 ACGGAATAC GATCACCACAG ACTGTCCAGG AAGACAGAAA CTAGGCAGAT GGGCTGGCCA TGGCTCCAA
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 CGGCTTGAG AGGC TCAAAAG GTGACCAACT CCCTTGGGAG GGGCCCGGT GATAAGGAAG GAATGTGAAT
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 TGACCTGAGG GGTACAGGCC TCTTTTCCAC TTCTTTCAG CGCCGACATG CTCAATGTCA CTTGCAAGG
 GCCCACTCTT AACGGGACCT TTGCCCCAGAG CAAATGCCCG CAAGTGGAGT GGCTGGGCTG GCTCAACACC
 ATCCAGCCCC CTCCTCTCTG GGTGCTGTT GTGCTGGCCA CCCTAGAGAA CATCTTGTC CTCAGCGTCT
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 GCTCTACAGC TTGGTGTACT GGGGGTGTAC GCTGCTCCTG AGCTCACCCA TGCTGGTGT CCGGACCATG
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 GCAGATCATG CAGGTGCTGC GGAACAAACGA GATGCAGAG TTCAAGGAGA TCCAGACGGAA GAGGAGGGCC
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 TGGATACGCT GCATCGCCTC GGCATCCTCT CCAGCTGCCA GGACGAGCGC ATCATCGATG TAATCACACA
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 CTGGGCAGGG AGCA GACAGT GAGAAACACG CAGCAGGGCT GCTGTGAATT TGTGTAAGGA TTGAGGGACA
 GTTGTCTTTC AGCACTGGCC CAGGAATGCC AAGGAGACAT CTATGCACGA CCTTGGGAAA TGAGTGTGTA
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 30 GGGGTAACT CACCACACG CAAGGACTCC AAAATCACAA CAGCATTACT GTTCTTATT GCTGCCACAC
 CTGAGCCAGC CTGCTCTTC CCAGGAGTGG AGGAGGCCCT GGGGAGGGAG AGGAGTGACT GAGCTTCCCT
 CCCGTGTGTT CTCCGTCCCT GCCCCAGCAA GACAACCTAG ATCTCCAGGA GAACTGCCAT CCACGTTTGG
 TGCAATGGCT GAGTGCACAA GTGAGTTGTT GCCCTGGGTT TCTTAAATCT ATCAGCTAGA ACTTTGAAGG
 ACAATTCTT GCATTAATAA AGGTTAACCC CTGAGGGGTC CCTTGATAAC AACCTGGAGA CCAGGATTT
 35 ATGGCTCCCC TCACIGATGG ACAAGGAGGT CTGTCACAA GAAGAATCAA TAAGCACATA TGAGCACTTC
 TGTATATCAG TATTGAGCAC TGTAGGCA -3' (FRAG. NO:2275) (SEQ. ID NO:2447)
 5'- CTGAGAAAAA CAGCCTGAGC TCCACCTCGG CTTCCTCTG CCCTGGCTGG TTGCTCTTAA CCCCTGTCTC
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 40 CAAGTGGAGT GGCCTGGGCTG GCTCAACACC ATCCAGCCCC CCTTCCTCTG GGTGCTGTTG GTGCTGGCCA
 CCCTAGAGAA CATCTTGTG CTCAGCGTCT TCTGCCCTGCA CAAGAGCAGC TGACGGTGG CAGAGATCTA
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 AACAACTTCG ACTGGCTCTT TGGGGAGACG CTCTGCCCG TGTTGAATGC CATTATCTCC ATGAACCTGT
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 5 CAAGGTTCCA GCTAACCAA TAACTATTGC ACAACCACCT GTCCCTGCCT CAGTCCCTC TTCTGTAACA
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 ATGTGAGGCA TCATACGCA GACGTAACTG GGATATGTTT ACTATAAGGA AAAGACACTG AGGTCTAGA -3'
 (FRAG. NO:2275) (SEQ. ID NO:2446)
 5' AAATGATAGA CGGTCAATAA TTGTTAAAT GCTTTTAAA ATGAATGCTT TAAGCCGGGT GCAGTGCCTC
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 15 TCTCAGAGAG GAAAGCTCCT AGGTCTTCTT TTCCCTCTGC AAACCTCCCG CCTTGAAGGT TCAGAAGGAC
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 20 AAACCCAGGT GCCCGGTGTT GCAGAGTGGC TGAAAGCTGG GATGGGGCAG ATCCCTGGCT ACATTGATGC
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	GCCACAGTTG	TCAGGAGTCA	GGCAGGGCAG	GGGCCGGGTG	GTGTCTTCTT	TGTGTTCTTG	CACTCAGGGC
	AGAGCTCAGC	ACACAGCAGA	CGCTAAAAAA	ACATTTAAAG	GATAGAACGA	TTGATTGTG	GGTCCCCCAG
5	TCTGGCTCCA	GGATGCCAGC	CAGCTGCTCC	TAGAACGAAA	CGGACTTTTC	CTGGAAATC	CCAGAGGTGA
	TGATCAGTAA	TCTCTCCCGT	GACTCGTAGT	TCAGCTCTTC	CTCCATGAGC	CTGACTATCA	GTGGACCTTC
	CAGAAAGAGC	CCCCTTTCTT	TCTCTCACCC	ACAGCACAGG	GCACGGGAA	AATGCCAAT	GAGTCCTGCC
	TCTGGGTGT	GCTTGGACT	TTTCAGTGTG	TCTCGCATCC	ACTCTTCAAA	TTGAATGTTG	CAACAGCCAT
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25	CCCCAAGTGG	AGTC GCTGGG	CTGGCTCAAC	ACCATCCAGC	CCCCCTTCC	CTGGGTGCTG	TTCGTGCTGG
	CCACCCCTAGA	GAACATCTT	GTCTCTAGCG	TCTTCTGCCT	GCACAAGAGC	AGCTCACCG	TGGCAGAGAT
	CTACCTGGGG	AACTTGGCCG	CAGCAGACCT	GATCCTGGCC	TGCGGGCTGC	CCTCTGGGC	CATCACCATC
	TCCAACAAC	TCGACTGGCT	CTTGGGGAG	ACGCTCTGCC	CGTGGTGAA	TGCCATTATC	TCCATGAACC
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30	CATGGGCCGG	ATGCGCGGCG	TGCGCTGGG	CAAGCTCTAC	AGCTGGTGA	TCTGGGGTG	TACGCTGCTC
	CTGAGCTCAC	CCAT'GCTGGT	TTTCCGGACC	ATGAAGGAGT	ACAGCGATGA	GGGCCACAAC	GTCACCGCTT
	GTGTCATCAG	CTACCCATCC	CTCATCTGGG	AAAGTGTAC	CAACATGTC	CTGAATGTCG	TGGGCTTCTT
	GTCGCCCTG	AGTGTATCA	CCTTCTGCAC	GATCAGATC	ATGCAGGTGC	TGCGGAACAA	CGAGATGCG
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	AGCCATCTCC	ATCT'GAAGG	AACTCAAAGA	CTCAAGTGGG	AACGACTGGG	CACTGCCACC	ACCAGAAAGC
	TGTTCGACGA	GACGGTCGAG	CAGGGTGTG	TGGGTGATAT	GGACAGCAGA	AGGGGGAGAC	CAAGGTTCCA

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 25 AAAGAACATC TGTCCTGTGA AAGACTCAAT GAGCTGTAT GTGTAAACAA GGAAGCATTT CACATCC
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 AAAAAAAA-3' (FRAG. NO:2275) (SEQ. ID NO:2444)
 5'- GAGCTCTTCA ATATTTAGT GAAAGCTATA GATGAGGCTC CATAGGGGAT AAAGCACAGA CACACCTTT
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 30 AGATTAAGGA GCCCAATGT GGTTGAACAG CCAGGTGAC AGATGAGTC ACCACACAGC CAGGCCAGGG
 AGGGCTTCA CTCAAGAGCC TACAGCCAGT TCACAGCAA GCCAGGGCTA GCGCAGGCC ACCCATAAAC
 TGATCTGAGA CTCITTTCC CTGTCCTCAT GATGATGGGA TCAGGCTGA TTGCTGGTT GTAGGCTTGT
 TATGAATCAA GTCACAGGGAG AGAGGAGCTG ATGGGCTGGG GGGACGCTCT CTGCCCTCC TGTCTCTTCC
 CCAGATCCAC TGGCCCCACT CTTATCTGTT CTCTCTGAA GGAAGGGTT TAAGGCTTCA AAAAAAAATG
 35 TTTGAAAGT CCCTGCCCT TCCAGCTCT ACCGTCAG CCCTGGGAGT GTAAAGTGCT GCAGATAGTT
 AGTAAGTCTT TGAGCAAAAC TGAGAAAGCC AGCCTGAGCC TTGACATGGG AGAACACCTCC GCCATACATC
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 40 AAGAAGATAA ATAATGATAA GAAATAAATG TTACCGGAGG CAAATTATT CACATGGGGC TCCCCAGGGC
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 CATGGAAATC TTCCAGAGC CTCCCTGGCC CCCAGGGCTC AGAGGGTGGC AGAGCGGAGA GCGAAGGTGG
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 45 CTCCAGCTCT GGCTCTGGG CTCCAGGGAG GGGTGGGGAC GGTGGTGACG GTGGGGACAT CAGGCTGCC
 CGCAGTACCA GGGAGCAGT GAAGTGCCA TGCCGCTTG TCCGGAGAAG GTGGGTGCCG GGCAGGGGCT
 GCTCCAGCCG CCTCACCTCT GCTGGGAGGA CAAACTGTCC CAGCACAGAG GGAGGGAGGG AGGGCAGGCA
 GCGGGGAGAA GTTCCCTGT GGTCTGGGG AGTTGGGAAA AGTCCCTTC CTTCCGGAGG GAGG-3'
 (FRAG.NO:2275) (SEQ. ID NO:2443)
 5'- GCCCTTCAAA GATGAGCTGT TCCCAGGCC ACTCCAGCTC TGGCTCTGG GCTCCGAGGA GGGGTGGGG
 50 CGGTGGTGAC GGTGGGGACA TCAGGCTGCC CCCAGGTAC AGGGAGCGAC TGAAGTGCC ATGCCGTTG
 CTCCGGAGAA GGTCGGTGC GGGCAGGGGC TGCTCCAGCC GCCTCACCTC TGCTGGGAGG ACAAAACTGTC
 CCAGCACAGA GGGAGGGAGG GAGGGCAGGC AGCAGGGAGA AGTTCCCTG TGTCGTGGG GAGTT -3' (FRAG.
 NO:2275) (SEQ. ID NC:2442)
 5'- AAATGATAGA CCGTCAATAA TTTGTTAAAT GCTTTTAAAT ATGAATGCTT TAAGCCGGGT GCAGTGCCTC
 55 ACATCTGAA TCCCAGCACT TTGGAGCCG GCGGGTGGAT TGTGTGAGGT CAGGAGTCG AGACCAACCT
 GGCCAACATG GCAAAACCTC ACTCTCTACC AAAAATACAA AAATTAGCCA GGCATGGTGG CAGGCACCTG
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 TGTGCTGCT CGTGCATCC TTTGCAAGTG TCCAAACCCCT GATCCCAGCT GTGCTTAGGG GTTCCTGCAA
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	TTTGAATTCC	CTGAACTGAC	CGTTGTCTGA	TCTCCACCTC	CCAACTGAAT	TAGGGGAGCT	GGGCTTCTGG
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5	ATAGACCACA	GCT TCCACA	CCCTTCCTAG	ACAGGGGTCA	CTTGGTATCC	TGGAGAGAGT	GTGAAGTCCT
	GGAATGAAA	GAGGGGGGAT	TAAGCCCCAC	CTCTAGCCAT	GGGACTGAGA	CAAGTCACCA	CCAACCCATC
	TGCGCTTGT	TTAC CTCTC	TGTGAGGCAA	GCACAGAGCC	CATGCCGTC	CCCCCTGGATG	GGAGTGATGT
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10	CTGGAAATAC	TCAGATGTGT	CTGTCTCCCT	TATTAGGTT	AAAGTCCCTC	AAGACCTGT	CTCCATCACAA
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	CCCCACCTGC	CTGC AATTCT	CCAAAGAACCC	TCCCCTTTAA	CAGTCCAGC	CTTTAACAGT	TCCAGTCTAA
	ACACATGACC	TTTC TCCTCT	AAATCAGCCC	CCCATCTCTG	CCTTTCAGG	AGATGGAAGC	CATGACACCT
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15	CCTCTGGAAT	CCAC TCTCTC	AGTCTCCATC	ATCCCAAGTC	GAAGCTAATG	GGCTAACTGG	TCCTTGCTTC
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	CCAACCTGAC	TGAGATATCC	TCTGACCCA	TCATCCCTCC	ACCCGTTTA	GTTCTGCTCA	CCCTCAGTGT
	TCTCATCAAT	AATCCACTCC	CCTCACAGGC	GCGTTTGGGA	CCCCATGTTT	TATGCTCTCA	CAGGACCTTT
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	AGCAGGCATC	TTCTGTATGA	TCCGATGGCT	TCTCAGAGCC	AGGGATGGC	CAGGATCCAT	CCCCTTGGCT
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	TCATGGTCA	AGA' TTCAGA	GCCCAGTAGA	GACAGCTTAT	CTCTGTTCCA	AGATGTTCTG	GGCCTTGGTT
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40	GCAATGAAA	AGGC CAAGAA	AGATGCTGCA	AAGATGTTAT	GACCTAGCCT	CAGAAATCAC	ACACCATCCC
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	CACCAAGCCC	CTCTCCAAGT	CTGTGTCCCA	CAACCCCCCT	GCTCCCTCCA	GGGCACCCCTC	CACCCCTCTGG
	GCCACAGTTG	TCAGGAGTC	GGCAGGGCAG	GGGCCGGGTG	GTGTCTCTT	TGTGTTCTG	CACTCAGGGC
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50	TCTGGCTCCA	GGATGCCAGC	CAGCTGCTCC	TAGAAGCAA	CGGACTTTTC	CTGGGAAATC	CCAGAGGTGA
	TGATCAGTAA	TCTC TCCCCT	GACTCGTAGT	TCAGCTCTTC	CTCCATGAGC	CTGACTATCA	GTGGACCTTC
	CAGAAAGAGC	CCC TTTTCT	TCTCTCACCC	ACAGCACAGG	GCACTGGGAA	AATGCCAAT	GAGTCCTGCC
	TCTGGGTGT	GCTT TGGACT	TTTCAGTGTG	TCTCGCATCC	ACTCTTCAC	TTGAATGTTG	CAACAGCCAT
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	TGCACATTGT	CTCT GATCCC	TATGACAACC	CTGAGAGGTA	GTGGTTTAA	CTGCCATGTT	ACAGGTGAGG
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60	TGAACCCAGT	AGGA CTATCT	GGCTGCAAAG	TCCCCACCC	CCTCGCCATC	TGTATCCTCC	AATCACTTC
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	ACCACCAAGAA	AGC T GTTCGA	TGAGACGGTC	GAGCAGGGTG	CTGTTGGTGA	TATGGACAGC	AGAAGGGGGA
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	GAGCATGGCT	GTGAGGATGG	GGTGAACCTA	CGCACAGCCA	AGGACTCCA	AATCACAA	GCATTACTGT
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 10 AAAAAAAA -3' (FRAG. NO:) (SEQ. ID NO 2431)
 5'-GGTBCBTTGBGCB TGTGGCGC-3' (FRAG. NO:2276) (SEQ. ID NO:2289)
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 15 5'-GGCCCAGAAGGGC AGCCCCGAGGCCAGGGATCAGGTCTGCTGCC-3'(FRAG.NO:2280)(SEQ.ID NO:2293)
 5'-GGAGATAATGGCA TCACCA CGCGGC-3' (FRAG. NO:2281) (SEQ. ID NO:2294)
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 5'-GGGTTCTGACCTGC AGCCCC-3' (FRAG. NO:2283) (SEQ. ID NO:2296)
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 20 5'-CAGTCACTCCTCTC CCTGCCCC-3' (FRAG. NO:2285) (SEQ. ID NO:2298)
 5'-CTTGCTGGGCAGGGACGG-3' (FRAG. NO:2286) (SEQ. ID NO:2299)
 5'-GGTBCBTTGBGCE TGTGGCGC-3' (FRAG. NO:2287) (SEQ. ID NO:2300)
 5'-GGTCCCGTTBBGBC TGCCCC-3' (FRAG. NO:2288) (SEQ. ID NO:2301)
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 25 5'-GGGTGGCCAGCAC GAACAGCACCCAGAGGAAGGGGGGC-3' (FRAG. NO:2290) (SEQ. ID NO:2303)
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 5'-GGAGATAATGGCA TCACCA CGCGGC-3' (FRAG. NO:2292) (SEQ. ID NO:2305)
 5'-GGCCCAGCGCAGC CGCGCATCCGGCCC-3' (FRAG. NO:2293) (SEQ. ID NO:2306)
 5'-GGGTTCTGACCTGC AGCCCC-3' (FRAG. NO:2294) (SEQ. ID NO:2307)
 30 5'-GTCTCCTGGCATT CCTGGGCC-3' (FRAG. NO:2295) (SEQ. ID NO:2308)
 5'-CAGTCACTCCTCTCCCTGCC-3' (FRAG. NO:2296) (SEQ. ID NO:2309)
 5'-CTTGCTGGGCAGGGACGG-3' (FRAG. NO:2297) (SEQ. ID NO:2310)
 5'-CCGTGTTGTCBGTGGTGCTG-3' (FRAG. NO:2298) (SEQ. ID NO:2311)
 5'-CCCGTTTBGGTBGGC-3' (FRAG. NO:2299) (SEQ. ID NO:2312)
 35 5'-GCTCCBBCBTTCCTCTCC-3' (FRAG. NO:2300) (SEQ. ID NO:2313)
 5'-TTGTTTCCGTTTC CTTG-3' (FRAG. NO:2301) (SEQ. ID NO:2314)
 5'-CCGTCTGTGGTT-3' (FRAG. NO:2302) (SEQ. ID NO:2315)

B2 Adrenergic Receptor Kinase Nucleic Acids and Antisense Oligonucleotide Fragments

5'- GCCCGCGCC CCAAGATGGC GGACCTGGAG GCGGTGCTGG CCGACGTGAG CTACCTGATG GCCATGGAGA
 40 AGAGCAAGGC CACGCCGGCC GCGCGCGCA GCAAGAAGAT ACTGCTGCC GAGCCCAGCA TCCGCAGTGT
 CATGCAGAAG TACC TGGAGG ACCGGGGCGA GGTGACCTTT GAGAAGATCT TTTCCCAGAA GCTGGGGTAC
 CTGCTCTTCC GAGACTTCTG CCTGAACAC CTGGAGGAGG CCAGGCCCTT GGTGGAATTG TATGAGGAGA
 TCAAGAAGTA CGAC AAGCTG GAGACGGAGG AGGAGCGTGT GGCCCGCAGC CGGGAGATCT TCGACTCAT
 CATCATGAAG GAGCTGCTGG CCTGCTCGCA TCCCTCTCG AAGAGTGCCA CTGAGCATGT CCAAGGCCAC
 45 CTGGGAAAGA AGCAGGTGCC TCCGGATCTC TTCCAGCCAT ACATCGAAGA GATTGTC GACATCGAAGAAC
 GGGACGTGTT CCAC AAATTG ATTGAGAGCG ATAAGTTCAC ACGGTTTGC CAGTGGAGA ATGTGGAGCT
 CAACATCCAC CTGACCATGA ATGACTTCAG CGTCATCGC ATCATTGGC GCGGGGGCTT TGGCGAGGTC
 TATGGGTGCC GGAAGGCTGA CACAGGAAG ATGTACGCCA TGAAGTGCCT GGACAAAAAG CGCATCAAGA
 TGAAGCAGGG GGAGACCTG GCCCTGAACG AGCGCATCAT GCTCTCGCTC GTCAGCACTG GGGACTGCC
 50 ATTCAATTGTC TGCAITGTCAT AC CGGTCCA CACGCCAGAC AAGCTCAGCT TCATCCTGGA CCTCATGAAC
 GGTGGGACC TGCACTACCA CCTCTCCAG CACGGGGTCT TCTCAGAGGC TGACATGCGC TTCTATGCGG
 CCGAGATCAT CCTGGCCTG GAGCACATGC ACAACCGCTT CGTGGTCTAC CGGGACCTGA AGCCAGCAA
 CATCCTCTG GACGAGCATG GCCACGTGCG GATCTGGAC CTGGGCTTG CCTGTGACTT CTCCAAGAAG
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 GCAGCACAAG ACCA AAGACA AGCATGAGAT CGACCGCATG ACGCTGACGA TGGCCGTGGA GCTGCCGAC
 TCCTTCTCCC CTGA ACTACG CTCCCTGCTG GAGGGGTTGC TGCAGAGGGA TGTCAACC GGAGTTGGCT
 GCCTGGCCG AGGGGCTCAG GAGGTGAAAG AGAGCCCTT TTTCCGCTCC CTGGACTGGC AGATGGTCTT
 CTTGCAGAAG TACC CTCCCC CGCTGATCCC CCCACGAGGG GAGGTGAACG CGGGCAGCG CTTCGACATT
 60 GGCTCCTTCG ATGAGGAGGA CACAAAAGGA ATCAAGTTAC TGGACAGTGA TCAGGAGCTC TACCGCAACT

TCCCCCTCAC CATCTCGGAG CGGTGGCAGC AGGAGGTGGC AGAGACTGTC TTGACACCA TCAACGCTGA
 GACAGACCGG CTGGAGGCTC GCAAGAAAGC CAAGAACAG CAGCTGGGCC ATGAGGAAGA CTACGCCCTG
 GGCAAGGACT GCA'CATGCA TGGCTACATG TCCAAGATGG GCAACCCCTT CCTGACCCAG TGGCAGCGGC
 GGTACTTCTA CCTGTTCCCC AACCGCCTCG AGTGGCGGGG CGAGGGCGAG GCCCGCAGA GCCTGCTGAC
 5 CATGGAGGAG ATCCAGTCGG TGGAGGAGAC GCAGATCAAG GAGCGAAGT GCCTGCTCCT CAAGATCCGC
 GGTGGGAAAC AGT'CATTTC GCAGTGCAG AGCACCCTG AGCTGGTGCA GTGGAAGAAG GAGCTGCGCG
 ACGCCTACCG CGAC GCCCAG CAGCTGGTC AGCGGGTGCC CAAGATGAAG ACAAGCCGC GCTCGCCCGT
 GGTGGAGCTG AGCAAGGTGC CGCTGGTCA CGCAGGGCAGT GCCAACGGCC TCTGACCCGC CCACCCGCCT
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 10 AAGGGCTTCC AGGC CCAGGA AACAGCAGAG GCACAGAAGT GAGAATGGGT GGGTGAGTTG GTGGGAAAC
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 15 AGAAGTAGAC AGA'TCACGG AGATTCTCAG GAGGCCAGAC AGGAGACTAT GGTGACAAAT TAGATTAGAG
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 GCCCACAGCA TGGI'AATGAG ATTTGAGCTT TATGTGCCA GGGCTGGAG GAGGGTCCTG TCACTTTGAA
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 GGAGAGTTT TACCGTAACT ACATGTGAA CCATCTGAA GGAACATCTG GATGGGATGG GGTACAGGGA
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 GTGTCAGGGC TGCC GCCCCA CTGGGGAGCC TGGGATCCAG AGATGTGACC CGAGGTGTG GTCAAGAGAAT
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 35 CCGAGGTAC GGGC'AGGGC TGAGCCCCG GTCGCAGGTC TGGTCTGGGG TCAGATTCCG CGCGGCCCTCC
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 GAGGCGCGGG CGG'CCTCGGG GGCGCGGGCC GGGCGCGGGC GCGAGCCGGC GCCATGGGGC GGCAGGGCCT GTGAGCGGGC
 GGAGCGGAGC GCGA'AGCGCG GGGCCGGGCC CGGAGCCGGC CGAGCAGGGC CAGGCCGGAG CGTCGGCCTC CGAGCCGGG
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 40 CCGGGCCGGG CCGAGCGCCG AGCGAGCAGG AGCGGCCGGCG CGGGCGCGG CGGGGGAGG AGGCAGCGCC
 GCCGCCAAGA TGGC'GGACCT GGAGGCGGTG CTGGCCGACG TGAGCTACCT GATGCCCATG GAGAAGAGCA
 AGGCCACGCC GGCC GCGCGC GCCAGCAAGA AGATACTGCT GCCCGAGCCC AGGTGAGGAG AAGCT-3' (FRAG.
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 5'-CCAGGAAGCT ACCTGGAGGA GGTGAGTCTT AGCGGATGAG TAGGAGTTGT CCACGGAGGA AGGTACACAG
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 CAGATTAAGG AGT'TGTTCA CCTAATCTGC TTTGGGCAGA GTGTTGGTGAG TCCTAGAGAC CCCCTCTAGGT
 CTCTCCTCTC AGTA GCCCCA GAAGGCCTGG AGAGCTGCTT CTGGGTGCCA AGCAGGGCAGT GACTCCATCA
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 50 AGAAGTAGAC AGA'TCACGG AGATTCTCAG GAGGCCAGAC AGGAGACTAT GGTGACAAAT TAGATTAGAG
 AAGGGGAGAG AATGAAGGAG CAGTTGGGGT AAAAGAAAAC TGAGGCTGAC ATGGGTATAT GGGTGGCGAG
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 GCCCACAGCA TGGI'AATGAG ATTTGAGCTT TATGTGCCA GGGCTGGAG GAGGGTCCTG TCACTTTGAA
 55 AGCAAAGAGA GGC'CTAGAG AGGGGCATGT TGAGATAGGA ATGCTGCCCT GAGACACCTG GCTTTCCCCA
 CTCTGGGTGG CTCTCAGCAG GGTGGGTTTC CCCTGCCAGG CAGCACTGAA CCTCTGTGCG CTTCCGGCTG
 GGAGAGTTT TACCGTAACT ACATGTGAA CCATCTGAA GGAACATCTG GATGGGATGG GGTACAGGGA
 AGGGAGCTGC CAAAGAGTGC GGCCAGGGAC CTGGGTCTAT GAGCTGGTT GGGGGTGGGG TTGGGTGCAG
 GGTACTTGTAT CCTGAGTGGG CCTTCTGCGG CCAGGATTGG TTCTAGAGTA GGAGGGTGG GATCGGGGAT
 60 GGGGGAAGCC TGT'ACTGCG CTGCAGTTGT CAGGTCCCAG GTTCTGGTG ACCTACTAAG GATTCTGGGT

CCAGTGTGGG TCCC'AGGTTA GACGTCCTAG TCCTGAGTCC GTGTCCACAG TTCTGGGTGT TGAGTCTAGG
 ACAGTGATCT GGAGTTGACA GTCCAATCTA GGCTCTGAGTC CTGACCCCCA GTCTAGAGTT CAGGGTCATG
 GTAGTAGCCT AGGCCTCAGAA TCAAGGTTGG GGTCAAGTAAC CAGGATGGGA TCGAGGTCAT GGTCCAAAT
 5 CTGGATCTGG GGACCTGTTG GGGGTCTGAG GTGAGTGTG CAGTCTGGGT ATGGCGTTGG AGACCCAGGG
 CTGTGATCTG AGG1CATGGT TAGAGTCTCA GGTGGTGGGC CAAGGTTGA GTCTGGGTG CTTGTTGGAG
 TCTGGTGTCA GGTCTGGAC TCGTCCAAG GTCAGGGAGT CCGGGGTTAT AGCCAGGGTC TGAGATGAAA
 GTCCCAGATG GTG1TCAGAG GTCTGAATCT GTGCTTGGT GAGCGTCCAG GTTCCCTGTG ATCACGTTG
 GTGTCAGGGC TGCC GCCCAG CTGGGGAGGC TGGGATCCAG AGATGTGACC CGAGGTTGTG GTCAGAGAAT
 10 GGGTCTCGGG TCG1CTTCGT GCCGGGTTCC TGTCTGTTG CAGGGCCGGG TCTCCGTCCA GCATCGAGGG
 CCGAGGTACAC GGGC'AGGGTC TGAGCCCCG GTCGCAGGTC TGGTTGGGG TCAGATTCCG CGCGGCCCTCC
 AGGGGGCGCC GTCGCCGCC GGCCTGGGCC CTCCGCGGCT CGCTGGCGT GTGCGCGCA GGCGGGCGCG
 GAGGCGCGGG CGGCCTCCGGG GGCAGCGGCC GGGCGCGGCC GGCAGCGGCC CCCGACTGC AGTCCCAGGG
 GGAGCGGAGC GCG1AGCGCG GGGCCGGGCC CGGAGCGGCC GGCATGGGC GGCGCCGCCT GTGAGCGGG
 15 GCGAGCGGAG CCGC'GGGCGC CGAGCAGGGC CAGGGGGAG CGTCGGCGCC CGAGGCCAG CGAGCCGCG
 CCGGGCCGGG CGCGAGCGCG AGCGAGCAGG AGCGGCGCG GCGGGCGCG CGGGGGAGG AGGCAGCGCC
 GCCGCAAGA TGGC'GGACCT GGAGGGCGGT CTGGCCGACG TGAGCTACCT GATGGCCATG GAGAAGAGCA
 AGGCCACGCC GGCCGCGCGC GCCAGCAAGA AGATACTGCT GCCCGAGGCC AGGTGAGGAG AAGCT-3' (FRAG.
 NO:_) (SEQ. ID NO:24'9)
 5'-GCCGCCGCCG CCAAGATGGC GGACCTGGAG GCGGTGCTGG CCGACGTGAG CTACCTGATG GCCATGGAGA
 20 AGAGCAAGGC CACGCCGGCC GCGCGGCCA GCAAGAAGAT ACTGCTGCC GAGCCCAGCA TCCGCAGTGT
 CATGCAGAAG TACCTGGAGG ACCGGGGCGA GGTGACCTT GAGAAGATCT TTTCCCAGAA GCTGGGGTAC
 CTGCTCTCC GAGACTTCTG CCTGAACCAC CTGGAGGAGG CCAGGCCCTT GGTGGAATT TATGAGGAGA
 TCAAGAAGTA CGAG1AAGCTG GAGACGGAGG AGGAGCGTGT GGCCCGCAGC CGGGAGATCT TCGACTCATA
 25 CATCATGAAG GAGCTGCTGG CCTGCTCGCA TCCCCTCTCG AAGAGTGCCA CTGAGCATGT CCAAGGCCAC
 CTGGGGAAAGA AGCAGGTGCC TCCGGATCTC TTCCAGCCAT ACATCGAAGA GATTGTCAA AACCTCCGAG
 GGGACGTGTT CCAC AAATTG ATTGAGAGCG ATAAGTTCAC ACGGTTTIGC CAGTGGAAAGA ATGTGGAGCT
 CAACATCCAC CTGA CCATGA ATGACTTCAG CGTGCACTCG ATCATTGGC GCGGGGGCTT TGGCGAGGTC
 TATGGGTGCC GGAAAGCTGA CACAGGCAAG ATGTACGCCA TGAAAGTGCCT GGACAAAAG CGCATCAAGA
 TGAAGCAGGG GGAGACCCCTG GCCCTGAACG AGGCATCAT GCTCTCGCT GTCAGCACTG GGGACTGCC
 30 ATTCAATTGTC TGCA1GTCTAT ACGCGTTCAC CACGCCAGAC AAGCTCAGCT TCATCCTGGAA CCTCATGAAC
 GGTGGGGACC TGCACCTACCA CCTCTCCAG CACGGGGTCT CGTGGCTAC CGGGACCTGA AGCCAGCCAA
 CCGAGATCAT CCTGGGCCCTG GAGCACATGC ACAACCGCTT CTGGGCCCTT CCTGTGACTT CTCCAAGAAG
 CATCCTCTG GACCGAGCATG GCCACGTGCG GATCTCGGAC CGGAGGTCTT GCAGAAGGGC GTGGCCTACG
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 GCAGCACAAAG ACCAAAGACA AGCATGAGAT CGACCGCATG ACGCTGACGA TGGCCGTGGA GCTGCCGAC
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 CTTGCAGAAG TACCCCTCCCC CGCTGATCCC CCCACGAGGG GAGGTGAACG CGGCCGACGC CTTCGACATT
 40 GGCTCCTTCG ATGAGGAGGA CACAAAAGGA ATCAAGTTAC TGGACAGTGA TCAGGAGCTC TACCGCAACT
 TCCCCCTCAC CATC1CGGGAG CGGTGGCAGC AGGAGGTGGC AGAGACTGTC TTCGACACCA TCAACGCTGA
 GACAGACCGG CTGCAAGGCTC GCAAGAAAGC CAAGAACAAAG CAGCTGGGCC ATGAGGAAGA CTACGCCCTG
 GGCAAGGACT GCAT1CATGCA TGGCTACATG TCCAAGATGG GCAACCCCTT CCTGACCCAG TGGCAGCGGC
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 45 CATGGAGGAG ATCC1AGTCGG TGGAGGAGAC GCAGATCAAG GAGCGCAAGT GCCTGCTCCT CAAGATCCGC
 GGTGGGAAAC AGT1CATTT GCAGTGGCAT AGCCACCTG AGCTGGTGCA GTGGAAGAAG GAGCTGCGCG
 ACGCCTACCG CGAC GCCCAG CAGCTGGTC AGCGGGTGC CAAGATGAAG AACAAAGCCGC GCTCGCCCGT
 GGTGGAGCTG AGCAAGGTGC CGCTGGTCCA GCGCGGCAGT GCCAACGGCC TCTGACCCGC CCACCCGCCT-3'
 (FRAG. NO:_) (SEQ. ID NO:2428)

50 CCR-2 CC Chemokine Receptor Nucleic Acids and Antisense Oligonucleotide Fragments

5'-CTTTGTGAAG AAGGAATTGG CAACACTGAA ACCTCCAGAA CAAAGGCTGT CACTAAGGTC CCGCTGCCTT
 GATGGATTAT ACAC1TTGACC TCAGTGTGAC AACAGTGACC GACTACTACT ACCCTGATAT CTTCTCAAGC
 CCCTGTGATG CGGA ACTTAT TCAGACAAAT GGCAAGTTGC TCCTTGCTGT CTTTATTGCA CTCCTGTTG
 TATTCACTCT TCTG1GGAAAC AGCCTGGTCA TCCTGGTCTT TGTGGTCTG AAGAAGCTGA GGAGCATCAC
 55 AGATGTATAC CTC1TGAACC TGGCCCTGTC TGACCTGCTT TTTGTCTTCT CCTTCCCTT TCAGACCTAC
 TATCTGCTGG ACCAGTGGGT GTTTGGACT GTAATGTGCA AAGTGGTGT TGGCTTTAT TACATTGGCT
 TCTACAGCAG CATC1TTTTCA ATCACCTCA TGAGTGTGGA CAGGTACCTG GCTGTGTCCT ATGCCGTGTA
 TGCCCTAAAG GTGAGGACGA TCAGGATGGG CACAACGCTG TGCCGGCAG TATGGCTAAC CGCCATTATG
 GCTACCATCC CAT1GCTAGT GTTTTACCAA GTGGCCTCTG AAGATGGTGT TCTACAGTGT TATTCACTT
 60 ACAATCAACA GAC1TTGAAAG TGGAAAGATCT TCACCAACTT CAAAATGAAC ATTGAGGCT TGTTGATCCC
 ATTACCACTC TTTA1GTTCT GCTACATTAA AATCTGCAC CAGCTGAAGA GGTGTCAAAA CCACAACAAG

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 TTCTTTCT CACT CCTTG CACAGTATGC ACATCTGGGA TGGATGTAGC ATAAGCCAAC AGCTGACTTA
 TGCCACCAT GTCA CAGAAA TCATTTCTT TACTCACTGC TGTGTGAACC CTGTTATCTA TGCTTTGTT
 5 GGGGAGAAAGT TCA AAGAACAC CCTCTCAGAA ATATTCAGA AAAGTTGCAG CCAAATCTTC AACTACCTAG
 GAAGACAAAT GCCT AGGGAG AGCTGTGAAA AGTCATCATC CTGCCAGCAG CACTCCTCCC GTTCCTCCAG
 CGTAGACTAC ATTGTGAG GATCAATGAA GACTAAATAT AAAAACATT TTCTGAATG GCATGCTAGT
 AGCAGTGTGAGC AAAAGGTGTT GTGTGAAAGG TTTCAAAAAA AAGTTCAGCA TGAAGGATGC CGTGTGTGTT
 GTTGCAACA CTTGGAACAC AATGACTGGA GACATAGTT TGCACTGCTG GCACAACATC AAGCCTGTGA
 10 TTGTGTTAT TGATGATGTT GAACAAGTGG TGGCTTGAG GGATTCTGTA TGCCAAGTGG AAAAAAAAGA
 TGTCTCCCGA ATTGACAGG TTATCA-3' (FRAG. NO.:_) (SEQ. ID NO:2462)

CCR-4 CC Chemokine Receptor Nucleic Acids and Antisense Oligonucleotide Fragments

5'-TTTCATCTCT CCCGGCTTAT TTGCTGGTTT CTCCGAATGC GGGCCTTGT TGTTCACGC TGGATCCCCA
 ACGCTAGAA CAGT'CGGTGG CACCGAGTTC GTCTTCTAT AAATATCGGA CTAATGCAT CTCTGTGATG
 15 GTAATACCCA CACC GTGTT TGAGAATGAA TGAGTGTATT TGTCAGTT AAAGCAACTAT CCTAGTGTATC TGTTACAAA
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 GTTACCGCTA TTATGAAATT ACTGAGCAAT ACATATCTAC ATCTGATCAG TCTCCAGAAT TATGCCAAT
 CCTACCTCT TCTG AAGTA TCTCCTAATT ATCTGCACCT GACCCCTAGTG ATGCTGTGAA TGTGCAAGTA
 TAGCTACATC CTCCGAAGGA AGGATCTTA CTCTTTTAC CTCCCTGAATG GGCTGCGTCT GCTGAAAGCG
 20 CGGGGGAATG GGC GGTTGGT AGCTTGGCCC TACTTCCAGC ATTGCCGCT ACTGGTTGGG TTACTCCAGC
 AAGTCACTCC CCTTCCCTGG GCCTCAGTGT CTCTACTGTA GCATTCAG GCATTCAGT CCATCCACTT
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 CCGCTTCCCT CAAACTTAGG AAATGCCCT TGCTTGTCA GGGAGGTCTT GTCCGGCTCC CCTCCCTCCT
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 CGCGTCTGCC CCTCTCCCCC ACCCCGCCTT CTCCCTCCCC GCCCCAGCGG CGCATGCGCC GCGCTCGGAG
 25 CGTGTTTTA TAAA AGTCCG GCGCGGCCA GAAACTTCAG TTTGTTGGCT GCGGCAGCAG GTAGCAAAGT
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 30 AGGAGAAACG ACTGAAAGA GCGTTCCAGT GGCTGCATGT GTCTCCCCCT TGAGTCCCGC CGCGCGCGGC
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 35 CAGTCTCCA GCACAGTAGG CAGAGGGCGG GAGAGGCGGG TGGACCCACC GCGCCGATCC TCTGAGGGGA
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 40 AGACTGGCAG GTGCAAGTGG GGAAACCGTT TGGCTCTCTC CGAGTCCAGT TGTGATGTTT AACCGTCGGT
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 45 GATCAGTGGC GGGG TAATGG GAAGCCACCC GGGAGAGTGA GGAAATGAAA CTTGGGGCGA GGACCACGGG
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 50 GCTT TAGGAG AATGAGTCTT TGCAACGCC CC GCGCCCTCCC CCGGTATCC TCCCTCTCC CCTCTCCCT
 CCCTGGCGA AAA CTTCTT ACAAAAGTT AATCACTGCC CCTCCTAGCA GCACCCACCC CACCCCCCAC
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 AGTGGCGGG GCAGAGGAGT TAGCCAAGAT GTGACTTTGA AACCCCTCAGC GTCTCAGTGC CCTTTGTTC
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 55 AGGAGAGTT TAGGATTCTA CATTAATTCT CTTGTGCCCT TAGCCCACCA CTTCAGAATT TCCTGAAGAA
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 GAAGTGAATG TCCATTCCCT TGCCCTTTT GCAGATATAC ACTTCAGATA ACTACACCGA GGAAATGGC
 TCAGGGACT ATGACTCCAT GAAGGAACCC TGTTCCGT AAGAAAATGC TAATTCAAT AAAATCTCC
 TGCCCACCAT CTACTCCATC ATCTCTTAA CTGGCATTGT GGGCAATGGA TTGGTCATCC TGGTCATGGG
 60 TTACCAAGAAG AAAC TGTGAGAA GCATGACCGA CAAGTACAGG CTGCACCTGT CAGTGGCCGA CCTCCTCTT
 GTCATCACGC TTCCCTCTG GGCAGTTGAT GCCGTGGCAA ACTGGTACTT TGGGAACCTC CTATGCAAGG

CAGTCCATGT CATC TACACA GTCAACCTCT ACAGCAGTGT CCTCATCTG GCCTTCATCA GTCTGGACCG
 CTACCTGGCC ATCGTCCACG CCACCAACAG TCAGAGGCCA AGGAAGCTGT TGGCTGAAAA GGTGGTCTAT
 GTTGGCGTCT GGATCCCTGC CCTCCTGCTG ACTATTCCCG ACTTCATCTT TGCCAACGTC AGTGAGGCAG
 5 ATGACAGATA TATCTGTGAC CGCTTCTACC CCAATGACTT GTGGGTGGTT GTGTTCCAGT TTCAAGCACAT
 CATGGTTGGC CTTAACCTGC CTGGTATTGT CATCCTGTCC TGCTATTGCA TTATCATCTC CAAGCTGTCA
 CACTCCAAGG GCCAACAGAA GCGCAAGGCC CTCAGAGCCA CAGTCATCTT CATCCTGGCT TTCTTCGCT
 GTTGGCTGCC TTACTACATT GGGATCAGCA TCGACTCCTT CATCCTCCTG GAAATCATCA AGCAAGGGTG
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 10 AACCCCATCC TCTATGCTT CCTTGGAGCC AAATTAAA CCTCTGCCA GCACGCACTC ACCTCTGTGA
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 15 AAAGGGAACG GAAACATTCCA GAGCGTGTAG TGAATCACGT AAAGCTAGAA ATGATCCCCA GCTGTTATG
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 20 TTCTGATTTC TGTTGACATT CTTTGGCTA GTAGAAGACA AAAGTAATAC ATTATGGTA TGCAAAAGCAC
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 TCAAATGGAA GTTIAGAAAT GGCCAGCCAG CACCTATTG TATGAAAGGT CATCTTCAG AGGATAAGACA
 TGTATAAAGA AGAAAGGTA TGCAGTCGTG TTTGGATTT ACTCCACCAT C-3' (FRAG. NO.:) (SEQ. ID NO: 2463)

25 CD-34 Nucleic Acids and Antisense Oligonucleotide Fragments

5'-AGGATGATGG TGATGGGGAA CTAATGGGG AAATATGGAA GGTCACAGGA AAAGTTAAC CAAGTTAGCA
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 30 GAAATGCTCA CACITCTAA CTGAGGTCT TACAGTAGAT TCCCTTGCA AGATTGTTAC TGGCTTACAA
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 GGCCACCGGC AAGCCTGCCA CAAAGGGTT AAAAGTAAAG TGGAAGTGGA GCTTGAAGAA GTGGGATGG
 GCCTCTCCAG GAAAGCTGAA CGAGGCATCT GGAGCCCAGA CAAACCTCCA CCTTTTTGG CCTCGACGGC
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 35 CAAGGAGAGG CGCIGCCTTG CCAAGACTAA AAAGGGAGGG GAGAAGAGAG GAAAAAAGCA AGAATCCCC
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 GCGTCTCTCT AGGAAGCGCG CGGGAAGGAT GCTGGTCCGC AGGGGCGCGC GCGCAGGGCC CAGGATGCC
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 40 CGCTGCCCTTG CCAA GACTAA AAAGGGAGGG GAGAAGAGAG GAAAAAAGCA AGAATCCCC ACCCCTCTCC
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 CAAGGCTGGG CAGTGTCCGA GAGAGCACCC CTCTCTGCAT CTGACCACTG GCTACCCCCA TGCTGGAGGT
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 CACACAGGAC CCCCTTCCCC TACCTCTGCCGC AATACAGGAA CCCCCAGGGG AAAGATGAGC
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 CTTGAACCAC TTCCCTCATC TCTCCTCCA GACACTGTGG ACTTGGTCAC CAGCTCCTCC CTTGTTCTCT
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 5 TTTGGGCTCC TTTTCTCCC TCTGGATCAA AGTAGGCAGG ACCATGGGAC CAGGCTTGG AGCTGAGCCT
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 GGCTTCCCTCC TCCCCTCCTGC CGACTCCTGG GTTGANCTGT TGCCCTAGTC CCCAACAGA TGCTTTCTG
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 10 CTAACCCCTA TCAC'CAGCTG CCTCTTCTGT GGGTGACCCA GTGCTTGTGTT TGCTGTGAT TTCTTTCCAG
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 TAGATATTTC TTCTGAAATAC AAAGTGATGT GTTTAAATAC TGCAATTAAA GTGATACTGA AACAC-3' (FRAG.No:_)
 (SEQ. ID NO:2466)
 5'-AGGATGATGG TGATGGGGAA CAAATGGGG AAATATGAA GGTACAGGA AAAGTTAAC CAAGTTAGCA
 AAAAGTTAAC ATAACACAAA AAGGTCTTC AGGAAAAAAA AAAGAAAAGA AAAGAAAAGA AAAGTCTCCA
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 CACACAGCAC AGGATCTGGT GAGGCTATCA CAAATGTGC CACATTGTTG TTAAGTTTA CCTGATTAAC
 GAAATGCTCA CACTCTAAA CTGAGGTCCT TACAGTAGAT TCCCTTGCAG AGATGTTAC TGGCTTACAA
 CTTAAAAATA AAGC AAAATC ACAAGGAAAG AAAAGTGGGG AAAAATCGG AGGAAACTTG CCCCTGCCCT
 GCCCACCGGC AAGUCGCCA CAAAGGGTT AAAAGTTAAC TGGAGTGGG GCTTGAAGAA GTGGGATGGG
 20 GCCTCTCCAG GAAAGCTGAA CGAGGCATCT GGAGCCGAA CAAACCTCA CCTTTTGGG CCTCGACGGC
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 CAAGGAGAGG CGCTGCCCTG CCAAGACTAA AAAGGGAGGG GAGAAGAGAG GAAAAAAGCA AGAATCCCCC
 ACCCTCTCC CGGGCGGAGG GGGCGGGAAAG AGCGCTCCT GGCCAAGCCG AGTAGTGTCT TCCACTCGGT
 GCGTCTCTC AGGAGCCGCG CGGGAAAGGAT GCTGGTCCGC AGGGGCGCG GCGCAGGGCC CAGGATGCCG
 25 CGGGGCTGGA CGCGCTTTG CTTGCTGAGT TTGCTGC-3' (FRAG. NO:_) (SEQ. ID NO:2464)
 5'-CCTTTTTGG CCI CGACGGC GGCAACCCAG CCTCCCTCCT AACGCCCTCC GCCTTGGG CCAACCAGGG
 GAGCTCAAGT TAGAGCAGC CAAGGAGAGG CGCTGCTTG CCAAGACTAA AAAGGGAGGG GAGAAGAGAG
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 30 AGTAGTGTCT TCCACTCGGT GCGTCTCTCT AGGAGCCGCG CGGGAAAGGAT GCTGGTCCGC AGGGGCGCG
 GCGAGGGCCC AGGATGCCG CGGGCTGGAC CGCGCTTGC TTGCTGAGTT TGCTGCCCTC TGGGTTCATG
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 ATGTATCCTA CCAAGAAACT ACAACACCTA GTACCCCTGG AAGTACCAAGC CTGACCCCTG TGTCTCAACA
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 35 CCAACGTTTC AACICCAGAG ACAACCTGA AGCCTAGCCT GTCACCTGGA AATGTTAG CACCTTCAAC
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 40 TGTCTACTGC TGGCTTGCG CAACAGAAC GAAATTCCA GCAAACCTCA ACTTATGAA AAGCACCAAT
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 45 GGCTCAGAAA AACGGGACCG GCCAGGCCAC CTCCAGAAC GGCCATTCAAG CAAGACAACA CGTGGTGGCT
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 CTGACCACTG GCTACCCCA TGCTGGAGGT GACATCTCTT ACGCCAACCT CTTCCCCACT GCACACACT
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 50 CCCAGGAACA ATCGATGCC TTGAGCACT CACACAGGAC CCCCTCCCC TACCCCTCC TCTCTGCCG
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 60 CCCCATATG GTCATAGCCC AGATCAGCT CTAACCCCTA TCACCACTG CCTCTCTGT GGGTCAATG
 GGTCTTGTGTT TGCTGTTGAT TTCTTCCAG AGGGGTTGAG CAGGGATCCT GGTTCATG ACGGTTGGAA
 ATAGAAATT CCACAGAAGA GAGTATTGG TAGATATT TTCTGAATAC AAAGTGATGT GTTTAAATAC

TGCAATTAAA GTGAT'ACTGA AACAC-3' (FRAG. No:_) (SEQ. ID NO:2465)

Eotaxin Antisense Nucleic Acids and Oligonucleotide Fragments

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5	GCCAAAGCTC	ACACCTTCAG	CCTCCAACAT	GAAGGTCTCC	GCAGCACTTC	TGTGGCTGCT	GCTCATAGCA
	GCTGCCTTCA	GCCCCCAGGG	GCTCGCTGGG	CCAGCTTCTG	TCCCAACCAC	CTGCTGCTT	AACCTGGCCA
	ATAGGAAGAT	ACCCCTTCAG	CGACTAGAGA	GCTACAGGAG	AATCACCAGT	GGCAAATGTC	CCCAGAAAGC
	TGTGATCTC	AAGACAAAC	TGGCCAAGGA	TATCTGTGCC	GACCCCAAGA	AGAAGTGGGT	GCAGGATTCC
10	ATGAAGTATC	TGGACCAAAA	ATCTCCAAC	CCAAAGCCAT	AAATAATCAC	CATTITGAA	ACCAAACCAAG
	AGCCTGAGTG	TTGCTTAATT	TGTTTCCCT	TCTTACAATG	CATTCTGAGG	TAACCTCATT	ATCAGTCCAA
	AGGGCATGGG	TTT'ATTATA	TATATATATA	TTTTTTTTT	AAAAAAAAC	GTATTGCATT	TAATTATATG
	AGGCTTAA	ACTTATCCTC	CATGAATATC	AGTTATTTT	AAACTGTAAC	GCTTGTGCA	GATTCTTAC
	CCCCTGGAG	CCCCAATTCG	ATCCCCGTG	ACGTGTGGGC	AATGTTCCCC	CTCTCCCTC	TCCTCCCTG
15	GAATCTGT	AAAGCTCTGG	CAAAGATGAT	CAGTATGAA	ATGTCATTGT	TCTTGTGAAC	CCAAAGTGTG
	ACTCATAAA	TGGAGTAAA	TGTTGTTTA	GGAATAC	ATGAAGGTCT	CCGCAGCACT	TCTGTGGCTG
	CTGCTCATAG	CAGCTGCCTT	CAGCCCCCAG	GGGCTCGCTG	GGCCAGCTTC	TGTCCCAACC	ACCTGCTGCT
	TTAACCTGGC	CAATAGGAAG	ATACCCCTTC	AGCGACTAGA	GAGCTACAGG	AGAATCACCA	GTGGCAAATG
	TCCCCAGAAA	GCTCTGATCT	TCAAGACAA	ACTGGCCAG	GATATCTGTG	CCGACCCCAA	GAAGAAGTGG
	GTGCAGGATT	CCATGAAGTA	TCTGACCAAA	AAATCTCCA	CTCCAAAGCC	ATAA	CCACATATTCCCTT
20	CCAAGGCAAG	ATCCAGATGG	ATTAAAAAT	GTACCAAGTC	CCTCTTA	GCTTGCCTCT	CTTCTGTTCT
	GCTTGACTTC	CTAGGATCTG	GAATCTGGTC	AGCAATCAGG	AATCCCTTC	TCGTGACCCC	CGCATGGGCA
	AAGGCTCCC	TGGGATCTCC	CACACTGTCT	GCTCCCTATA	AAAGGCGAGC	AGATGGGCCA	GAGGAGCAGA
	GAGGCTGAGA	CCAACCCAGA	AACCACCA	TCTCACGCCA	AAGCTCACAC	CTTCAGCCTC	CAACATGAAG
	GTCTCCGAG	CACITCTGTG	GCTGCTGCTC	ATAGCAGCTG	CCTTCAGCCC	CCAGGGGCTC	GCTGGGCCAG
25	GTAAGCCCCC	CAACTCTTA	CAGGAAAGGT	AAGTAACCA	CCTCCAGCT	ACTAGGTCA	CAAGAATCTT
	TACAGACTCA	CTGCAATTTC	TCCATTGAA	AAATAGGGAA	ACAGGTTTG	TGGGGGACAA	AGAAATGCT
	CAACCGTCAC	ATCCAGTCAC	TGGAAGAGGC	AGAACTAGAA	AGCTCCCGAG	TCTTTCCCC	ACATTCAAGA
	GGGCCGCTGG	GTGCATCTT	ACCCAGCTAT	CCTTACAGTG	TTTGGGAATG	GGGAATGGCT	CTGTCTTACT
	GTGGGCATGG	TGGGCACTTT	TGGCAGTGGG	AGAGAAGGAA	AATCTGTTGA	TTAGAAGCTC	AGTATGTTAA
30	TTCGACTCCA	GGACAGCTT	CAGAGACAGT	GGCTAAGAGA	AGAACGAGGT	CCCAGGGAT	CTCTTGAGGT
	GACTTATTTT	GACA CTCTTT	GGGAAAGTTA	TCTAGGAGAT	TTGTTCCATA	ACTCATTTTC	CCATACTCTG
	GTGACAAATT	TACIGAGTGT	ATCGGTCCCA	CTGAGCCAGT	GCATAGCATG	GTAACAAACAA	GTTCTAAATT
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35	ATTGATGGAT	ACTGTGATAA	AGCAGAAGAA	AGCTCTCAGG	AGTCTTGAT	AGGCAATGCA	CTGTGGCTCA
	AAAATGACAC	CCA'CACTTT	GTCTCCTTCT	TTATTGATCA	AAACTAATTAA	ATGCCTCCAA	CCAAACAAAA
	GTGGCCAAGA	ATATGCAAGTC	TACCTTGTTG	CTCAAAACAG	AGGATGGAGA	ATATTGGTG	AAAATTACCA
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40	TCCAGACACA	TAAGACTTCA	GAGCAGAGGG	ATTCTCCCTC	CACCTCTCGC	AATTCTTG	TTTCTCCTAA
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	TTTTTCCCC	AAAAITCAGC	TTCTGTCCCA	ACCACCTGCT	GCTTAACT	GGCCAATAGG	AAGATACCCC
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	TAAAGTTCAC	CCTCCCTAG	ACAAAAAAAT	AATGCTTAGG	GCACAGAGTC	AAGAACTGTG	GGAGTCATAG
45	ACTCTGATAG	TTTGACCTCT	ATGGTCCAAAT	TCATTAATTT	TCACAAGTGA	GTGTTCACTC	CCAGCTCCCT
	GCCTGGGAGA	TTGCTGTAGT	CATATCAATT	TCTTCAAGTC	AAGAGCAAAG	ATGGTTTAC	TGGGCCTTTA
	AGAGCAGCAA	CTAACCCAAAG	AGTCTCATCC	TTCTCCTCT	CCGTAGCAAC	CCTTGTCCA	GGGGCAGATG
	GTCCTTAAAT	ATTAGGGTC	AAATGGGCAG	AATTTCAAA	ACAATCCTT	CCAATTGCA	CCTGATTCTC
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50	CATGAAGTAT	CTGCAACAA	AATCTCCAAC	TCCAAAGCCA	TAATAATCA	CCATTTCGA	AACCAAACCA
	GAGCCTGAGT	GTTCCTTAAT	TTGTTTCCC	TTCTTACAAT	GCATTCTGAG	GTAACCTCAT	TATCAGTCCA
	AAGGGCATGG	GT'TTATTAT	ATATATATAT	ATATATTTTT	TTTAAAAAA	AAACGTATTG	CATTAAATT
	ATTGAGGCTT	TAACACTTAT	CCTCCATGAA	TATCAGTTAT	TTTAAACTG	AAAGCTTTG	TGCAGATTCT
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55	CCTGGAATCT	TGTAAAGGTC	CTGGCAAAGA	TGATCAGTAT	GAAAATGTCA	TTGTTCTGT	GAACCCAAAG
	TGTGACTCAT	TAATGGAAG	TAATGTTGTT	TTAGGAATAC	ATAAAGTATG	TGCATATT	ATTATAGTCA
	CTAGTTGTA	TTTTTTGTTG	GGAAATCCAC	ACTGAGCTGA	GGGG-3'	(FRAG. NO:_)	(SEQ. ID
	NO: 2494)						
	5'-GCATTTTTTC	AACTTTTATG	ATTTATTAA	CTTGTGGAAC	AAAAATAAAC	CAGAAACCAC	CACCTCTCAC
60	GCCAAAGCTC	ACACCTTCAG	CCTCCAACAT	GAAGGTCTCC	GCAGCACTTC	TGTGGCTGCT	GCTCATAGCA
	GCTGCCTTCA	GCCCCCAGGG	GCTCGCTGGG	CCAGCTTCTG	TCCCAACCAC	CTGCTGCTT	AACCTGGCCA

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 5 AGCCTGAGTG TTGCTTAATT TGTTTCCCT TCTTACAATG CATTCTGAGG TAACCTCATT ATCAGTCCAA
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 10 5'-ATGAAGGTCT CCCTCAGCACT TCTGTGCTG CTGCTCATAG CAGCTGCCCT CAGCCCCAG GGGCTCGCTG
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 GAGCTACAGG AGAATCACCA GTGGCAAATG TCCCCAGAAA GCTGTGATCT TCAAGACCAA ACTGGCCAAG
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 CTCCAAAGCC ATAA-3' (FRAG. NO:_) (SEQ. ID NO:2492)
 15 5'-CCACATATTCCCTCTCT CCAAGGGCAAG ATCCAGATGG ATTAAAAAAAT GTACCAAGTC CCTCCTACTA
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 20 CTCAGCCTC CAACATGAAG GTCTCCCGAG CACTTCTGTG GCTGCTGCTC ATAGCAGCTG CCTTCAGGCC
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 25 GGGATGGCT CTGCTTAACT GTGGGCATGG TGGGCATTT TGGCAGTGG AGAGAAGGAA AATCTGTTGA
 TTAGAAGCTC AGTATGTTAA TTCGACTCCA GGACAGCTTT CAGAGACAGT GGCTAAGAGA AGAACGAGGT
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 ACTCATTTTC CCATACTCTG GTGACAAATT TACTGAGTGT ATCGGTCCCA CTGAGCCAGT GCATAGCATG
 30 GTAACAAACAA GTTCTAAATT ATCAATGACT TAACAGAATT AACTAAATTAA ACAAAAGTTA CTTTCTCACT
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 40 AAAGCTGTGA TGTAAAGTAAA TAAAGTTCAC CCTCCCCTAG AAAAAAAAT AATGTCTAGG GCACAGAGTC
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 GTGTTCACTC CCAGCTCCCT GCCTGGGAGA TTGCTGTAGT CATATCAATT TCTTCAGTC AAGAGCAAAG
 ATGGTTTAC TGGGCCTTA AGAGCAGCAA CTAACCCAAG AGTCTCATCC TTCCCTCTCT CCGTAGCAAC
 CCTTTGTCCA GGGGCAGATG GTCTTAAAT ATTTAGGGTC AAATGGGCAG AATTTCAAA AACAAATCCTT
 45 CCAATTGCTAT CCTGATTCTC CCCACAGCTT CAAGACAAA CTGGCAAGG ATATCTGTGC CGACCCCAAG
 AAGAAGTGGG TGCAGGATT CATGAAGTAT CTGGACCAAA AATCTCCAAC TCCAAAGCCA TAAATAATCA
 CCATTTTGA ACCAAACCA GAGCCTGAGT GTTGTAAATT TTGTTTCCC TTCTTACAAT GCATTCTGAG
 GTAACCTCAT TATCAGTCCA AAGGGCATGG GTTTTATTAT ATATATATAT ATATATTTT TTTTAAACTG
 AAACGTATTG CATITAATT TATGAGGCTT TAAACATTAT CCTCCATGAA TATCAGTTAT TTTTAAACTG
 TAAAGCTTTG TGCAGATTCT TTACCCCCCTG GGAGCCCCAA TTCGATCCCC TGTACGTGT GGGCAATGTT
 50 CCCCTCTCC TCTCTCTC CCTGGAATCT TGTAAAGGTC CTGGCAAAGA TGATCAGTAT GAAAATGTCA
 TTGTTCTGT GAACCAAAG TGTGACTCAT TAAATGGAAG TAATGTTGTT TAGGAATAC ATAAAGTATG
 TGCAATTATT ATTATAGTCA CTAGTTGAA TTTTTTGTG GGAAATCCAC ACTGAGCTGA GGGGG-3' (FRAG.NO:_)
 (SEQ. ID NO:2493)

FK-506 Binding Protein Nucleic Acids and Oligonucleotide Fragments

55 5'- GCCAGGTGCG TGTTGGTCCA CGCCGCCCGT CGGCCGCCCGCC GCCCGCTCAG CGTCCGCCGC CGCCATGGGA
 GGCCGGAGCC GAGCGGGGT CGGGCAGCAG CAGGGACCCC CCAGAGGGCGG GGCCTGTGGG ACCGCTATGG
 GCGTGGAGAT CGACACCAC TCCCCCGAG ACGGAAGGAC ATTCCCCAAG AAGGGCCAAA CGTGTGTGGT
 GCACTACACA GGAATGCTCC AAAATGGGAA GAAGTTTGAT TCATCCAGAG ACAGAAACAA ACCTTTCAAG
 TTCAGAATTG GCAAACAGGA AGTCATCAAAG GTTGTGAAG AGGGTGCAGC CCAGATGAGC TTGGGGCAGA
 60 GGGCGAAGCT GACCTGCACT CCTGATGTGG CATATGGAGC CACGGGCCAC CCCGGTGTCA TCCCTCCCAA
 TGCCACCCCTC ATCTTGACG TGGAGCTGCT CAACTTAGAG TGAAGGCAGG AAGGAACCTCA AGGTGGCTG

AGATGGCTGC TGCCTCACCCCT CCTAGCCTGC TCTGCCACTG GGACGGCTCC TGCTTTGGG GCTCTTGATC
 AGTGTGCTAA CCTCACTGCC TCATGGCATC ATCCATTCTC TCTGCCAAG TTGCTCTGTA TGTGTTCGTC
 AGTGTTCATG CGAAATTCTTG CTTGAGGAAA CTTCGGTTGC AGATTGAAGC ATTTCAGGTT GTGCATTITG
 5 TGTGATGCAT GTACTAGCCT TTCCCTGATGA CAGAACACAG ATCTCTTGT CGCACAAATCT ACAC TGCCCT
 ACCTTCACTT AAACACACACA CACAAGGTGC TCAGACATGA AATGTACATG GCGTACCGTA CACAGAGGGA
 CTTGAGGCCAG TTACCTTGC TGTCACTTC TCTCTTATAA ATTCTGTTAG CTGCTCACTT AAACAATGTC
 CTCTTGAGA AAATGAAAAA TAAAGGCTCT GTGCTTGACA GAATTGGGC CGCCGCCAGG TCGCTGTTGG
 10 TCCACGCCGC CGCIGCGGCC GCCCCCCCAG TCAGCGTCC CGGCCGCCAT GGGAGTGCAG GTGAAACCCA
 TCTCCCCAGG AGACGGGCGC ACCTTCCCCA AGCGCGGCCA GACCTGCGTG GTGCACTACA CGGGGATGCT
 TGAAGATGGA AAGAAATTG ATTCCTCCCG GGACAGAAAC AAGCCCTTA AGTTTATGCT AGGCAAGCAG
 GAGGTGATCC GAGCCTGGGA AGAAGGGTT GCCAGATGA GTGTGGGTCA GAGAGCCAA CTGACTATAT
 CTCCAGATTA TGCCATGGT GCCACTGGC ACCCAGGCAT CATCCCACCA CATGCCACTC TCGTCTTGA
 15 TGTGGAGCTT CTAAACTGG AATGACAGGA ATGGCCTCT CCCTTAGCTC CCTGTTCTTG GATCTGCCAT
 GGAGGGATCT GGTGCGCTCA GACATGTCA CATGAGTCCA TATGGAGCTT TTCTGTATGT TCCACTCCAC
 TTTGTATAGA CATCTGCCCT GACTGAATGT GTTCTGTAC TCAGCTTGC TTCCGACACC TCTGTTCTC
 CTTCCCCCTT CTCCPCGTAT GTGTGTTAC CTAAACTATA TGCCATAAAC CTCAAGTTAT TCATTTTATT
 TTGTTTCTAT TTGGGGTGA AGATTCACTT TCAGTCTTT GGATATAGGT TTCAAATTAA GTACATGGTC
 AAGTATTAAAC AGCACAAGTG GTAGGTTAAC ATTAAAGATAG GAATTGGGT TGGGGGGGGG GTTGCAAGA
 20 ATATTTATT TTAATTTTTT GGATGAAATT TTATCTATT ATATATTAAA CATTCTTGCT GCTGCGCTGC
 AAAGCCATAG CAGATTGAG GCGCTGTTA GGACTGAATT ACTCTCAAG TTGAGAGATG TCTTGGGTT
 AAATTAAGG CGCTACCTAA AACTGAGGTG GGGATGGGA GAGCCTTGC CTCCACCACTT CCCACCCACC
 CTCCCCCTAA ACCCTCTGCC TTTGAAAGTA GATCATGTT ACTGCAATGC TGGACACTAC AGGTATCTGT
 CCCTGGGCCA GCAGGGACCT CTGAAGCCTT CTTGTGGCC TTTTTTTT TTCACTCTGT GGTTTTCTA
 25 ATGGACTTTC AGGAATTG TAATCTCATA ACTTTCCAAG CACCCAGTGA AAGCCCAGCC ATCATGACAA
 AATTGACAGT TTCAATTGAA GGTGCTGTT GTAGACTTAA CAGCTTCAAGG ATCTCTGT TTTTGTATGCT
 ATCCCTGAAT GTTCTCTAA GAAAATGATG CTGGTCATCG CTCAGCCCCCT TCTCAACCTCT TTGCTGTCT
 TGGCTCCCTC TGCIGATCTC AGTTTCTGG CTTTCTCTCC CCAGCACCAT TTATGAGTCT CAAGTTTAT
 GTGTAGTGTAT TTGCTGAGAA ATCGTTGCTG CACCCCTTCCC TATTGCAATA AAAGGCTTT ATGCCGAAT TC
 30 GAGACGGGCG CACCTTCCCC AAGCGCGGCC AGACCTGCGT GGTGCACTAC ACCGGGATGC TTGAAGATGG
 AAAGAAAATTG GATTCCTCCC GGGACAGAAA CAAGCCCTT AAGTTTATGC TAGGCAAGCA GGAGGTGATC
 CGAGGCTGGG AAGAAAGGGT TGCCCAGATG AGTGTGGTC AGAGAGCCAA ACTGACTATA TCTCCAGATT
 ATGCCTATGG TGCCACTGGG CACCCAGGCA TCATCCCACC ACATGCCACT CTCGCTTCTG ATGTGGAGCT
 35 TCTAAAATG GAAAGACAGG AATGGCCTCC TCCCTTAGCT CCGTGTCTT GGATCTGCCR TGGAGGGATC
 TGGTGCCTCC AGACATGTGC ACATGARTCC ATATGGAGCT TTCTGTATG TTCACTCCA CTTTGTATAG
 ACATCTGCCCT TGACTGAATG TGTTCTGTCA CTCAGCTTG CTTCCGACAC CTCTGTTCC TCTTCCCCCT
 TCTCTCGTA TGTGTGTTA CCTAAACTAT ATGCCATAAA CCTCAAGTTA TTCA-3' (FRAG.NO:_) (SEQ. ID
 NO:2499)
 5'- GCCAGGTCGC TG'TGGTCCA CGCCGCCCGT CGGCCGCCGC GCGCGCTCAG CGTCCGCCGC CGCCATGGGA-3'
 (FRAG. No:_) (SEQ. ID NO: 2495)
 5'-GGCCGGAGCC GA'GCCGGGGT CGGGCAGCAG CAGGGACCCC CCAGAGGCAGG GGCGCTGTGGG CCGCTATGG
 GCGTGGAGAT CGACACCAC TCCCCCGAG ACGGAAGGAC ATTCCCCAAG AAGGGCCAA CGTGTGTGGT
 GCACTACACA GGAATGCTCC AAAATGGAA GAAGTTTGTAT TCATCCAGAG ACAGAAACAA ACCTTTCAAG
 45 TTCAGAATTG GCAAACAGGA AGTCATCAAA GGTTTGAAG AGGGTGCAGC CCAGATGAGC TTGGGGCAGA
 GGGCGAAGCT GACCTGCACT CCTGATGTGG CATATGGAGC CACGGGCCAC CCCGGTGTCA TCCCTCCCAA
 TGCCACCCCT ATCTTGACG TGGAGCTGCT CAACTTAGAG TGAAGGCAGG AAGGAACCTCA AGGTGGCTGG
 AGATGGCTGC TGCICACCC CCTAGCCTGC TCTGCCACTG GGACGGCTCC TGCTTTGGG GCTCTTGATC
 AGTGTGCTAA CCTCACTGCC TCATGGCATC ATCCATTCTC TCTGCCCAAG TTGCTCTGTA TGTGTTCGTC
 50 AGTGTTCATG CGAAATTCTTG CTTGAGGAAA CTTCGGTTGC AGATTGAAGC ATTTCAGGTT GTGCAATTG
 TGTGATGCAT GTAGTAGCCT TTCCCTGATGA CAGAACACAG ATCTCTGT CGCACAAATCT ACAC TGCCCT
 ACCTTCACTT AAACACACACA CACAAGGTGC TCAGACATGA AATGTACATG GCGTACCGTA CACAGAGGGA
 CTTGAGGCCAG TTACCTTGC TGTCACTTT CTCCTTATAA ATTCTGTTAG CTGCTCACTT AAACAATGTC
 CTCTTGAGA AAATGAAAAA TAAAGGCTCT GTGCTGACA-3' (FRAG. NO:_) (SEQ. ID NO:2496)
 5'-GAATTCCGGGC CGCCGCCAGG TCGCTGTTGG TCCACGCCGC CCGTCGCCGC GCGCCGCCGC TCAGCGTCCG
 55 CCGCCGCCAT GGGAGTGCAG GTGGAAACCA TCTCCCCAGG AGACGGGCCG ACCTTCCCCA AGCGCGGCCA
 GACCTGCGTG GTGCACTACA CGGGGATGCT TGAAGATGGA AAGAAATTG ATTCCCTCCCG GGACAGAAAC
 AAGCCCTTA AGTTTATGCT AGGCAAGCAG GAGGTGATCC GAGGCTGGGA AGAAGGGTT GCCCAGATGA
 GTGTGGGTCA GAGAGCCAAA CTGACTATAT CTCCAGATTA TGCCCTATGGT GCCACTGGGC ACCCAGGCAT
 CATCCACCA CATGCCACTC TCGTCTCGA TGTGGAGCTT CTCCTACTGG AATGACAGGA ATGGCCTCCT
 60 CCCTTAGCTC CCTGTTCTTG GATCTGCCAT GGAGGGATCT GGTGCCTCCA GACATGTGCA CATGAGTCCA
 TATGGAGCTT TTCCCTGATGT TCCACTCCAC TTTGTATAGA CATCTGCCCT GACTGAATGT GTTCTGTAC
 TCAGCTTGC TTCCGACACC TCTGTTTCTC CTTCCCCCTT CTCCTCGTAT GTGTGTTTAC CTCCTACTATA

TGCCATAAAC CTCAGTTAT TCATTTTATT TTGTTTCAT TTTGGGTGA AGATTCAGTT TCAGTCTTT
 GGATATAAGGT TTCCAATTAA GTACATGGTC AAGTATTAAC AGCACAAGTG GTAGGTTAAC ATTAGAATAG
 GAATTGGTGT TGGGGGGGG GTTTCAAGA ATATTTTATT TTAATTTTT GGATGAAATT TTTATCTATT
 5 ATATATAAA CATCTTGCT GCTGCCTGC AAAGCCATAG CAGATTGAG GCGCTGTTGA GGACTGAATT
 ACTCTCCAAG TTGAGAGATG TCTTGGGTT AAATTAAG CCCTACCTAA AACTGAGGTG GGGATGGGA
 GAGCCTTGTC CTCCACCATT CCCACCCACC CTCCCCCTAA ACCCTCTGCC TTTGAAAGTA GATCATGTC
 ACTGCAATGC TGGA CACTAC AGGTATCTGT CCCTGGCCA GCAGGGACCT CTGAAGCCTT CTTTGTGGCC
 TTTTTTTTT TTCA CCTGT GGTTTTCTA ATGGACTTTC AGGAATTITG TAATCTCATA ACTTTCCAAG
 10 CTCCACCACT TCCTAAATCT TAAGAACTT AATTGACAGT TTCAATTGAA GGTGCTGTT GTAGACTTAA
 CACCCAGTGA AAGCCAGCC ATCATGACAA ATCCTGAAAT GTTCTCTTAA GAAAATGATG CTGGTCATCG
 CAGCTTCAGC ATC'CCTGTT TTTTGATGCT TGGCTCCCTC TGCTGATCTC AGTTCCCTGG CTTTCCTCC
 15 CTCAGCCCCCT TCTCACCCCT TTGCTGTCCT GTGTAGTGT TTGGTGAGAA ATCGTTGCTG CACCCCTCC
 CCAGCACCCT TTATGAGTCT CAAGTTTAT TATTGCAATA AAAGTGCTT ATGCCCGAAT TC-3' (FRAG.NO:_)
 (SEQ. ID NO:2497)

5' GCCGCCGCCA TGGGAGTGCA GGTGGAAACC ATCTCCCCAG GAGACGGGCG CACCTCCCC AAGCGCGGCC
 AGACCTCGGT GGTC CACTAC ACCGGGATGC TTGAAGATGG AAAGAAATTG GATTCTCCC GGGACAGAAA
 CAAGCCCTT AAGTITATGC TAGGCAAGCA GGAGGTGATC CGAGGCTGGG AAGAAGGGT TGCCAGATG
 AGTGTGGGT AGAGAGCAA ACTGACTATA TCTCCAGATT ATGCCCTATGG TGCCACTGGG CACCCAGGCA
 20 TCATCCCACC ACATGCCACT CTCGTCTCG ATGTGGAGCT TCTAAAATG GAATGACAGG AATGGCCTCC
 TCCCTTAGCT CCCTTTCTT GGATCTGCCR TGGAGGGATC TGGTGCCTCC AGACATGTGC ACATGARTCC
 ATATGGAGCT TTCTCTGATG TTCCACTCCA CTTTGTATAG ACATCTGCC TGACTGAATG TGTTCTGTCA
 CTCAGCTTG CTTCCGACAC CTCTGTTCC TCTTCCCCCT TCTCCTCGTA TGTGTGTTA CCTAAACTAT
 ATGCCATAAA CCTCAAGTTA TTCA-3' (FRAG. NO:_)(SEQ. ID NO:2498)

wherein B is adenine, or, more preferably, replaces adenine and is an "equivam\llent" or a "universal" base, and adenine A_{2a} receptor agonist or only minimally antagonist, an adenine A_{2b} receptor antagonist, an adenine A₃ receptor antagonist, or an adenine A₁ receptor antagonist. Similarly, adenine (A) may always be replaced by an "alternative", "equivalent" and/or "universal" base having a smal. fraction, preferably less than 0.3 of the activity of adenine at the adenine receptor(s), as described above.

25 In one preferred embodiment, the links between neighboring mononucleotides are phosphodiester links. In another preferred, at least one mononucleotide phosphodiester residue of the anti-sense oligonucleotide(s) is substituted by a methylphosphonate, phosphotriester, phosphorothioate, phosphorodithioate, boranophosphate, formacetal, thioformacetal, thioether, carbonate, carbamate, sulfate, sulfonate, sulfamate, sulfonamide, sulfone, sulfite, sulfoxide, sulfide, hydroxylamine, 2'-O-methyl, 30 methylene(methyimino), methyleneoxy (methylimino), phosphoramidate residues, and combinations thereof. The oligos having one or more phosphodiester residues substituted by one or more of the other residues are general y longer lasting, given that these residues are more resistant to hydrolysis than the phosphodiester residue. In some cases up to about 10%, about 30%, about 50%, about 75%, and even all phosphodiester residues may be substituted (100%). Typically, the multiple target anti-sense 35 oligonucleotide (oligo) of the invention comprises at least about 7 mononucleotides, in some instances up to 60 and more mononucleotides, preferably about 10 to about 36, and more preferably about 12 to about 21 mononucleotides. However, other lengths are also suitable depending on the length of the target macromolecule. Examples of the MTA oligos of the invention are provided in Table 3 below, which 40 includes ninety-four sequences (SEQ ID NOS.: 2316 through 2410).

45 **Table 3: MTA Oligos, Location Targeted & Target**

MTA Oligo	SEQ. ID No.	Location	Compound Targeted	Target
HUMNFKBP65A AS				
CCC GGC CCC GCC TCG TGC C	3019	5'=1	EPI 2192	
CGT CCB TGC CGC GGG CCC	3020	5'=28 (AUG)	EPI 2193	
GCC CGG CTG CTT GGG CTG CTC TGC CGG G	3021	5'=65	EPI 2194	
TCT GTG CTC CTC TCG CCT GGG	3022	5'=137	EPI 2195	
TGG TGG GGT GGG TCT TGG TGG	3023	5'=159	EPI 2196	
CTG TCC CTG GTC CTG TG	3024	5'=196	EPI 2197	

	GGT CCC GCT TCT TC	3025	5'=362	EPI 2198
	GGG GTT GTT GTT GGT CTG G	3026	5'=401	EPI 2199
	TGT CCT CTT TCT GC	3026	5'=656	EPI 2200
	GCC TCG GGC CTC CC	3027	5'=697	EPI 2201
5	GGC TGG GGT CTG CGT	3028	5'=769	EPI 2202
	GGC CGG GGG TCG GTG GGT CCG CTG	3029	5'=953	EPI 2203
	GGG CTG GGG TGC TGG CTT GGG G	3030	5'=1022	EPI 2204
	GGG GCT GGG GCC TGG GCC	3031	5'=1208	EPI 2205
	GCC TGG GTG GCC TTG GGG GC	3032	5'=1272	EPI 2206
10	GCT GGG TCT GTG CTG TTG CC	3033	5'=1362	EPI 2207
	GTT GTG TGG GGG GCC	3034	5'= 1451	EPI 2208
	GCT GGG TCG GGG GGC CTC TGG GCT GTC	3035	5'=1511	EPI 2209
	GCC CCG GGG CCC CC	3036	5'=1550	EPI 2210
	TGG CTC CCC CCT CC	3037	5'=1772	EPI 2211
15	GCT CCC CCC TTT CC	3038	5'=1863	EPI 2212
	CGG ACG AAG ACA GAG A	3039	5'=1979	EPI 2213
	GGC TTT GTG GGC TC	3040	5'=2011	EPI 2214
	GCC TGC TCT CCC CC	3041	5'=2312	EPI 2215
	CCC GGC CCC GCC BCG BBC C	3042	intron	EPI 2192-01A HSU50136C4Synth
20	CCC GGC CCC GCC BCG	3043	intron	EPI 2192-01B
	CCC GGC CCC GCC BCG BBC C	3044	5'untr	EPI 2192-02A HUMLIPOX5LO
	CCC GGC CCC GCC BCG	3045	5'untr	EPI 2192-02B
	CCC GBC CCC GCC TCB BG	3046	trans	EPI 2192-03A HSNFKBS Subunit
	CCC GBC CCC GCC TC	3047	trans	EPI 2192-03B
25	CCG GCC CCG CCT C	3048	5'untr	EPI 2192-04 TGF β R1
	CCC GBB CCC GCB TBG TGC C	3049	5'trans	EPI 2192-05A HSU581981l enhan
	CCC GCB TBG TGC C	3050	5'untr	EPI 2192-05B
	CCC GGB CCC BCC BBG TGC C	3051	3'trans	EPI 2192-06 HSVECAD
	CBG BBC CCG CCT CGT GCC	3052	intron	EPI 2192-07A NFKB2
30	C CCG CCT CGT GCC	3053	intron	EPI 2192-07B NFKB2
	CCG GCB CCG CCT CBT GCC	3054	5'trans	EPI 2192-08 Carboxypep
	CCG GCC CCG CCB CBT GCC	3055	3'trans	EPI 2192-09 HumADRA2Ca2AdrKid
	CCC GBC CCC GBC TCG	3056	5'untrs	EPI 2192-10 HUMFK506B
	CCC GGC CBC GBC TCG	3057	5'untrs	EPI 2192-11 HSNBARKS1 β AdrKin
35	CCC GGC CCB GCC TBG	3058	5'UTR	EPI 2192-12 HSNFXN1 (NFKB1)
	CCC GGC BCB GBC TCG TBC C	3059	3'UTR	EPI 2192-13 HSILF(transcrp. Factor ILF)
	CCC GGC CCC GCC BCG	3060		EPI-2192-14 NFKB/C4Syn/5-LO/ TGF β rec1 MTA
40	CCC GGC CCC GCC BCG	3061		EPI-2192-15NFKB/C4Syn/5-LO/MTA
	TCC BTG CCG CGG GC	3062	3' trans	EPI-2193-01 METONcogene
	TCC BTG CCB CGG GCC	3063	3' trans	EPI-2193-02 HSFGFR2 (IG)
	TCC BTG CCB CGG GCC	3064	mid cod	EPI-2193-03 5-LO
	TCC BTG CCB CBG GCC	3065	mid cod	EPI-2193-04 HUMTK14
45	GTC CBT GBC GCG G	3066	3'trans	EPI-2193-05 HUMTNFR
	TC CBT GBC GCG GG	3067	AUG	Probl.HUMPTCH cardiacK+channel
	TCT GBG CTC CTC TBB CCT GGG	3068	intr	EPI-2195-01 humCSPAcytotox. Ser.Protease
50	CTG TGC BCC TBB CBC CTG GG	3069	intr	EPI-2195-02 HSINOSX08induc.NOS
	TGT GBT CCB CTB GBC TGG G	3070		EPI-2195-03 HUMACHRM2musc.m2 acetylch.rec.
	TCT GTB CTC BBC TCB CCT G	3071		EPI-2195-04 s86371s1 Neurokinin3Recept
55	TGC TCC TCB CBB CTG GG inflam.factor	3072		EPI-2195-05 HUMMIP1 Amacro

Table 3: MTA Oligos, Location Targeted & Target (Cont'd)

MTA Oligo	SEQ. ID No.	Location	Compound Targeted	Target
CTC CTC TBG CCT GG	3073		EPI-2195-06	HSNBARKS4 β-Adr Rec Kinase
GTG CTC CBB TCB BCT GGG	3074		EPI-2195-07	HSTNFR2SO6TNF R2
GTG CBC CBB TCB CCT GGG	3075		EPI-2195-08	humfkbp fk506 binding prot.
TCT GTG CBC CTC TBG BCT	3076	exon	EPI-2195-09	HSNBARKS1β-Adr. Recept.Kinase
CTG TBB TCC TBB CBC CTG G	3077	intron	EPI-2195-10	HUMIL8
TGT GCT BBT CBC BCB TGG G	3078		EPI-2195-11	HSU50157 PDE4
GTG CBC CBC TCB CCT G	3079	intron/exon	EPI-2195-12	IL-2 R
CTG TGC BCC TCT C	3080	3'UTR	EPI-2203-05	IL-6 R HSIL6R
CBG TGC BCC BCT CBC CTG	3081	intr/ex	EPI-2203-06A	HSIL2rG6
G TGC BCC BCT CBC CTG	3082	intr/ex	EPI-2203-06B	HSIL2rG6
CBC CTC TCB CCT GGG	3083	coding	EPI-2203-07A	HUMIL71
C CTC TCB CCT GCG	3084	coding	EPI-2203-07B	IL-7 HUMIL71
GCT CCB CTC GCC T	3085	coding	EPI-2203-08	IL-6 R HSI6REC
TGC TCC TCB CGC C	3086	intron PDGF A	EPI-2303-09	Chain HUMPDGFAF
GTT GTT GBT CTG G	3087	3'utr	EPI-2199-01	GATA-4Transcrip. Factor for IL-5
GGT TGB BBT TGG TCT TGG	3088	Coding	EPI-2199-02	TNFα HUMTNFA
GGT TGT TGB TGB TCT G	3089	Far 5'UTR	EPI-2199-03	HSSUBP1G(Sub Pr)
GGG TTG BBG TTG BTC TGG	3090	Coding	EPI-2199-04	NeutrophilAdh. R HUMNARIA
GGG TTG BBG TTG BTC TGG	3091	HSHM2	EPI-2199-05	m2 Muscarinic R
TTG TTG TBG BTC TGG	3092	HUML1CAM	EPI-2199-06	L1 LeukAadhProt
GGG TBG BBG BGT CCG CTG	3093	coding	EPI-2203-01	HUMGATA2A
GGG TCB GBG GBT CBG CTG	3094	S71424S2	EPI-2203-02	IGE eps
GGG TBG GTG GGT C	3095	coding	EPI-2203-03	HSGCSFR2
GGG TCG GBG GGT CBG C	3096	HUMITGF	EPI-2203-04	TGFβ3
GGG TGG GCT T	3097	HUMNK65PRO	EPI-2206-01	NFKB/NK & TCell Activating Prot
GGG TGG GCT TGG G	3098	HUMPEREEB	EPI 2206-02	NFKB/Prostagl. EP3 Rec
CCTGGGTGGGBBTGGG	3099		EPI 2206-03	HSNF2B/GCSF NFKB/GranuLocCSF/ Transcr.FactorNF2B
CCTGGGBTGGGCBTGGG	3100		EPI-2206-04	HUMLAP/NFKB Leuk.Adhes.Prot
GCCTGBTGBTCTTGGG	3101		EPI2206-05	NFKB/Endothel N2 S63833
CCCAVGVCCVCCCAGGC	3102		EPI 2206-06	NFKBAS13/B Lymph SerThrProt.Kinase
AGCCCACCCAGGC	3103		EPI2206-07	NFKBAS13/GCSF1 HSGCSFR1Rec
BCCTGGGTGGGCTB	3104		EPI2206-08	NFKBAS13/GCSF1/ NK7TCELLACT.Prot
GGTGGGCTTGGG	3105		EPI 2206-09	NFKBAS13/ HSTGFB1 TGFB
CCBBGGTGGGCTTGGG	3106		EPI 2206-10	NFKBAS13/ HSTGFB1 TGFB1
CTGGGTGGGBBTGGG	3107		EPI 2206-11	NFKBAS13/ HSGCSFR1 GCSFR1
CCBGGGTGGGCTTGG	3108		EPI 2206-12	NFKBAS13/HUMCD30A LymphActAntigCoding
GGGTGGGCTTGG	3109		EPI-2206-12B	NFKBAS13/HUMCD30A
CCTGBTGBTGGCCTGG	3110		EPI 2206-13	NFKBAS13/HUMCAM1V Vasc.Endoth.Cell Adh.Molec

B: Universal Base

The MTA oligos of Table 3 are suitable for use with two or more of the targets listed in Table 4 below.

Table 4: Targets for the MTA Oligos of Table 3

Compound	Target
EPI 2010	Adenosine A1 receptor
EPI 2045	Adenosine A3 receptor
EPI 2873, EPI 2193	NF _K B
EPI 1873	Interleukin-1
EPI 1857	Interleukin -5
EPI 2945	Interleukin -4
EPI 2977	Interleukin -8
EPI 2031	5-Lipoxygenase
EPI 1898	Leukotriene C-4 Synthase
EPI 1856	Eotaxin
EPI 1131	ICAM
EPI 1085	VCAM
EPI 2085	TNF α
EPI 1908	PAF
EPI 1925	IL-4 receptor
EPI 2643	β 2 adrenergic receptor kinase
EPI 2934	Tryptase
EPI 2033	Major Basic Protein
EPI 2795	Eosinophil Peroxidase

Nf_KB: nuclear factor kB

ICAM: intracellular adhesion molecule

VCAM: vascular cell adhesion molecule

TNF: tumor necrosis factor

PAF: platelet activating factor

5

The mRNA sequence of the targeted protein may be derived from the nucleotide sequence of the gene expressing the protein, whether for existing targets or those to be found in the future. Sequences for many target genes of different systems are presently known. See, GenBank data base, NIH, the entire sequences of which are incorporated here by reference. The sequences of those genes, whose sequences are not yet available, may be obtained by isolating the target segments applying technology known in the art. Once the sequence of the gene, its RNA and/or the protein are known, anti-sense oligonucleotides are produced as described above and utilized to validate the target by in vivo administration and testing for a reduction of the production of the targeted protein in accordance with standard techniques, and of specific functions. As already described above, the anti-sense oligonucleotides may be of any suitable length, e.g., from about 7 to about 60 nucleotides in length, depending on the particular target being bound and the mode of delivery thereof. The anti-sense oligonucleotide preferably is directed to an mRNA region containing a junction between intron and exon or to regions vicinal to the junction. Where the anti-sense oligonucleotide is directed to an intron/exon junction, it may either entirely overlie the junction or may be sufficiently close to the junction to inhibit splicing out of the intervening exon during processing of precursor mRNA to mature mRNA, e.g., with the 3' or 5' terminus of the anti-sense oligonucleotide being positioned within about, for example, 10, 5, 3, or 2 nucleotide of the intron/exon junction. Also preferred are anti-sense oligonucleotides which overlap the initiation codon and, more generally, those that target the coding region of the target mRNA. When practicing the present invention, the anti-sense oligonucleotides administered may be related in origin to the species to which it is administered. When treating humans, human anti-sense may be used if desired. Anti-sense oligos to endogenous sequences from other species,

however, are also encompassed.

Pharmaceutical compositions comprising an anti-sense oligonucleotide as given above effective to reduce expression of an A₁ or A₃ adenosine receptor by passing through a cell membrane and binding specifically with mRNA encoding an A₁ or A₃ adenosine receptor in the cell so as to prevent its translation are another aspect of the present invention. Such compositions are provided in a suitable pharmaceutically acceptable carrier, e.g., sterile pyrogen-free saline solution. The anti-sense oligonucleotides may be formulated with a hydrophobic carrier capable of passing through a cell membrane, e.g., in a liposome, with the liposomes carried in a pharmaceutically acceptable aqueous carrier. The oligonucleotides may also be coupled to a substance which inactivates mRNA, such as a ribozyme. Such oligonucleotides may be administered to a subject to inhibit the activation of a target, such as the adenosine receptors, which subject is in need of such treatment for any of the reasons discussed herein. Furthermore, the pharmaceutical formulation may also contain chimeric molecules comprising anti-sense oligonucleotides attached to molecules which are known to be internalized by cells. These oligonucleotide conjugates utilize cellular uptake pathways to increase cellular concentrations of oligonucleotides. Examples of macromolecules used in this manner include transferrin, asialoglycoprotein (bound to oligonucleotides via polylysine) and streptavidin. In the pharmaceutical formulation, the anti-sense compound may be contained within a lipid particle or vesicle, such as a liposome or microcrystal. The particles may be of any suitable structure, such as unilamellar or plurilamellar, so long as the anti-sense oligonucleotide is contained therein. Positively charged lipids such as N-[1-(2, 3-dioleyloxy) propyl]-N, N, N-trimethylammoniummethylsulfate, or "DOTAP," are particularly preferred for such particles and vesicles. The preparation of such lipid particles is well known. See, e.g., U.S. Patent Nos. 4,880,635 to Janoff et al.; 4,906,477 to Kurono et al.; 4,911,928 to Wallach; 4,917,951 to Wallach; 4,920,016 to Allen et al.; 4,921,757 to Wheatley et al.; etc.

Subjects may be administered the active composition by any means which transports the anti-sense nucleotide composition to the lung. The anti-sense compounds are particularly disclosed herein may be administered to the lungs of a patient by any suitable means, but are preferably administered by generating an aerosol comprised of respirable particles, the respirable particles comprised of the anti-sense compound, which particles the subject inhales. The respirable particles may be liquid or solid. The particles may optionally contain other therapeutic ingredients. Particles comprised of anti-sense compound for practicing the present invention should include particles of respirable size: that is, particles of a size sufficiently small to pass through the mouth and larynx upon inhalation and into the bronchi and alveoli of the lungs. In general particles ranging from about .5 to about 10 microns in size are respirable. Particles of non-respirable size which are included in the aerosol tend to deposit in the throat and be swallowed, and the quantity of non-respirable particles in the aerosol is preferably minimized. For nasal administration, a particle size in the range of 10-500 nm is preferred to ensure retention in the nasal cavity. Thus, particles of about 4, about 10, about 25, about 50 to about 75, about 100, about 250, about 500, and other specific ranges therewithin, are preferred. Others, however, are also contemplated within the confines of this invention.

Liquid pharmaceutical compositions of active compound for producing an aerosol can be prepared by combining the anti-sense compound with a suitable vehicle, such as sterile pyrogen free water. Other therapeutic compounds may optionally be included. Solid particulate compositions containing respirable dry particles of micronized anti-sense compound may be prepared by grinding dry anti-sense compound with a mortar and pestle, and then passing the micronized composition through a 400 mesh screen to break up or separate out large agglomerates. A solid particulate composition comprised of the anti-sense compound may optionally contain a dispersant which serves to facilitate the formation of an aerosol. A suitable dispersant is lactose, which may be blended with the anti-sense compound in any suitable ratio (e.g., a 1 to 1 ratio by weight). Again, other therapeutic compounds may also be included.

The dosage of the anti-sense compound administered will depend upon the disease being treated, the condition of the subject, the particular formulation, the route of administration, the timing of administration to a subject, etc. In general, intracellular concentrations of the oligonucleotide of from about

0.01, about 0.05, about 0.1, about 0.2, about 1 to about 5 μM , about 50 μM , about 100 μM or more, and more particularly about 0.2 to about 0.5 μM , are desired. For administration to a subject such as a human, a dosage of from about 0.01, about 0.1 or about 1 mg/Kg up to about 50, about 100, or about 150 mg/Kg and even higher doses are typically employed depending on the route of administration as is known in the art.

5 Depending on the solubility of the particular formulation of active compound administered, the daily dose may be divided among one or several unit dose administrations. Administration of the anti-sense compounds may be carried out therapeutically (i.e., as a rescue treatment) or prophylactically. Aerosols of liquid particles comprising the anti-sense compound may be produced by any suitable means, such as with a nebulizer. See, e.g., U.S. Patent No. 4,501,729. Nebulizers are commercially available devices which
10 transform solutions or suspensions of the active ingredient into a therapeutic aerosol mist either by means of acceleration of a compressed gas, typically air or oxygen, through a narrow venturi orifice or by means of ultrasonic agitation. Suitable formulations for use in nebulizers consist of the active ingredient in a liquid carrier, the active ingredient comprising up to 40% w/w of the formulation, but preferably less than 20% w/w. The carrier is typically water or a dilute aqueous alcoholic solution, preferably made isotonic
15 with body fluids by the addition of, for example, sodium chloride. Optional additives include preservatives if the formulation is not prepared sterile, for example, methyl hydroxybenzoate, antioxidants, flavoring agents, volatile oils, buffering agents and surfactants.

In one preferred embodiment, the pharmaceutical composition comprises nucleic acid(s) which comprise the anti-sense oligo(s) described above and one or more surfactants. Suitable surfactants or surfactant components for enhancing the uptake of the anti-sense oligonucleotides of the invention include synthetic and natural as well as full and truncated forms of surfactant protein A, surfactant protein B, surfactant protein C, surfactant protein D and surfactant Protein E, di-saturated phosphatidylcholine (other than dipalmitoyl), dipalmitoylphosphatidylcholine, phosphatidylcholine, phosphatidylglycerol, phosphatidylinositol, phosphatidylethanolamine, phosphatidylserine; phosphatidic acid, ubiquinones, lysophosphatidylethanolamine, lysophosphatidylcholine, palmitoyl-lysophosphatidylcholine, dehydroepiandrosterone, dolichols, sulfatidic acid, glycerol-3-phosphate, dihydroxyacetone phosphate, glycerol, glycero-3-phosphocholine, dihydroxyacetone, palmitate, cytidine diphosphate (CDP) diacylglycerol, CDP choline, choline phosphate; as well as natural and artificial lamellar bodies which are the natural carrier vehicles for the components of surfactant, omega-3 fatty acids, polyenic acid, polyenoic acid, lecithin, palmitinic acid, non-ionic block copolymers of ethylene or propylene oxides, polyoxypropylene, monomeric and polymeric, polyoxyethylene, monomeric and polymeric, poly(vinyl amine) with dextran and/or alkanoyl side chains, Brij 35, Triton X-100 and synthetic surfactants ALEC, Exosurf, Survan and Atovaquone, among others. These surfactants may be used either as a single, or as part of a multiple component, surfactant in a formulation, or as covalently bound additions to the 5' and/or
35 3' ends of the anti-sense oligo(s). Aerosols of solid particles comprising the active compound may likewise be produced with any solid particulate medicament aerosol generator. Aerosol generators for administering solid particulate medicaments to a subject produce particles which are respirable, as explained above, and generate a volume of aerosol containing a predetermined metered dose of a medicament at a rate suitable for human administration. One illustrative type of solid particulate aerosol generator is an insufflator. Suitable formulations for administration by insufflation include finely comminuted powders which may be delivered by means of an insufflator or taken into the nasal cavity in the manner of a snuff. In the insufflator, the powder (e.g., a metered dose thereof effective to carry out the treatments described herein) is contained in capsules or cartridges, typically made of gelatin or plastic, which are either pierced or opened in situ and the powder delivered by air drawn through the device upon
40 inhalation or by means of a manually-operated pump. The powder employed in the insufflator consists either solely of the active ingredient or of a powder blend comprising the active ingredient, a suitable powder diluent, such as lactose, and an optional surfactant. The active ingredient typically comprises from 0.1 to 100 w/w of the formulation. A second type of illustrative aerosol generator comprises a metered dose inhaler. Metered dose inhalers are pressurized aerosol dispensers, typically containing a suspension or

solution formulation of the active ingredient in a liquefied propellant. During use these devices discharge the formulation through a valve adapted to deliver a metered volume, typically from 10 to 150 ml, to produce a fine particle spray containing the active ingredient. Suitable propellants include certain chlorofluorocarbon compounds, for example, dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane and mixtures thereof. The formulation may additionally contain one or more co-solvents, for example, ethanol, surfactants, such as oleic acid or sorbitan trioleate, antioxidants and suitable flavoring agents. The aerosol, whether formed from solid or liquid particles, may be produced by the aerosol generator for example at a rate of from about 10, about 30, about 70 to about 100, about 150, about 150 liters per minute, more preferably from about 30 to 150 liters per minute, and most preferably about 60 liters per minute. Aerosols containing greater amounts of medicament, however, may be administered more rapidly as is known in the art.

The relevant disclosures of all scientific publications and patent references cited in this patent are specifically intended to be incorporated herein by reference, particularly in reference to preparatory methods and technologies which are enabling of the invention. The following examples are provided to illustrate the present invention, and should not be construed as limiting thereon.

EXAMPLES

In the following examples, :M means micromolar, ml means milliliters, :m means micrometers, mm means millimeters, cm means centimeters, EC means degrees Celsius, :g means micrograms, mg means milligrams, g means grams, kg means kilograms, M means molar, and h or hr. means hours.

20 **Example 1: Design and Synthesis of Anti-sense Oligonucleotides**

The design of anti-sense oligonucleotides against the A₁ and A₃ adenosine receptors may require the solution of the complex secondary structure of the target A₁ receptor mRNA and the target A₃ receptor mRNA. After generating this structure, anti-sense nucleotide are designed which target regions of mRNA which might be construed to confer functional activity or stability to the mRNA and which optimally may overlap the initiation codon. Other target sites are readily usable. As a demonstration of specificity of the anti-sense effect, other oligonucleotides not totally complementary to the target mRNA, but containing identical nucleotide compositions on a w/w basis, are included as controls in anti-sense experiments.

The mRNA secondary structure of the adenosine A₁ receptor was analyzed and used as described above, to design a phosphorothioate anti-sense oligonucleotide. The anti-sense oligonucleotide which was synthesized was designated HAdA₁AS and had the following sequence: 5' -GAT GGA GGG CGG CAT GGC GGG-3' (**SEQ ID NO:1**). As a control, a mismatched phosphorothioate anti-sense nucleotide designated HAdA1MM1 was synthesized with the following sequence: 5' -GTA GCA GGC GGG GAT GGG GGC-3' (**SEQ ID NO:2**). Each oligonucleotide had identical base content and general sequence structure. Homology searches in GENBANK (release 85.0) and EMBL (release 40.0) indicated that the anti-sense oligonucleotide was specific for the human and rabbit adenosine A₁ receptor genes, and that the mismatched control was not a candidate for hybridization with any known gene sequence.

The secondary structure of the adenosine A₃ receptor mRNA was similarly analyzed and used as described above to design two phosphorothioate anti-sense oligonucleotides. The first anti-sense oligonucleotide (HAdA3AS1) synthesized had the following sequence: 5' -GTT GTT GGG CAT CTT GCC-3' (**SEQ ID NO:3**). As a control, a mismatched phosphorothioate anti-sense oligonucleotide (HAdA3MM1) was synthesized, having the following sequence: 5' -GTA CTT GCG GAT CTA GGC-3' (**SEQ ID NO:4**). A second phosphorothioate anti-sense oligonucleotide (HAdA3AS2) was also designed and synthesized, having the following sequence: 5' -GTG GGC CTA GCT CTC GCC-3' (**SEQ ID NO:5**). Its control oligonucleotide (HAdA3MM2) had the sequence: 5' -GTC GGG GTA CCT GTC GGC-3' (**SEQ ID NO:6**). Phosphorothioate oligonucleotides were synthesized on an Applied Biosystems Model 396 Oligonucleotide Synthesizer, and purified using NENSORB chromatography (DuPont, MD).

Example 2: In Vivo Testing of Adenosine A₁

Receptor Anti-sense Oligos

The anti-sense oligonucleotide against the human A₁ receptor (**SEQ ID NO:1**) described above, was tested for efficacy in an in vitro model utilizing lung adenocarcinoma cells HTB-54. HTB-54 lung adenocarcinoma cells were demonstrated to express the A₁ adenosine receptor using standard northern blotting procedures and receptor probes designed and synthesized in the laboratory.

HTB-54 human lung adenocarcinoma cells (106/100 mm tissue culture dish) were exposed to 5.0 μM HAdAlAS or HAdAlMM1 for 24 hours, with a fresh change of media and oligonucleotides after 12 hours of incubation. Following 24 hour exposure to the oligonucleotides, cells were harvested and their RNA extracted by standard procedures. A 21-mer probe corresponding to the region of mRNA targeted by the anti-sense (and therefore having the same sequence as the anti-sense, but not phosphorothioated) was synthesized and used to probe northern blots of RNA prepared from HAdAlAS-treated, HAdAlMM1-treated and non-treated HTB-54 cells. These blots showed clearly that HAdAlAS but not HAdAlMM1 effectively reduced human adenosine receptor mRNA by >50%. This result showed that HAdAlAS is a good candidate for a anti-asthma drug since it depletes intracellular mRNA for the adenosine A₁ receptor, which is involved in asthma.

Example 3: In Vivo Efficacy of Adenosine A₁ Receptor Anti-sense Oligos

A fortuitous homology between the rabbit and human DNA sequences within the adenosine A₁ gene overlapping the initiation codon permitted the use of the phosphorothioate anti-sense oligonucleotides initially designed for use against the human adenosine A₁ receptor in a rabbit model. Neonatal New Zealand white Pasteurella-free rabbits were immunized intraperitoneally within 24 hours of birth with 312 antigen units/ml house dustmite (*D. farinae*) extract (Berkeley Biologicals, Berkeley, CA), mixed with 10% kaolin. Immunizations were repeated weekly for the first month and then biweekly for the next 2 months. At 3-4 months of age, eight sensitized rabbits were anesthetized and relaxed with a mixture of ketamine hydrochloride (44 mg/kg) and acepromazine maleate (0.4 mg/kg) administered intramuscularly. The rabbits were then laid supine in a comfortable position on a small molded, padded animal board and intubated with a 4.0-mm intratracheal tube (Mallinkrodt, Inc., Glens Falls, NY). A polyethylene catheter of external diameter 2.4 mm with an attached latex balloon was passed into the esophagus and maintained at the same distance (approximately 16 cm) from the mouth throughout the experiments. The intratracheal tube was attached to a heated Fleisch pneumotachograph (size 00; DOM Medical, Richmond, VA), and flow was measured using a Validyne differential pressure transducer (Model DP-45161927; Validyne Engineering Corp., Northridge, CA) driven by a Gould carrier amplifier (Model 11-4113; Gould Electronic, Cleveland, OH). The esophageal balloon was attached to one side of the differential pressure transducer, and the outflow of the intratracheal tube was connected to the opposite side of the pressure transducer to allow recording of transpulmonary pressure. Flow was integrated to give a continuous tidal volume, and measurements of total lung resistance (RL) and dynamic compliance (Cdyn) were calculated at isovolumetric and flow zero points, respectively, using an automated respiratory analyzer (Model 6; Buxco, Sharon, CT). Animals were randomized and on Day 1 pretreatment values for PC50 were obtained for aerosolized adenosine. Anti-sense (HAdAlAS) or mismatched control (HAdAlMM) oligonucleotides were dissolved in sterile physiological saline at a concentration of 5000 :g (5 mg) per 1.0 ml. Animals were subsequently administered the aerosolized anti-sense or mismatch oligonucleotide via the intratracheal tube (approximately 5000 :g in a volume of 1.0 ml), twice daily for two days. Aerosols of either saline, adenosine, or anti-sense or mismatch oligonucleotides were generated by an ultrasonic nebulizer (DeVilbiss, Somerse , PA), producing aerosol droplets 80% of which were smaller than 5 :m in diameter. In the first arm of the experiment, four randomly selected allergic rabbits were administered anti-sense oligonucleotide and four the mismatched control oligonucleotide. On the morning of the third day, PC50 values (the concentration of aerosolized adenosine in mg/ml required to reduce the dynamic compliance of the bronchial airway 50% from the baseline value) were obtained and compared to PC50 values obtained for these animals prior to exposure to oligonucleotide. Following a 1 week interval, animals were crossed

over, with those previously administered mismatch control oligonucleotide now administered anti-sense oligonucleotide, and those previously treated with anti-sense oligonucleotide now administered mismatch control oligonucleotide. Treatment methods and measurements were identical to those employed in the first arm of the experiment. It should be noted that in six of the eight animals treated with anti-sense oligonucleotide, adenosine-mediated bronchoconstriction could not be obtained up to the limit of solubility of adenosine, 20 mg/ml. For the purpose of calculation, PC50 values for these animals were set at 20 mg/ml. The values given therefore represent a minimum figure for anti-sense effectiveness. Actual effectiveness was higher. The results of this experiment are illustrated in Table 5 below.

Table 5: Effect of Adenosine A₁ Receptor Anti-sense Oligo
up on PC50 Values in Asthmatic Rabbits

Mismatch Control		A ₁ Receptor Anti-sense Oligo	
Pre Oligonucleotide	Post Oligonucleotide	Pre Oligonucleotide	Post Oligonucleotide
3.56 ± 1.02	5.16 ± 1.03	2.36 ± 0.68	>19.5 ± 0.34**

The results are presented as the mean (n=8) ± SEM.

The significance was determined by repeated-measures analysis of variance (ANOVA), and Tukey's protected test.

**Significantly different from all other groups, p<0.01

In both arms of the experiment, animals receiving the anti-sense oligonucleotide showed an order of magnitude increase in the dose of aerosolized adenosine required to reduce dynamic compliance of the lung by 50%. No effect of the mismatched control oligonucleotide upon PC50 values was observed. No toxicity was observed in any animal receiving either anti-sense or control inhaled oligonucleotide. These results show clearly that the lung has exceptional potential as a target for anti-sense oligonucleotide-based therapeutic intervention in lung disease. They further show, in a model system which closely resembles human asthma, that downregulation of the adenosine A₁ receptor largely eliminates adenosine-mediated bronchoconstriction in asthmatic airways. Bronchial hyperresponsiveness in the allergic rabbit model of human asthma is an excellent endpoint for anti-sense intervention since the tissues involved in this response lie near to the point of contact with aerosolized oligonucleotides, and the model closely simulates an important human disease.

Example 4: Specificity of A₁-adenosine Receptor Anti-sense Oligonucleotide

At the conclusion of the cross-over experiment of Example 3 above, airway smooth muscle from all rabbits was quantitatively analyzed for adenosine A₁ receptor number. As a control for the specificity of the anti-sense oligonucleotide, adenosine A₂ receptors, which should not have been affected, were also quantified. Airway smooth muscle tissue was dissected from each rabbit and a membrane fraction prepared according to the method of Kleinstein et al. (Kleinstein, J. and Glossmann, H., Naunyn-Schmiedeberg's Arch. Pharmacol. 305: 191-200 (1978)), the relevant portion of which is hereby incorporated in its entirety by reference, with slight modifications. Crude plasma membrane preparations were stored at 70°C until the time of assay. Protein content was determined by the method of Bradford (M. Bradford, Anal. Biochem. 72, 240-254 (1976), the relevant portion of which is hereby incorporated in its entirety by reference). Frozen plasma membranes were thawed at room temperature and were incubated with 0.2 U/ml adenosine deaminase for 30 minutes at 37°C to remove endogenous adenosine. The binding of [³H] DPCPX (A₁ receptor-specific) or [³H] CGS-21680 (A₁ receptor-specific) was measured as previously described by Ali et al. (Ali, S. et al., J. Pharmacol. Exp. Ther. 268, Am. J. Physiol 266, L271-277 (1994), the relevant portion of which is hereby incorporated in its entirety by reference). The animals treated with adenosine A₁ anti-sense oligonucleotide in the cross-over experiment had a nearly 75% decrease in A₁ receptor number compared to controls, as assayed by specific binding of the A₁-specific antagonist DPCPX. There was no change in adenosine A₂ receptor number, as assayed by specific binding of the A₂ receptor-specific agonist 2-[p-(2-carboxyethyl)-phenethylamino]-5'-(N-ethylcarboxamido) adenosine (CGS-21630). This is illustrated in Table 6 below.

Table 6: Specificity of Action of Adenosine A₁
Receptor Oligonucleotide Anti-sense

Mismatch Control Oligonucleotide	A ₁ Anti-sense Oligonucleotide
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A₁-Specific Binding	1105 ± 48**	293 ± 18
A₂-Specific Binding	302 ± 22	442 ± 171

The results are presented as the mean (n = 8) ± SEM.

The significance was determined by repeated-measures analysis of variance (ANOVA), and Tukey's protected test

**Significantly different from mismatch control, p<0.01.

5 The above results illustrate the effectiveness of anti-sense oligonucleotides in treating airway disease. Since the anti-sense oligos described above, eliminate the receptor systems responsible for adenosine-mediated bronchoconstriction, it may be less imperative to eliminate adenosine from them. However, it would be preferable to eliminate adenosine from even these oligonucleotides to reduce the dose needed to attain a similar effect. Described above are other anti-sense oligonucleotides targeting 10 mRNA of proteins involved in inflammation. Adenosine has been eliminated from their nucleotide content to prevent its liberation during degradation.

Example 5: Anti-sense Oligos directed to other Target Nucleic Acids

This work was conducted to demonstrate that the present invention is broadly applicable to anti-sense oligonucleotides ("oligos") specific to nucleic acid targets broadly. The following experimental 15 studies were conducted to show that the method of the invention is broadly suitable for use with anti-sense oligos designed as taught by this application and targeted to any and all adenosine receptor mRNAs. For this purpose, various anti-sense oligos were prepared to adenosine receptor mRNAs exemplified by the adenosine A₁, A_{2b} and A₃ receptor mRNAs. Anti-sense Oligo I was disclosed above (SEQ. ID NO:1). Five additional anti-sense phosphorothioate oligos were designed and synthesized as indicated above.

20 1- Oligo II (SEQ. ID NO: 7) also targeted to the adenosine A₁ receptor, but to a different region than Oligo I.

2- Oligo V (SEQ. ID NO: 10) targeted to the adenosine A_{2b} receptor.

3- Oligos III (SEQ. ID NO: 8) and IV (SEQ. ID NO: 9) targeted to different regions of the adenosine A₃ receptor.

4- Oligo I-PD (SEQ. ID NO: 1681)(a phosphodiester oligo of the same sequence as Oligo I).

25 These anti-sense oligos were designed for therapy on a selected species as described above and are generally specific for that species, unless the segment of the target mRNA of other species happens to contain a similar sequences. All anti-sense oligos were prepared as described below, and tested in vivo in a rabbit model for bronchoconstriction, inflammation and allergy, which have breathing difficulties and impeded lung airways, as is the case in ailments such as asthma, as described in the above-identified application.

30 **Example 6: Design & Sequences of other Anti-sense Oligos**

Six oligos and their effects in a rabbit model were studied and the results of these studies are reported and discussed below. Five of these oligos were selected for this study to complement the data on Oligo I (SEQ ID NO: 1) provided in Examples 1 to 4 above. This oligo is anti-sense to one region of the adenosine A₁ receptor mRNA. The oligos tested are identified as anti-sense Oligos I (SEQ ID NO: 1) and II (SEQ. ID No: 7) targeted to a different region of the adenosine A₁ receptor mRNA, Oligo V (SEQ. ID No:8) targeted to the adenosine A_{2b} receptor mRNA, and anti-sense Oligos III and IV (SEQ. ID NOS: 9 and 10) targeted to two different regions of the adenosine A₃ receptor mRNA. The sixth oligo (Oligo I-PD) is a phosphodiester version of Oligo I (SEQ. ID NO:1). The design and synthesis of these anti-sense oligos was performed in accordance with Example 1 above.

40 **(I) Anti-sense Oligo I**

The anti-sense oligonucleotide I referred to in Examples 1 to 4 above is targeted to the human A₁ adenosine receptor rRNA (EPI 2010). Anti-sense oligo I is 21 nucleotide long, overlaps the initiation codon, and has the following sequence: 5'-GAT GGA GGG CGG CAT GGC GGG-3' (SEQ.ID NO:1). The oligo I was previously shown to abrogate the adenosine-induced bronchoconstriction in allergic rabbits, and to reduce allergen-induced airway obstruction and bronchial hyperresponsiveness (BHR), as discussed above and shown by Nyce, J. W. & Metzger, W. J., Nature, 385:721 (1977), the relevant portions of which reference are incorporated in their entireties herein by reference.

45 **(II) Anti-sense Oligo II**

A phosphorothioate anti-sense oligo (**SEQ. ID NO:7**) was designed in accordance with the invention to target the rabbit adenosine A₁ receptor mRNA region +936 to +956 relative to the initiation codon (start site). The anti-sense oligo II is 21 nucleotide long, and has the following sequence: **5'-CTC GTC GCC GTC GCC GGC GGG-3' (SEQ. ID NO:7)**.

5 **(III) Anti-sense Oligo III**

A phosphorothioate anti-sense oligo other than that provided in Example 1 above (**SEQ. ID NO:8**) was designed in accordance with the invention to target the anti-sense A₃ receptor mRNA region +3 to + 22 relative to the initiation codon start site. The anti-sense oligo III is 20 nucleotide long, and has the following sequence: **5'-GGG TGG TGC TAT TGT CGG GC-3' (SEQ. ID NO:8)**.

10 **(IV) Anti-sense Oligo IV**

Yet another phosphorothioate anti-sense oligo (**SEQ. ID NO:9**) was designed in accordance with the invention to target the adenosine A₃ receptor mRNA region + 386 to + 401 relative to the initiation codon (start site). The anti-sense oligo IV is 15 nucleotide long, and has the following sequence: **5'-GGC CCA GGG CCA GCC-3' (SEQ. ID NO:9)**

15 **(V) Anti-sense Oligo V**

A phosphorothioate anti-sense oligo (**SEQ. ID NO:10**) was designed in accordance with the invention to target the adenosine A_{2b} receptor mRNA region -21 to -1 relative to the initiation codon (start site). The anti-sense oligonucleotide V is 21 nucleotide long, and has the following sequence: **5'-GGC CGG GCC AGC CGG GCC CGG-3' (SEQ. ID NO:10)**.

20 **(VI) A₁ Mismatch Oligos**

Two different mismatched oligonucleotides having the following sequences were used as controls for anti-sense oligo I (**SEQ. ID NO: 1**) described in Example 5 above: A₁ MM2:**5'-GTA GGT GGC GGG CAA GGC GGG-3' (SEQ. ID NO:2421)**, and A₁ MM3:**5'-GAT GGA GGC GGG CAT GGC GGG-3' (SEQ. ID NO:2422)**. Anti-sense oligo I and the two mismatch anti-sense oligos had identical base content and general sequence structure. Homology searches in GENBANK (release 85.0) and EMBL (release 40.0) indicated that the anti-sense oligo I was specific, not only for the human, but also for the rabbit, adenosine A₁ receptor genes, and that the mismatched controls were not candidates for hybridization with any known human or animal gene sequence.

25 **(VII) Anti-sense Oligo A₁-PD (Oligo VI)**

30 A phosphodiester anti-sense oligo (**Oligo VI; SEQ. ID NO:2420**) having the same nucleotide sequence as Oligo I was designed as disclosed in the above-identified application. Anti-sense oligo I-PD is 21 nucleotide long, overlaps the initiation codon, and has the following sequence: **5'- GAT GGA GGG CGG CAT GGC GGG-3' (SEQ. ID NO:2420)**.

35 **III) Controls**

Each rabbit was administered 5.0 ml aerosolized sterile saline following the same schedule as for the anti-sense oligos in (II), (III), and (IV) above.

Example 7: Synthesis of Anti-sense Oligos

Phosphorothioate anti-sense oligos having the sequences described in (a) above, were synthesized on an Applied Biosystems Model 396 Oligonucleotide Synthesizer, and purified using NENSORB chromatography (Di Pont, DE). TETD (tetraethylthiuram disulfide) was used as the sulfurizing agent during the synthesis. Anti-sense oligonucleotide II (**SEQ. ID NO:7**), anti-sense oligonucleotide III (**SEQ. ID NO: 8**) and anti-sense oligonucleotide IV (**SEQ. ID NO: 9**) were each synthesized and purified in this manner.

Example 8: Preparation of Allergic Rabbits

45 Neonatal New Zealand white Pasteurella-free rabbits were immunized intraperitoneally within 24 hours of birth with 0.5 ml of 312 antigen units/ml house dust mite (*D. farinae*) extract (Berkeley Biologicals, Berkeley, CA) mixed with 10% kaolin as previously described (Metzger, W. J., in Late Phase Allergic Reactions, Dorsch, W., Ed., CRC Handbook, pp. 347-362, CRC Press, Boca Raton (1990); Ali,

S., Metzger, W. J. and Mustafa, S. J., Am. J. Resp. Crit. Care Med. 149: 908 (1994)), the relevant portions of which are incorporated in their entireties here by reference. Immunizations were repeated weekly for the first month and then biweekly until the age of 4 months. These rabbits preferentially produce allergen-specific IgE antibody, typically respond to aeroallergen challenge with both an early and late-phase 5 asthmatic response, and show bronchial hyper responsiveness (BHR). Monthly intraperitoneal administration of allergen (312 units dust mite allergen, as above) continues to stimulate and maintain allergen-specific IgE antibody and BHR. At 4 months of age, sensitized rabbits were prepared for aerosol administration as described by Ali et al. (Ali, S., Metzger, W. J. and Mustafa, S. J., Am. J. Resp. Crit. Care Med. 149 (1994)), the relevant section being incorporated in its entirety here by reference.

10 **DOSE-RESPONSE STUDIES**

Example 9: Experimental Setup

Aerosols of either adenosine (0-20 mg/ml), or anti-sense or one of two mismatch oligonucleotides (5 mg/ml) were separately prepared with an ultrasonic nebulizer (Model 646, DeVilbiss, Somerset, PA), which produced aerosol droplets, 80% of which were smaller than 5:μm in diameter. Equal volumes of the 15 aerosols were administered directly to the lungs via an intratracheal tube. The animals were randomized, and administered aerosolized adenosine. Day 1 pre-treatment values for sensitivity to adenosine were calculated as the dose of adenosine causing a 50% loss of compliance (PC₅₀ Adenosine). The animals were then administered either the aerosolized anti-sense or one of the mismatch anti-sense oligos via the intratracheal tube (5 mg/1.0 ml), for 2 minutes, twice daily for 2 days (total dose, 20 mg). Post-treatment 20 PC₅₀ values were recorded (post-treatment challenge) on the morning of the third day. The results of these studies are provided in Example 21 below.

Example 10: Crossover Experiments

For some experiments utilizing anti-sense oligo I (**SEQ ID NO: 1**) and a corresponding mismatch control oligonucleotide A₁MM2, following a 2 week interval, the animals were crossed over, with those 25 previously administered the mismatch control A₁MM2, now receiving the anti-sense oligo I, and those previously treated with the anti-sense oligo I, now receiving the mismatch control A₁MM2 oligo. The number of animals per group was as follows. For mismatch A₁MM2 (Control 1), n=7, since one animal was lost in the second control arm of the experiment due to technical difficulties, for mismatch A₁MM3 n=4 (Control 2) and for A₁AS anti-sense oligo I, n=8. The A₁MM3 oligo-treated animals were analyzed 30 separately and were not part of the cross-over experiment. The treatment methods and measurements employed following the cross-over were identical to those employed in the first arm of the experiment. In 6 of the 8 animals treated with the anti-sense oligo I (**SEQ. ID NO: 1**), no PC₅₀ value could be obtained for adenosine doses of up to 20 mg/ml, which is the limit of solubility of adenosine. Accordingly, the PC₅₀ values for these animals were assumed to be 20 mg/ml for calculation purposes. The values given, 35 therefore, represent a minimum figure for the effectiveness of the anti-sense oligonucleotides of the invention. Other groups of allergic rabbits (n=4 for each group) were administered 0.5 or 0.05 mg doses of the anti-sense oligo (**SEQ ID NO: 1**), or the A₁MM2 oligo in the manner and according to the schedule described above (the total doses being 2.0 or 0.2 mg). The results of these studies are provided in Example 22 below.

40 **Example 11: Anti-sense Oligo Formulation**

Each one of anti-sense oligos were separately solubilized in an aqueous solution and administered as described for anti-sense oligo I (**SEQ. ID No:1**) in (e) above, in four 5 mg aliquots (20 mg total dose) by means of a nebulizer via endotracheal tube, as described above. The results obtained for anti-sense oligo I and its mismatch controls confirmed that the mismatch controls are equivalent to saline, as described in 45 Example 19 below and in Table 1 of Nyce & Metzger, Nature 385: 721-725 (1997). Because of this finding, saline was used as a control for pulmonary function studies employing anti-sense oligos II, III and IV (**SEQ. IS NOS; 7, 8 and 9**).

Example 12: Specificity of Oligo I for Adenosine A₁ Receptor (Receptor Binding Studies)

Tissue from airway smooth muscle was dissected to primary, secondary and tertiary bronchi from rabbits which had been administered 20 mg oligo I (**SEQ ID NO: 1**) in 4 divided doses over a period of 48 hours as described above. A membrane fraction was prepared according to the method of Ali et al. (Ali, S., et al., Am. J. Resp. Crit. Care Med. 149: 908 (1994), the relevant section relating to the preparation of the membrane fraction is incorporated in its entirety hereby by reference). The protein content was determined by the method of Bradford and plasma membranes were incubated with 0.2 U/ml adenosine deaminase for 30 minutes at 37EC to remove endogenous adenosine. See, Bradford, M. M. Anal. Biochem. 72, 240-254 (1976), the relevant portion of which is hereby incorporated in its entirety by reference. The binding of [³H]DPCPX, [³H]NPC17731, or [³H]CGS-21680 was measured as described by Jarvis et al. See, Jarvis, M.F., et al., Pharmacol. Exptl. Ther. 251, 888-893 (1989), the relevant portion of which is fully incorporated herein by reference. The results of this study are shown in Table 8 and discussed in Example 20 below.

**Example 13: Pulmonary Function Measurements
(Compliance C_{DYN} and Resistance)**

At 4 months of age, the immunized animals were anesthetized and relaxed with 1.5 ml of a mixture of ketamine HCl (35 mg/kg) and acepromazine maleate (1.5 mg/kg) administered intramuscularly. After induction of anesthesia, allergic rabbits were comfortably positioned supine on a soft molded animal board. Salve was applied to the eyes to prevent drying, and they were closed. The animals were then intubated with a 4.0 mm intermediate high-low cuffed Murphy 1 endotracheal tube (Mallinckrodt, Glen Falls, NY), as previously described by Zavala and Rhodes. See, Zavala and Rhodes, Proc. Soc. Exp. Biol. Med. 144: 509-512 (1973), the relevant portion of which is incorporated herein by reference in its entirety. A polyethylene catheter of OD 2.4 mm (Becton Dickinson, Clay Adams, Parsippany NJ) with an attached thin-walled latex balloon was passed into the esophagus and maintained at the same distance (approximately 16 cm) from the mouth throughout the experiment. The endotracheal tube was attached to a heated Fleisch pneumotach (size 00; DEM Medical, Richmond, VA), and the flow (v) measured using a Validyne differential pressure transducer (Model DP-45-16-1927, Validyne Engineering, Northridge, CA), driven by a Gould carrier amplifier (Model 11-4113, Gould Electronics, Cleveland, OH). An esophageal balloon was attached to one side of the Validyne differential pressure transducer, and the other side was attached to the outflow of the endotracheal tube to obtain transpulmonary pressure (P_{tp}). The flow was integrated to yield a continuous tidal volume, and the measurements of total lung resistance (R_t) and dynamic compliance (C_{dyn}) were made at isovolumetric and zero flow points. The flow, volume and pressure were recorded on an eight channel Gould 2000 W high-frequency recorder and C_{dyn} was calculated using the total volume and the difference in P_{tp} at zero flow, and R_t was calculated as the ratio of P_{tp} and V at midtidal lung volumes. These calculations were made automatically with the Buxco automated pulmonary mechanics respiratory analyzer (Model 6, Buxco Electronics, Sharon, CT), as previously described by Giles et al. See, Giles et al., Arch. Int. Pharmacodyn. Ther. 194: 213-232 (1971), the relevant portion of which describing these calculations is incorporated in toto hereby by reference. The results obtained upon administration of oligo II on allergic rabbits are shown and discussed in Example 26 below.

Example 14: Measurement of Bronchial Hyperresponsiveness (BHR)

Each allergic rabbit was administered histamine by aerosol to determine their baseline hyperresponsiveness. Aerosols of either saline or histamine were generated using a DeVilbiss nebulizer (DeVilbiss, Somerset, PA) for 30 seconds and then for 2 minutes at each dose employed. The ultrasonic nebulizer produced aerosol droplets of which 80% were <5 micron in diameter. The histamine aerosol was administered in increasing concentrations (0.156 to 80 mg/ml) and measurements of pulmonary function were made after each dose. The B4R was then determined by calculating the concentration of histamine (mg/ml) required to reduce the C_{dyn} 50% from baseline (PC₅₀ Histamine).

Example 15: Cardiovascular Effect of Anti-sense Oligo I

The measurement of cardiac output and other cardiovascular parameters using CardiomaxJ utilizes the principal of thermal dilution in which the change in temperature of the blood exiting the heart after a venous injection of a known volume of cool saline is monitored. A single rapid injection of cool
5 saline was made into the right atrium via cannulation of the right jugular vein, and the corresponding changes in temperature of the mixed injectate and blood in the aortic arch were recorded via cannulation of the carotid artery by a temperature-sensing miniprobe. Twelve hours after the allergic rabbits had been treated with aerosols of oligo I (EPI 2010; SEQ. ID NO: 1) as described in (d) above, the animals were anesthetized with 0.5 ml/kg of 80% Ketamine and 20% Xylazine. This time point coincides with previous
10 data showing efficacy for SEQ. ID NO: 1, as is clearly shown by Nyce & Metzger, (1997), supra, the pertinent disclosure being incorporated in its entirety here by reference. A thermocouple was then inserted into the left carotid artery of each rabbit, and was then advanced 6.5 cm and secured with a silk ligature. The right jugular vein was then cannulated and a length of polyethylene tubing was inserted and secured.
15 A thermodilution curve was then established on a CardiomaxJ II (Columbus Instruments, Ohio) by injecting sterile saline at 20EC to determine the correctness of positioning of the thermocouple probe. After establishing the correctness of the position of the thermocouple, the femoral artery and vein were isolated. The femoral vein was used as a portal for drug injections, and the femoral artery for blood pressure and heart rate measurements. Once constant baseline cardiovascular parameters were established, CardiomaxJ measurements of blood pressure, heart rate, cardiac output, total peripheral resistance, and
20 cardiac contractility were made.

Example 16: Duration of Action of Oligo I (SEQ. ID NO: 1)

Eight allergic rabbits received initially increasing log doses of adenosine by means of a nebulizer via an intra-tracheal tube as described in (f) above, beginning with 0.156 mg/ml until compliance was reduced by 50% (PC_{50} Adenosine) to establish a baseline. Six of the rabbits then received four 5 mg aerosolized
25 doses of (SEQ. ID NO: 1) as described above. Two rabbits received equivalent amounts of saline vehicle as controls. Beginning 18 hours after the last treatment, the PC_{50} Adenosine values were tested again. After this point, the measurements were continued for all animals each day, for up to 10 days. The results of this study are discussed in Example 25 below.

Example 17: Reduction of Adenosine A_{2b} Receptor**Number by Anti-sense Oligo V**

Sprague Dawley rats were administered 2.0 mg respirable anti-sense oligo V (SEQ ID NO:10) three times over two days using an inhalation chamber as described above. Twelve hours after the last administration, lung parenchymal tissue was dissected and assayed for adenosine A_{2b} receptor binding using [311]-NECA as described by Nyce & Metzger (1997), supra. Controls were conducted by administration of equal volumes of saline. The results are significant at p<0.05 using Student's paired t test, and are discussed in Example 28 below.

Example 18: Comparison of Oligo I & Corresponding Phosphodiester Oligo VI (SEQ. ID NO:1681)

Oligo I (SEQ ID NO:1) countered the effects of adenosine and eliminated sensitivity to it for
40 adenosine amounts up to 20 mg adenosine/5.0 ml (the limit of solubility of adenosine). Oligo VI (SEQ ID NO:1681), the phosphodiester version of the oligonucleotide sequence, was completely ineffective when tested in the same manner. Both compounds have identical sequence, differing only in the presence of phosphorothioate residues in Oligo I (SEQ ID NO:1), and were delivered as an aerosol as described above and in Nyce & Metzger (1997), supra. Significantly different at p<0.001, Student's paired t test. The results
45 are discussed in Example 29 below.

RESULTS OBTAINED FOR ANTI-SENSE OLIGO I (SEQ. ID NO: 1)

Example 19: Results of Prior Work

The nucleotide sequence and other data for anti-sense oligo I (SEQ. ID NO: 1), which is specific for the adenosine A₁ receptor, were provided above. The experimental data showing the effectiveness of oligo I in down regulating the receptor number and activity were also provided above. Further information on the characteristics and activities of anti-sense oligo I is provided in Nyce, J. W. and Metzger, W. J., Nature 385:721 (1997), the relevant parts of which relating to the following results are incorporated in their entireties herein by reference. The Nyce & Metzger (1997) publication provided data showing that the anti-sense oligo I (SEQ. ID NO: 1):

- (1) The anti-sense oligo I reduces the number of adenosine A₁ receptors in the bronchial smooth muscle of allergic rabbits in a dose-dependent manner as may be seen in Table 5 below.
- (2) Anti-sense Oligo I attenuates adenosine-induced bronchoconstriction and allergen-induced bronchoconstriction.
- (3) The Oligo I attenuates bronchial hyperresponsiveness as measured by PC₅₀ histamine, a standard measurement to assess bronchial hyperresponsiveness. This result clearly demonstrates anti-inflammatory activity of the anti-sense oligo I as is shown in Table 5 above.
- (4) As expected, because it was designed to target it, the anti-sense oligo I is totally specific for the adenosine A₁ receptor, and has no effect at all at any dose on either the very closely related adenosine A₂ receptor or the related bradykinin B₂ receptor. This is seen in Table 5 below.
- (5) In contradistinction to the above effects of the Oligo I, the mismatch control molecules MM2 and MM3 (SEQ. ID NO:1682 and SEQ. ID NO:1683) which have identical base composition and molecular weight but differed from the anti-sense oligo I (SEQ ID NO: 1) by 6 and 2 mismatches, respectively. These mismatches, which are the minimum possible while still retaining identical base composition, produced absolutely no effect upon any of the targeted receptors (A₁, A₂ or B₂).

These results, along with a complete lack of prior art on the use of anti-sense oligonucleotides, such as oligo I, targeted to the adenosine A₁ receptor, are unexpected results. The showings presented in this patent clearly enable and demonstrate the effectiveness, for their intended use, of the claimed agents and method for treating a disease or condition associated with lung airway, such as bronchoconstriction, inflammation, allergy(ies), and the like.

Example 20: Oligo I Significantly Reduces Response to Adenosine Challenge

The receptor binding experiment is described in Example 12 above, and the results shown in Table 5 below which shows the binding characteristics of the adenosine A₁-selective ligand [³H]DPCPX and the bradykinin E₂-selective ligand [³H]NPC 17731 in membranes isolated from airway smooth muscle of A₁ adenosine receptor and B₂ bradykinin receptor anti-sense- and mismatch-treated allergic rabbits.

Table 5: Binding Characteristics of Three Anti-Sense Oligos

Treatment ¹	A ₁ receptor		B ₂ receptor	
	Kd	B _{max}	Kd	B _{max}
Adenosine A₁	Receptor			
20 mg	0.36±0.029 nM	19±1.52 fmoles*	0.39±0.031 nM	14.8±0.99fmoles
2 mg	0.38±0.030 nM	32±2.56 fmoles*	0.41±0.028 nM	15.5±1.08
0.2 mg	0.37±0.030 nM	49±3.43 fmoles	0.34±0.024 nM	15.0±1.06
A₁MM1 (Control)				
20 mg	0.34±0.027 nM	52.0±3.64 fmoles	0.35±0.024 nM	14.0±1.0 fmoles
2 mg	0.37±0.033 nM	51.8±3.88 fmoles	0.38±0.028 nM	14.6±1.02
B₂A (Bradykinin Receptor)				
20 mg	0.36±0.028 nM	45.0±3.15 fmoles	0.38±0.027 nM	8.7±0.62

2 mg	0.39±0.035 nM	44.3±2.90 fmoles	0.34±0.024 nM	11.9±0.76
0.2 mg	0.40±0.028 nM	47.0±3.76 fmoles	0.35±0.028 nM	15.1±1.05 fmoles
B₂MM				
20 mg	0.39±0.031 nM	42.0±2.94 fmoles	0.41±0.029 nM	14.0±0.98 fmoles
2 mg	0.41±0.035 nM	40.0±3.20 fmoles	0.37±0.030 nM	14.8±0.99 fmoles
0.2 mg	0.37±0.029 nM	43.0±3.14 fmoles	0.36±0.025 nM	15.1±1.35 fmoles
Saline Control	0.37±0.041	46.0±5.21	0.39±0.047 nM	14.2±1.35 fmoles

¹ Refers to total oligo administered in four equivalently divided doses over a 48 hour period. Treatments and analyses were performed as described in methods. Significance was determined by repeated-measures analysis of variance (ANOVA), and Tukey's protected t test. n = 4-6 for all groups.

⁵ * Significantly different from mismatch control- and saline-treated groups, p<0.001;

**Significantly different from mismatch control- and saline-treated groups, p<0.05.

Example 21: Dose-response Effect of Oligo I

Anti-sense oligo I (SEQ ID NO:1) was found to reduce the effect of adenosine administration to the animal in a dose-dependent manner over the dose range tested as shown in Table 6 below.

Table 6: Dose-Response Effect to Anti-sense Oligo I

Total Dose (mg)	PC ₅₀ Adenosine (mg Adenosine)
Anti-sense Oligo I	
0.2	8.32±7.2
2.0	14.0±7.2
20	19.5±0.34
A₁MM2 oligo (control)	
0.2	2.51±0.46
2.0	3.13±0.71
20	3.25±0.34

20 The above results were studied with the Student's paired t test and found to be statistically different, p=0.05

The oligo I (SEQ. ID NO:1), an anti-adenosine A₁ receptor oligo, acts specifically on the adenosine A₁ receptor, but not on the adenosine A₂ receptors. These results stem from the treatment of rabbits with anti-sense oligo I (SEQ. ID NO:1) or mismatch control oligo (SEQ. ID NO:1682; A₁MM2) as described in Example 9 above and in Nyce & Metzger (1997), supra (four doses of 5 mg spaced 8 to 12 hours apart via nebulizer via endotracheal tube), bronchial smooth muscle tissue excised and the number of adenosine A₁ and adenosine A₂ receptors determined as reported in Nyce & Metzger (1997), supra.

Example 22: Specificity of Oligo I (SEQ. ID NO:1) for Target Gene Product

30 Oligo I (SEQ. ID No:1) is specific for the adenosine A₁ receptor whereas its mismatch controls had no activity. Figure 1 depicts the results obtained from the cross-over experiment described in Example 10 above and in Nyce & Metzger (1997), supra. The two mismatch controls (SEQ. ID NO:1682 and SEQ. ID NO:1683) evidenced no effect on the PC₅₀ Adenosine value. On the contrary, the administration of anti-sense oligo I (SEQ. ID NO:1) showed a seven-fold increase in the PC₅₀ Adenosine value. The results clearly indicate that the anti-sense oligo I (SEQ. ID NO: 1) reduces the response (attenuates the sensitivity) to exogenously administered adenosine when compared with a saline control. The results provided in Table 6 above clearly establish that the effect of the anti-sense oligo I is dose dependent (see, column 3 of Table 5). The Oligo I was also shown to be totally specific for the adenosine A₁ receptor, (see, top 3 rows of Table), inducing no activity at either the closely related adenosine A₂ receptor or the bradykinin B₂ receptor (see, lines 8-10 of Table 6 above). In addition, the results shown in Table 6 establish that the anti-sense oligo I (SEQ. ID NO:1) decreases sensitivity to adenosine in a dose dependent manner, and that it does this in an

anti-sense oligo-dependent manner since neither of two mismatch control oligonucleotides (A₁MM2; SEQ. ID NO:1682 and A MM3; SEQ. ID NO:1683) show any effect on PC_{50 Adenosine} values or on attenuating the number of adenosine A₁ receptors.

Example 23: Effect on Aeroallergen-induced Bronchoconstriction & Inflammation

The Oligo I (SEQ. ID NO:1) was shown to significantly reduce the histamine-induced effect in the rabbit model when compared to the mismatch oligos. The effect of the anti-sense Oligo I (SEQ. ID No:1) and the mismatch oligos (A₁MM2, SEQ. ID NO:1682 and A₁MM3, SEQ. ID NO:1682) on allergen-induced airway obstruction and bronchial hyperresponsiveness was assessed in allergic rabbits. The effect of the anti-sense oligo I (SEQ. ID NO:1) on allergen-induced airway obstruction was assessed. As calculated from the area under the plotted curve, the anti-sense oligo I significantly inhibited allergen-induced airway obstruction when compared with the mismatched control (55%, p<0.05; repeated measures ANOVA, and Tukey's t test). A complete lack of effect was induced by the mismatch oligo A₁MM2 (Control) on allergen induced airway obstruction. The effect of the anti-sense oligo I (SEQ. ID NO:1) on allergen-induced BHR was determined as above. As calculated from the PC_{50 Histamine} value, the anti-sense oligo I (SEQ. ID NO:1) significantly inhibited allergen-induced BHR in allergic rabbits when compared to the mismatched control (61%, p<0.05; repeated measures ANOVA, Tukey's t test). A complete lack of effect of the A₁MM mismatch control on allergen-induced BHR was observed. The results indicated that anti-sense oligo I (SEQ. ID NO:1) is effective to protect against aeroallergen-induced bronchoconstriction (house dust mite). In addition, the anti-sense oligo I (SEQ. ID NO:1) was also found to be a potent inhibitor of dust mite-induced bronchial hyper responsiveness, as shown by its effects upon histamine sensitivity which indicates anti-inflammatory activity for anti-sense oligo I (SEQ. ID NO:1).

Example 24: Anti-sense Oligo I is Free of Deleterious Side Effects

The Oligo I (SEQ. ID NO:1) was shown to be free of side effects that might be toxic to the recipient. No changes in arterial blood pressure, cardiac output, stroke volume, heart rate, total peripheral resistance or heart contractility (dPdT) were observed following administration of 2.0 or 20 mg oligo I (SEQ. ID NO:1). The addition, the results of the measurement of cardiac output (CO), stroke volume (SV), mean arterial pressure (MAP), heart rate (HR), total peripheral resistance (TPR), and contractility (dPdT) with a CardiomaxJ apparatus (Columbus Instruments, Ohio) were assessed. These results evidenced that oligo I (SEQ. ID NO:1) has no detrimental effect upon critical cardiovascular parameters. More particularly, this oligo does not cause hypotension. This finding is of particular importance because other phosphorothioate anti-sense oligonucleotides have been shown in the past to induce hypotension in some model systems. Furthermore, the adenosine A₁ receptor plays an important role in sinoatrial conduction within the heart. Attenuation of the adenosine A₁ receptor by anti-sense oligo I (SEQ. ID NO:1) might be expected to result, therefore, in deleterious extrapulmonary activity in response to the downregulation of the receptor. This is not the case. The anti-sense oligo I (SEQ. ID NO:1) does not produce any deleterious intrapulmonary effects and renders the administration of the low doses of the present anti-sense oligo free of unexpected, undesirable side effects. This demonstrates that when oligo I (SEQ. ID NO:1) is administered directly to the lung, it does not reach the heart in significant quantities to cause deleterious effects. This is in contrast to traditional adenosine receptor antagonists like theophylline which do escape the lung and can cause deleterious, even life-threatening effects outside the lung.

Example 25: Long Lasting Effect of Oligo I

The Oligo I (SEQ. ID NO:1) evidenced a long lasting effect as evidenced by the PC₅₀ and Resistance values obtained upon its administration prior to adenosine challenge. The duration of the effect was measured for with respect to the PC₅₀ of adenosine anti-sense oligo I when administered in four equal doses of 5 mg each by means of a nebulizer via an endotracheal tube, as described above. The effect of the agent is significant over days 1 to 8 after administration. When the effect of the anti-sense oligo I (SEQ. ID

5 NO:1) had disappeared, the animals were administered saline aerosols (controls), and the PC₅₀ Adenosine values for all animals were measured again. Saline-treated animals showed base line PC₅₀ adenosine values (n=6). The duration of the effect (with respect to Resistance) was measured for six allergic rabbits which were administered 20 mg of anti-sense oligo I (**SEQ. ID NO: 1**) as described above, upon airway resistance measured as also described above. The mean calculated duration of effect was 8.3 days for both PC₅₀ adenosine (p<0.05) and resistance (p<0.05). These results show that anti-sense oligo I (**SEQ. ID NO:1**) has an extremely long duration of action, which is completely unexpected.

Example 26: Anti-sense Oligo II

10 Anti-sense oligo II, targeted to a different region of the adenosine A₁ receptor mRNA, was found to be highly active against the adenosine A₁-mediated effects. The experiment measured the effect of the administration of anti-sense oligo II (**SEQ. ID NO:7**) upon compliance and resistance values when 20 mg anti-sense oligo II or saline (control) were administered to two groups of allergic rabbits as described above. Compliance and resistance values were measured following an administration of adenosine or saline as described above in Example 13. The effect of the anti-sense oligo of the invention was different 15 from the control in a statistically significant manner, p<0.05 using paired t-test, compliance; p<0.01 for resistance. The results showed that anti-sense oligo II (**SEQ. ID NO:7**), which targets the adenosine A₁ receptor, effectively maintains compliance and reduces resistance upon adenosine challenge.

Example 27: Antisense Oligos III and IV

20 Oligos III (**SEQ. ID NO:8**) and IV (**SEQ. ID NO:9**) were shown to be in fact specifically targeted to the adenosine A₃ receptor by their effect on reducing inflammation and the number of inflammatory cells present upon separate administration of 20 mg of the anti-sense oligos III (**SEQ. ID NO:8**) and IV (**SEQ. ID NO:9**) to allergic rabbits as described above. The number of inflammatory cells was determined in their bronchial lavage fluid 3 hours later by counting at least 100 viable cells per lavage. The effect of 25 anti-sense oligos III (**SEQ. ID NO:8**) and IV (**SEQ. ID NO:9**) upon granulocytes, and upon total cells in bronchial lavage were assessed following exposure to dust mite allergen. The results showed that the anti-sense oligo IV (**SEQ. ID NO:9**) and anti-sense oligo III (**SEQ. ID NO:8**) are very potent anti-inflammatory agents in the asthmatic lung following exposure to dust mite allergen. As is known in the art, granulocytes, especially eosinophils, are the primary inflammatory cells of asthma, and the administration of anti-sense oligos III (**SEQ. ID NO:8**) and IV (**SEQ. ID NO:9**) reduced their numbers by 30 40% and 66%, respectively. Furthermore, anti-sense oligos IV (**SEQ. ID NO:9**) and III (**SEQ. ID NO:8**) also reduced the total number of cells in the bronchial lavage fluid by 40% and 80%, respectively. This is also an important indicator of anti-inflammatory activity by the present anti-adenosine A₃ agents of the invention. Inflammation is known to underlie bronchial hyperresponsiveness and allergen-induced 35 bronchoconstriction in asthma. Both anti-sense oligonucleotides III (**SEQ. ID NO:8**) and IV (**SEQ. ID NO:9**), which are targeted to the adenosine A₃ receptor, are representative of an important new class of anti-inflammatory agents which may be designed to specifically target the lung receptors of each species.

Example 28: Anti-sense Oligo V

40 The anti-sense oligo V (**SEQ. ID NO:10**), targeted to the adenosine A_{2b} adenosine receptor mRNA was shown to be highly effective at countering adenosine A_{2b}-mediated effects and at reducing the number of adenosine A_{2b} receptors present to less than half.

Example 29: Unexpected Superiority of Substituted over Phosphodiester-residue Oligo I-DS (SEQ. ID NO:1681)

45 Oligos I (**SEQ. ID NO:1**) and I-DS (**SEQ. ID NO:1681**) were separately administered to allergic rabbits as described above, and the rabbits were then challenged with adenosine. The phosphodiester oligo I-DS (**SEQ. ID NO:1681**) was statistically significantly less effective in countering the effect of adenosine whereas oligo I (**SEQ. ID NO:1**) showed high effectiveness, evidencing a PC₅₀ Adenosine of 20 mg.

Example 30: Anti-sense Oligo VI

For the present work, I designed an additional anti-sense phosphorothioate oligo targeted to the adenosine A₁ receptor (Oligo VI). This anti-sense oligo was designed for therapy on a selected species as described in the above patent application and is generally specific for that species, unless the segment of the adenosine receptor mRNA of other species elected happens to have a similar sequence. The anti-sense oligos were prepared as described below, and tested in vivo in a rabbit model for bronchoconstriction, inflammation and lung allergy, which have breathing difficulties and impeded lung airways, as is the case in ailments such as asthma, as described in the above-identified application. One additional oligo and its effect in a rabbit model was studied and the results of the study are reported and discussed below. The present oligo (anti-sense oligo VI) was selected for this study to complement the data on SEQ ID NO: 1 (Oligo I), which is anti-sense to the adenosine A₁ receptor mRNA provided in the above-identified patent application. This additional oligo is identified as anti-sense Oligo VI, and is targeted to a different region of the adenosine A₁ receptor mRNA than Oligo I. The design and synthesis of this anti-sense oligo was performed in accordance with the teaching, particularly Example 1, of the above-identified patent application. The anti-sense Oligo VI is a phosphorothioate designed to target the coding region of the rabbit adenosine A₁ receptor mRNA region +964 to +984 relative to the initiation codon (start site). The Oligo VI was prepared as described in the above-indicated application, and is 20 nucleotides long. The Oligo VI is directed to the adenosine A₁ receptor gene, and has the following sequence: 5'-CGC CGG CGG GTG CGG GCC GG-3' (SEQ. ID NO: _). The phosphorothioate anti-sense Oligo VI having the sequence described in (5) above, was synthesized on an Applied Biosystems Model 396 Oligonucleotide Synthesizer, and purified using NENSORB chromatography (DuPont, DE). TETD (tetraethylthiuram disulfide) was used as the sulfurizing agent during the synthesis.

Example 31: Preparation of Allergic Rabbits

Neonatal New Zealand white Pasturella-free rabbits were immunized intraperitoneally within 24 hours of birth with 0.5 ml of 312 antigen units/ml house dust mite (*D. farinae*) extract (Berkeley Biologicals, Berkeley, CA) mixed with 10% kaolin as previously described (Metzger, W. J., in Late Phase Allergic Reactions, Dorsch, W., Ed., CRC Handbook, pp 347-362, CRC Press, Boca Raton, 1990; Ali, S. Et al., Am. J. Resp. Crit. Care Med. 149: 908 (1994)). The immunizations were repeated weekly for the first month and then bi-weekly until the animals were 4 months old. These rabbits preferentially produce allergen-specific IgE antibody, typically respond to aeroallergen challenge with both an early and late-phase asthmatic response, and show bronchial hyper responsiveness (BHR). Monthly intraperitoneal administration of alergen (312 units dust mite allergen, as above) continues to stimulate and maintain allergen-specific IgE antibody and BHR. At 4 months of age, sensitized rabbits were prepared for aerosol administration as described by Ali et al. (1994), supra.

Example 32: Adenosine Aerosol Preparation

An adenosine aerosol (20 mg/ml) was prepared with an ultrasonic nebulizer (Model 646, DeVilbiss, Somerville, PA), which produced aerosol droplets, 80% of which were smaller than 5:μm in diameter. Equal volumes of the aerosols were administered directly to the lungs via an intratracheal tube to all three rabbits. The animals were then administered the aerosolized adenosine and Day 1 pre-treatment values for sensitivity to adenosine were calculated as the dose of adenosine causing a 50% loss of compliance (PC₅₀ Adenosine). The animals were then administered the aerosolized anti-sense via the intratracheal tube (5 mg/1.0 ml), for 2 minutes, twice daily for 2 days (total dose, 20 mg). Post-treatment PC₅₀ values were recorded (post-treatment challenge) on the morning of the third day. The results of these studies are provided in (9) below.

Example 33: Anti-sense Oligo Formulation

Each one of the anti-sense oligos were separately solubilized in an aqueous solution and administered as described for anti-sense oligo I in (e) above, in four 5 mg aliquots (20 mg total dose) by means of a nebulizer via endotracheal tube, as described above.

Example 34: Oligo VI Reduces Response to Adenosine Challenge as well or Better than Oligo I

Oligo VI was tested in three allergic rabbits of the characteristics and readied as described in (7) above and in the above-indicated patent application. Oligo VI targets a section of the coding region of the A₁ receptor which is different from Oligo I. Both these target sequences were selected randomly from many possible coding region target sequences. The three rabbits were treated identically as previously indicated for Oligo I. Briefly, 5 mg of Oligo VI were nebulized to the rabbits twice per day at 8 hour intervals, for two days. Thereafter, PC₅₀ adenosine studies were performed on the morning of the third day and compared to pre-treatment PC₅₀ values. This protocol is described in more detail in Nyce and Metzger (Nyce & Metzger, Nature 385: 721-725 (1997)). The results obtained for the three rabbits are shown in Table 7 below.

Table 7: PC₅₀ Adenosine before & after Aerosolized Adenosine Treatment

Treatment Time	PC ₅₀ Adenosine (mg)
Pre-treatment	3.0 ±2.1
Post-treatment	>20.0*

* maximum achievable dose due to adenosine insolubility in saline

All three animals treated with Oligo VI completely eliminated sensitivity to adenosine up to the measurable level of the agent shown in Table 7 above. That is, the administration of the Oligo VI abrogated the adenosine-induced bronchoconstriction in the three allergic rabbits. The actual efficacy of Oligo VI is, therefore, greater than could be measured in the experimental system used. By comparing with the previously submitted results for the Oligo I, it may be seen that the Oligo VI was found to be as effective, or more, than Oligo I.

Example 34: Conclusions

The work described and results discussed in the examples clearly indicates that all anti-sense oligonucleotides designed in accordance with the teachings of the above-identified application were found to be highly effective at countering or reducing effects mediated by the receptors they are targeted to. That is, each and all of the two anti-sense oligos targeting an adenosine A₁ receptor mRNA, 1 anti-sense oligo targeting an adenosine A_{2b} receptor mRNA, and the 2 anti-sense oligos targeting an A₃ receptor mRNA were shown capable of countering the effect of exogenously administered adenosine which is mediated by the specific receptor they are targeted to. The activity of the anti-sense oligos of this invention, moreover, is specific to the target and substitutively fails to inhibit another target. In addition, the results presented also show that the administration of the present agents results in extremely low or non-existent deleterious side effects or toxicity. This represents 100% success in providing agents that are highly effective and specific in the treatment of bronchoconstriction and/or inflammation. This invention is broadly applicable in the same manner to all gene(s) and corresponding mRNAs encoding proteins involved in or associated with airway diseases. A comparison of the phosphodiester and a version of the same oligonucleotide wherein the phosphodiester bonds are substituted with phosphorothioate bonds evidenced an unexpected superiority for the phosphorothioate oligonucleotide over the phosphodiester anti-sense oligo.

Example 35: In Vivo Response to Adenosine Challenge with & without Oligo I Pretreatment

Two hyper responsive monkeys (ascaris sensitive) were challenged with inhaled adenosine, with and without pre-treatment with anti-sense oligo I (**SEQ.ID NO: 1**). The PC₄₀ adenosine was calculated from the data collected as being equivalent to that amount of adenosine in mg that causes a 40% decrease in dynamic compliance in hyper-responsive airways. The Oligo I (**SEQ. ID NO:1**; EPI 2010) was subsequently administered at 10 mg/day for 2 days by inhalation. On the third day, the PC adenosine was again measured. The PC₄₀ adenosine value prior to treatment with Oligo I was compared side-by-side with

to the PC₄₀ adenosine taken after administration of Oligo I (Figure not shown). The results of the experiment conducted with two animals showed that any sensitivity to adenosine was completely eliminated by the administration of the oligo of this invention in one animal, and substantially reduced in the second.

5 **Example 36: Extension of the experimental Results**

The method of the present invention is also practiced with anti-sense oligonucleotides targeted to many genes, mRNAs and their corresponding proteins as described above, in essentially the same manner as given above, for the treatment of various conditions in the lungs. Examples of these are Human A2a adenosine receptor, Human A2b adenosine receptor, Human IgE receptor β , Human Fc-epsilon receptor CD23 antigen (IgE receptor), Human IgE receptor, α subunit, Human IgE receptor, Fc epsilon R, Human histidine decarboxylase, Human beta tryptase, Human tryptase-I, Human prostaglandin D synthase, Human cyclooxygenase-2, Human eosinophil cationic protein, Human eosinophil derived neurotoxin, Human eosinophil peroxidase, Human intercellular adhesion molecule-1 (CAM-1), Human vascular cell adhesion molecule 1 (VCAM-1), Human endothelial leukocyte adhesion molecule (ELAM-1), Human P Selectin, Human endothelial monocyte activating factor, Human IL3, Human IL4, Human IL5, Human IL6, Human monocyte-derived neutrophil chemotactic factor, Human neutrophil elastase (medullasin), Human neutrophil oxidase factor, Human cathepsin G, Human defensin 1, Human defensin 3, Human macrophage inflammatory protein-1-alpha, Human muscarinic acetylcholine receptor HM1, Human muscarinic acetylcholine receptor HM3, Human fibronectin, Human interleukin 8, Human GM-CSF, Human tumor necrosis factor α , Human leukotriene C4 synthase, Human major basic protein, and many more.

The foregoing examples are illustrative of the present invention, and are not to be construed as limiting thereof. The invention is defined by the following claims, with equivalents of the claims to be included therein.

**WHAT IS CLAIMED AS NOVEL & UNOBlOUS
IN UNITED STATES LETTERS PATENT IS:**

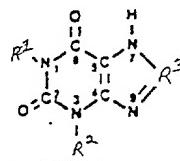
1. A pharmaceutical composition, comprising
an oligonucleotide(s) (oligo(s)) which is (are) effective for alleviating bronchoconstriction and/or
5 lung inflammation, allergy(ies), or surfactant depletion or hyposecretion, when administered to a mammal,
the oligo containing about 0 to about 15% adenosine (A) and being anti-sense to a target selected from the
group consisting of the initiation codon, the coding region, the 5'-end and the 3'-end genomic flanking
regions, the 5' and 3' intron-exon junctions, and regions within 2 to 10 nucleotides of the junctions of a
10 gene encoding a target polypeptide associated with lung airway dysfunction or anti-sense to the
polypeptide mRNA; combinations of the oligos; and mixtures of the oligos; and
a pharmaceutically or veterinarianly acceptable carrier or diluent.
2. The composition of claim 1, wherein the oligo is A-free.
3. The composition of claim 1, wherein the target is selected from the group consisting of
the initiation codon, the coding region, the 5'-end and the 3'-end genomic flanking regions, the 5' and 3'
15 intron-exon junctions, and regions within 2 to 10 nucleotides of the junctions of an oncogene(s) and a
gene(s) encoding a target polypeptide(s) associated with lung airway dysfunction or anti-sense to the
oncogene mRNA and the polypeptide mRNA; combinations of the oligos; and mixtures of the oligos; the
20 polypeptides being selected from the group consisting of peptide factors and transmitters, antibodies,
cytokines and chemokines, enzymes, binding proteins, adhesion molecules, their receptors, and malignancy
associated proteins.
4. The composition of claim 3, wherein the target is selected from the group consisting of
the initiation codon, the coding region, the 5'-end and the 3'-end genomic flanking regions, the 5' and 3'
25 intron-exon junctions, and regions within 2 to 10 nucleotides of the junctions of an oncogene(s) and a
gene(s) encoding a target polypeptide(s) associated with lung airway dysfunction or anti-sense to the
oncogene mRNA and the polypeptide mRNA; combinations of the oligos; and mixtures of the oligos;
wherein the polypeptides are selected from the group consisting of transcription factors, stimulating and
activating peptide factors, cytokines, cytokine receptors, chemokines, chemokine receptors, adenosine
30 receptors, bradykinin receptors, endogenously produced specific and non-specific enzymes,
immunoglobulins and antibodies, antibody receptors, central nervous system (CNS) and peripheral nervous
and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide
transmitters, adhesion molecules, defensins, growth factors, vasoactive peptides and receptors, binding
proteins, and malignancy associated proteins.
5. The agent of claim 4, wherein the encoded polypeptide(s) is(are) selected from the group
consisting of adenosine receptors A1, A2a, A2b and A3, bradykinin receptors B1 and B2, Nf6B
35 Transcription Factor, Interleukin-8 Receptor (IL-8 R), Interleukin 5 Receptor (IL-5 R), Interleukin 4
Receptor (IL-4 R), Interleukin 3 Receptor (IL-3 R), Interleukin-1 β (IL-1 β), Interleukin 1 β Receptor (IL-
1 β R), Eotaxin, Tryptase, Major Basic Protein, β 2-adrenergic Receptor Kinase, Endothelin Receptor A,
Endothelin Receptor B, Preproendothelin, Bradykinin B2 Receptor, IgE High Affinity Receptor,
Interleukin 1 (IL-1), Interleukin 1 Receptor (IL-1 R), Interleukin 9 (IL-9), Interleukin-9 Receptor (IL-9 R),
40 Interleukin 11 (IL-11), Interleukin-11 Receptor (IL-11 R), Inducible Nitric Oxide Synthase, Cyclo-
oxygenase-1 (COX 1), Cyclo-oxygenase-2 (COX-2), Intracellular Adhesion Molecule 1 (ICAM-1)
Vascular Cellular Adhesion Molecule (VCAM), Rantes, Endothelial Leukocyte Adhesion Molecule
(ELAM-1), Monocyte Activating Factor, Neutrophil Chemotactic Factor, Neutrophil Elastase, Defensin 1,
45 2 and 3, Muscarinic Acetylcholine Receptors, Platelet Activating Factor, Tumor Necrosis Factor α , 5-
lipoxygenase, Phosphodiesterase IV, Substance P, Substance P Receptor, Histamine Receptor, Chymase,
CCR-1 CC Chemokine Receptor, CCR-2 CC Chemokine Receptor, CCR-3 CC Chemokine Receptor,
CCR-4 CC Chemokine Receptor, CCR-5 CC Chemokine Receptor, Prostanoid Receptors, GATA-3
Transcription Factor, Neutrophil Adherence Receptor, MAP Kinase, Interleukin-9 (IL-9), NFAT
Transcription Factor, STAT 4, MIP-1 α , MCP-2, MCP-3, MCP-4, Cyclophilins, Phospholipase A2, Basic

Fibroblast Growth Factor, Metalloproteinase, CSBP/p38 MAP Kinase, Tryptose Receptor, PDG2, Interleukin-3 (IL-3), Interleukin-1 β (IL-1 β), Cyclosporin A-Binding Protein, FK5-Binding Protein, α 4 β 1 Selectin, Fibronectin, α 4 β 7 Selectin, Mad CAM-1, LFA-1 (CD11a/CD18), PECAM-1, LFA-1 Selectin, C3bi, PSGL-1, E-selectin, P-Selectin, CD-34, L-Selectin, p150,95, Mac-1 (CD11b/CD18), Fucosyl transferase, VLA-4, CD-18/CD11a, CD11b/CD18, ICAM2 and ICAM3, C5a, CCR3 (Eotaxin Receptor), CCR1, CCR2, CCR4, CCR5, LTB-4, AP-1 Transcription Factor, Protein kinase C, Cysteinyl Leukotriene Receptor, Tachykinin Receptors (tach R), I6B Kinase 1 & 2, STAT 6, c-mas and NF-Interleukin-6 (NF-IL-6).

6. The composition of claim 1, wherein one or more As is(are) substituted by a universal base selected from the group consisting of heteroaromatic bases which bind to a thymidine base but have antagonist activity and less than about 0.3 of the adenosine base agonist or antagonist activity at the adenosine A₁, A_{2a}, A_{2b} and A₃ receptors.

7. The composition of claim 6, wherein the heteroaromatic bases are selected from the group consisting of pyrimidines and purines, which may be substituted by O, halo, NH₂, SH, SO, SO₂, SO₃, COOH and branched and fused primary and secondary amino, alkyl, alkenyl, alkynyl, cycloalkyl, heterocycloalkyl, aryl, heteroaryl, alkoxy, alkenoxy, acyl, cycloacyl, arylacyl, alkynoxy, cycloalkoxy, aroyl, arylthio, arylsulfoxyl, halocycloalkyl, alkylcycloalkyl, alkenylcycloalkyl, alkynylcycloalkyl, haloaryl, alkylaryl, alkenylaryl, alkynylaryl, arylalkyl, arylalkenyl, arylalkynyl, arylcycloalkyl, which may be further substituted by O, halo, NH₂, primary, secondary and tertiary amine, SH, SO, SO₂, SO₃, cycloalkyl, heterocycloalkyl and heteroaryl.

8. The composition of claim 7, wherein the pyrimidines and purines are substituted at a position selected from the group consisting of positions 1, 2, 3, 4, 7, and 8, and the pyrimidines and purines are selected from the group consisting of theophylline, caffeine, dyphylline, etophylline, acephylline, piperazine, bamifylline, enprofylline and xantine having the chemical formula



30 wherein R¹ and R² are independently H, alkyl, alkenyl or alkynyl and R³ is H, aryl, dicycloalkyl, dicycloalkenyl, dicycloalkynyl, cycloalkyl, cycloalkenyl, cycloalkynyl, O-cycloalkyl, O-cycloalkenyl, O-cycloalkynyl, NH₂-alkylamino-ketoxyalkyloxy-aryl and mono and dialkylaminoalkyl-N-alkylamino-SO₂ aryl.

9. The composition of claim 8, wherein the universal base is selected from the group consisting of 3-nitropyrrole-2'-deoxynucleoside, 5-nitro-indole, 2-deoxyribosyl-(5-nitroindole), 2-deoxyribofuranosyl-(5-nitroindole), 2'-deoxyinosine, 2'-deoxynebularine, 6H, 8H-3,4-dihydropyrimido [4,5-c] oxazine-7-one or 2-amino-6-methoxyaminopurine.

10. The composition of claim 1, where one or more methylated cytocine(s) (^mC) is(are) substituted for a C in one or more CpG dinucleotide(s), if present in the oligo(s).

11. The composition of claim 1, wherein one or more mononucleotide(s) of the oligo(s) is(are) linked or modified by one or more methylphosphonate, 5'-N-carbamate, phosphotriester, phosphorothioate, phosphorodithioate, boranophosphate, formacetal, thioformacetal, thioether, carbonate, carbamate, sulfate, sulfonate, sulfamate, sulfonamide, sulfone, sulfite, sulfoxide, sulfide, hydroxylamine, methylene(methyimino) (MMI), methoxymethyl (MOM), methoxyethyl (MOE), methyleneoxy (methylimino) (MOMII), 2'-O-methyl, phosphoramidate, C-5 substituted residues, or combinations thereof.

12. The composition of claim 11, wherein the mononucleotide residues are linked by phosphorothioate residues.

13. The composition of claim 1, wherein the anti-sense oligo comprises about 7 to about 60 mononucleotides.

14. The composition of claim 1, wherein the anti-sense oligo comprises fragments 1, 3, 5, 7 and 8 to 2313 (SEQ. ID NOS: 1 through 2419).
15. The composition of claim 1, wherein the anti-sense oligo is operatively linked to, or complexed with, an agent selected from the group consisting of cell internalized or up-taken agents and cell targeting agents.
16. The composition of claim 15, wherein the cell internalized or up-taken agent is selected from the group consisting of transferrin, asialoglycoprotein and streptavidin.
17. The composition of claim 1, wherein the oligo is operatively linked to a vector that is a prokaryotic or eukaryotic vector.
18. The composition of claim 1, wherein the oligo(s) is(are) hybridized to a ribonucleic acid.
19. A cell, carrying the oligo of claim 1.
20. The composition of claim 1, wherein the carrier or diluent is selected from the group consisting of gaseous, liquid, and solid carriers or diluents.
21. The composition of claim 20, further comprising an agent selected from the group consisting of other therapeutic agents, surfactants, flavoring and coloring agents, fillers, volatile oils, buffering agents, dispersants, RNA inactivating agents, anti-oxidants, flavoring agents, propellants and preservatives.
22. The composition of claim 21, comprising one or more oligo(s), a surfactant, and a carrier or diluent for the oligo and the surfactant.
23. The composition of claim 21, wherein the agent is an RNA inactivating agent which comprises an enzyme, optionally an ribozyme.
24. The composition of claim 1, wherein the anti-sense oligo is present in an amount of about 0.01 to about 99.99 w/w of the composition.
25. The composition of claim 1, which is a systemic or topical formulation.
26. The formulation of claim 25, selected from the group consisting of oral, intrabuccal, intrapulmonary, rectal, intrauterine, intratunor, intracranial, nasal, intramuscular, subcutaneous, intravascular, intrathecal, inhalable, transdermal, intradermal, intracavitary, implantable, iontophoretic, ocular, vaginal, intraarticular, otical, intravenous, intramuscular, intraglandular, intraorgan, intralymphatic, implantable, slow release and enteric coating formulations.
27. The formulation of claim 26, which is an oral formulation, wherein the carrier is selected from the group consisting of solid and liquid carriers.
28. The oral formulation of claim 27, which is selected from the group consisting of a powder, dragees, tablets, capsules, sprays, aerosols, solutions, suspensions and emulsions, optionally oil-in-water and water-in-oil emulsions.
29. The formulation of claim 25, which is a topical formulation, wherein the carrier is selected from the group consisting of creams, gels, ointments, sprays, aerosols, patches, solutions, suspensions and emulsions.
30. The formulation of claim 26, which is an injectable formulation, wherein the carrier is selected from the group consisting of aqueous and alcoholic solutions and suspensions, oily solutions and suspensions and oil-in-water and water-in-oil emulsions.
31. The formulation of claim 26, which is a rectal formulation, optionally a suppository.
32. The formulation of claim 26, which is a transdermal formulation, wherein the carrier is selected from the group consisting of aqueous and alcoholic solutions, oily solutions and suspensions and oil-in-water and water-in-oil emulsions.
33. The transdermal formulation of claim 32, which is an iontophoretic transdermal formulation, wherein the carrier is selected from the group consisting of aqueous and alcoholic solutions, oily solutions and suspensions and oil-in-water and water-in-oil emulsions, and wherein the formulation further comprises a transdermal transport promoting agent.
34. The formulation of claim 26, which is provided in an implant, a capsule or a cartridge.

35. The composition of claim 20, wherein the carrier is selected from the group consisting of aqueous and alcoholic solutions and suspensions, oily solutions and suspensions and oil-in-water and water-in-oil emulsions.

36. The formulation of claim 20, wherein the carrier comprises a hydrophobic carrier.

5 37. The formulation of claim 36, wherein the carrier comprises lipid vesicles, optionally liposomes, or particles, optionally microcrystals.

38. The formulation of claim 37, wherein the carrier comprises liposomes, and the liposomes comprise the anti-sense oligo.

10 39. The formulation of claim 26, which is a respirable or inhalable formulation, optionally an aerosol.

40. The composition of claim 1, in single or multiple unit form.

41. The composition of claim 1, in bulk.

42. A kit, comprising
a delivery device;

15 in a separate container(s), the oligo(s) of claim 1; and
instructions for adding a carrier and for use of the kit.

43. The kit of claim 42, wherein the formulation is a respirable formulation and the delivery device comprises a nebulizer which delivers single metered doses of the formulation.

20 44. The kit of claim 43, wherein the nebulizer comprises an insufflator and the composition is provided in a piercable or openable capsule or cartridge.

45. The kit of claim 44, wherein the delivery device comprises a pressurized inhaler and the composition comprises a suspension, solution or dry formulation of the oligo.

25 46. The kit of claim 45, further comprising, in a separate container, an agent selected from the group consisting of other therapeutic agents, surfactants, anti-oxidants, flavoring agents, fillers, volatile oils, dispersants, antioxidants, propellants, preservatives, buffering agents, RNA inactivating agents, cell-internalized or up-taken agents and coloring agents.

47. The kit of claim 46, comprising, in separate containers, one or more oligos, one or more surfactants, and a carrier or diluent, and optionally other therapeutic agents.

48. The kit of claim 42, wherein the device is a transdermal delivery device, and the kit further comprises a transdermal delivery agent, a transdermal carrier or diluent, and instructions for preparing a transdermal delivery formulation.

49. The kit of claim 42, wherein the device is an iontophoretic delivery device, and the kit further comprises iontophoretic agents and instructions for preparing an iontophoretic formulation.

50. An in vivo method of delivering an anti-sense oligonucleotide(s) (oligo(s)) to one or 35 more target polynucleotide(s), comprising administering into the respiratory system of a subject one or more oligo(s) that are anti-sense to the polynucleotide(s), in an amount effective to reach and hybridize to the target polynucleotide(s), and reduce the production or availability, or to increase the degradation, of the target mRNA, or to reduce the amount of the target polypeptide present in the lungs.

51. An in vivo method of delivering an anti-sense oligonucleotide (oligo) to a target 40 polynucleotide associated with bronchoconstriction and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction, comprising administering to a subject the composition of claim 1, that comprises an amount of the oligo(s) effective to reach and hybridize to the target polynucleotide(s), and reduce or inhibit the polynucleotide(s)' transcription and/or expression and, thereby, alleviating bronchoconstriction and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction.

52. The method of claim 51, wherein the administered composition comprises an amount of 45 the oligo(s) and is administered under conditions effective for alleviating bronchoconstriction and/or lung inflammation, allergy(ies) and/or surfactant depletion or hyposecretion, when administered to a mammal.

53. The method of claim 51, wherein the composition is administered into the subject's respiratory system.

54. The method of claim 53, wherein the composition is administered directly into the subject's lung (s).

55. The method of claim 51, wherein the administered composition comprises an amount of the oligo(s) and is administered under conditions effective to reduce the production or availability, or to increase the degradation, of the target mRNA or to reduce the amount of the target polypeptide present in the lungs.

56. The method of claim 51, wherein the agent is administered as a respirable aerosol.

57. The method of claim 51, wherein the pulmonary obstruction, and/or bronchoconstriction and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction are associated with a disease or condition selected from the group consisting of pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and cancer.

58. The method of claim 57, wherein the disease or condition is associated with an allergy(ies), and the oligo is anti-sense to a target selected from the group consisting of the initiation codon, the coding region, the 5'-end and the 3'-end genomic flanking regions, the 5' and 3' intron-exon junctions, and regions within 2 to 10 nucleotides of the junctions of a gene(s) encoding an immunoglobulin(s) and antibody(ies) and immunoglobulin and antibody receptors or are anti-sense to the immunoglobulin(s) and antibody(ies) and immunoglobulin and antibody receptors mRNA; combinations of the oligo(s); and mixtures of the oligos.

59. The method of claim 57, wherein the disease or condition is associated with a malignancy or cancer, and the oligo is anti-sense to a target selected from the group consisting of the initiation codon, the coding region, the 5'-end and the 3'-end genomic flanking regions, the 5' and 3' intron-exon junctions, and regions within 2 to 10 nucleotides of the junctions of an oncogene(s) and/or encodes a malignancy associated protein, or is(are) anti-sense to the oncogene or malignancy associated protein mRNA; combinations of the oligo(s); and mixtures of the oligos and the oligo(s) is(are) administered in an amount effective to reduce either the level of the protein mRNA or of the malignancy associated protein, or to reduce the growth of or provide beneficial characteristics to malignant cells.

60. The method of claim 51, wherein the composition is administered transdermally or systemically.

61. The method of claim 60, wherein the composition is administered orally, intracavarily, intranasally, intraanally, intravaginally, intrauterally, intraarticularly, transdermally, intrabucally, intravenously, subcutaneously, intramuscularly, intravascularly, intratumorously, intraglandularly, intraocularly, intracranial, into an organ, intravascularly, intrathecally, intralymphatically, intraotically, by implantation, by inhalation, intradermally, intrapulmonarily, intraotically, by slow release, by sustained release and by a pump.

62. The method of claim 51, wherein the subject is a non-human mammal.

63. The method of claim 51, wherein the mammal is a human.

64. The method of claim 51, wherein the oligo is administered in amount of about 0.005 to about 150 mg/kg body weight.

65. The method of claim 51, wherein the oligo is obtained by

(a) selecting fragments of a target nucleic acid having at least 4 contiguous nucleic acids selected from the group consisting of G and C;

45 (b) obtaining a first oligonucleotide 4 to 60 nucleotides long which comprises the selected fragment and has a C and G nucleic acid content of up to and including about 15%; and

(c) obtaining a second oligonucleotide 4 to 60 nucleotides long comprising a sequence which is anti-sense to the selected fragment, the second oligonucleotide having an A base content of up to and including about 15%.

65. The method of claim 64, wherein the oligo is A-free.

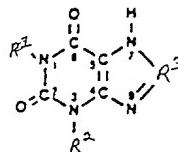
66. The method of claim 51, wherein the target is selected from the group consisting of the initiation codon, the coding region, the 5'-end and the 3'-end genomic flanking regions, the 5' and 3' intron-exon junctions, and regions within 2 to 10 nucleotides of the junctions of an oncogene or a gene encoding a target polypeptide associated with lung airway dysfunction or anti-sense to the polypeptide or oncogene mRNA; combinations of the oligo(s); and mixtures of the oligos; wherein the polypeptide is selected from the group consisting of transcription factors, stimulating and activating factors, interleukins, interleukin receptors, chemokines, chemokine receptors, endogenously produced specific and non-specific enzymes, immunoglobulins, antibody receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, adhesion molecules defensines, growth factors, vasoactive peptides, peptide receptors and binding proteins, and malignancy associated proteins.

67. The method of claim 51, wherein one or more As in the oligo(s) is(are) substituted by a universal base selected from the group consisting of heteroaromatic bases which bind to a thymidine base but have less than about 0.3 of the adenosine base agonist or antagonist activity at an adenosine A₁, A_{2a}, A_{2b} and A₃ receptors.

68. The method of claim 67, wherein the heteroaromatic bases are selected from the group consisting of pyrimidines and purines, which may be substituted by O, halo, NH₂, SH, SO, SO₂, SO₃, COOH and branched and fused primary and secondary amino, alkyl, alkenyl, alkynyl, cycloalkyl, heterocycloalkyl, aryl, heteroaryl, alkoxy, alkenoxy, acyl, cycloacyl, arylacyl, alkynoxy, cycloalkoxy, aroyl, arylthio, arylsulfonyl, halocycloalkyl, alkylcycloalkyl, alkenylcycloalkyl, alkynylcycloalkyl, haloaryl, alkylaryl, alkenylaryl, alkynylaryl, arylalkyl, arylalkenyl, arylalkynyl, arylcycloalkyl, which may be further substituted by O, halo, NH₂, primary, secondary and tertiary amine, SH, SO, SO₂, SO₃, cycloalkyl, heterocycloalkyl and heteroaryl.

69. The method of claim 67, wherein the pyrimidines and purines are substituted at positions 1, 2, 3, 4, 7 and 8 and the pyrimidines and purines are selected from the group consisting of theophylline, caffeine, dyphylline, etophylline, acephylline piperazine, bamifylline, enprofylline and xantine having the chemical formula

30



35 wherein R¹ and R² are independently H, alkyl, alkenyl or alkynyl and R³ is H, aryl, dicycloalkyl, dicycloalkenyl, dicycloalkynyl, cycloalkyl, cycloalkenyl, cycloalkynyl, O-cycloalkyl, O-cycloalkenyl, O-cycloalkynyl, NH₂-alkylamino-ketoxyalkyloxy-aryl and mono and dialkylaminoalkyl-N-alkylamino-SO₂ aryl.

70. The method of claim 69, wherein the universal base is selected from the group consisting of 3-nitropyrole-2'-deoxynucleoside, 5-nitro-indole, 2-deoxyribosyl-(5-nitroindole), 2-deoxyribofuranosyl-(5-nitroindole), 2'-deoxyinosine, 2'-deoxynebularine, 6H, 8H-3,4-dihydropyrimido[4,5-c]oxazine-7-one or 2-amino-6-methoxyaminopurine.

71. The method of claim 51, further comprising substituting a methylated cytocine (³C) for a C in one or more CpG dinucleotide(s), if present in the oligo(s).

72. The method of claim 51, further comprising substituting by, or modifying one or more nucleotide residue(s) of the oligo(s) with, methylphosphonate, phosphotriester, phosphorothioate, phosphorodithioate, organophosphate, formacetal, thioformacetal, thioether, carbonate, carbamate, sulfate, sulfonate, sulfamate, sulfonamide, sulfone, sulfite, sulfoxide, sulfide, hydroxylamine, methylene(methyimino) (MMI), methoxymethyl (MOM), methoxyethyl (MOE), methyleneoxy

(methylimino) (MOMI), methoxy methyl (MOM), 2'-O-methyl, phosphoramidate, C-5 substituted residues, or combinations thereof.

73. The method of claim 51, further comprising operatively linking to, or complexing the oligo(s) with, an agent selected from the group consisting of cell internalized and up-taken agent(s) and cell targeting agents.

74. The method of claim 73, wherein the cell internalized or up taken agent is selected from the group consisting of transferrin, asialoglycoprotein, and streptavidin.

75. The method of claim 73, wherein the cell targeting agent is a vector, optionally a prokaryotic or eukaryotic vector.

76. A method of treating a disease or condition associated with a target selected associated with a disease or condition afflicting lung airways, comprising conducting the method of claim 56.

77. The method of claim 76, wherein the amount of oligo(s) administered is (are) effective to reduce the production or availability, or to increase the degradation, of the mRNA, or to reduce the amount of the polypeptide present in the lungs.

78. The method of claim 77, wherein the amount of oligo(s) administered is (are) effective to reduce the production or availability, or to increase the degradation, of the mRNA, or to increase the amount of the surfactant present in the subject's lungs.

79. The composition of claim 4, wherein the oligo(s) is(are) anti-sense to the initiation codon, the coding region, the 5'-end and the 3'-end genomic flanking regions, the 5' and 3' intron-exon junctions, and regions within 2 to 10 nucleotides of the junctions of a gene(s) encoding an adenosine A1, A2a, A2b and/or A3 receptor, or anti-sense to the adenosine A1, A2a, A2b and/or A3 receptor mRNA.

80. The composition of claim 79, wherein all nucleotide linking residues are phosphorothioates.

81. The composition of claim 1, wherein the oligo is a DNA.

82. The composition of claim 1, wherein the oligo is an RNA.

83. The composition of claim 1, wherein the oligo comprises about 7 to up to about 60 mononucleotides.

84. The composition of claim 79, wherein the oligo(s) is selected from the group consisting of fragment(s) SEQ ID NOS: 1, 3, 5, 7, 8, and/or 11 through 2419, optionally wherein at least one mononucleotide residue is substituted or modified by methylphosphonate, phosphotriester, phosphorothioate, phosphorodithioate, boranophosphate, formacetal, thioformacetal, thioether, carbonate, carbamate, sulfate, sulfonate, sulfamate, sulfonamide, sulfone, sulfite, sulfoxide, sulfide, hydroxylamine, methylene(methylimino), (MMI), methoxymethyl (MOM), methoxyethyl (MOE), methyleneoxy (methylimino) (MOMA), methoxy methyl (MOM), 2'-O-methyl, phosphoramidate residues and/or combinations thereof.

85. The method of claim 51, wherein the oligo is administered topically to the airway, respiratory or pulmonary epithelium of the subject.

86. The composition of claim 1, wherein the oligo has a particle size of about 5-10 μm or in the range of 10-500 μm .

87. The composition of claim 1, further comprising a propellant.

88. The method of claim 50, wherein the oligo has a particle size of about 5-10 μm or in the range of 10-500 μm .

89. The method of claim 50, further comprising adding to the oligo a propellant.

90. The method of claim 51, wherein the oligo has a particle size of about 5-10 μm or in the range of 10-500 μm .

91. The method of claim 51, further comprising adding to the oligo a propellant.

**LOW ADENOSE ANTI-SENSE OLIGONUCLEOTIDE, COMPOSITIONS, KIT
& METHOD FOR TREATMENT OF AIRWAY DISORDERS ASSOCIATED
WITH BRONCHOCONSTRICKTION, LUNG INFLAMMATION,
ALLERGY(IES) & SURFACTANT DEPLETION**

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ABSTRACT OF THE INVENTION

An in vivo method of selectively delivering a nucleic acid to a target gene or mRNA, comprises the topical administration, e. g. to the respiratory system, of a subject of a therapeutic amount of an oligonucleotide (oligo) that is anti-sense to the initiation codon region, the coding region, the 5' or 3' intron-exon junction; or regions within 2 to 10 nucleotides of the junctions of the gene, or antisense to a mRNA complementary to the gene in an amount effective to reach the target polynucleotide and reducing or inhibiting express on. In addition a method of treating an adenosine mediated effect, comprises topically administering to a subject an anti-sense oligo in an amount effective to treat the respiratory, pulmonary, or airway disease. In order to minimize triggering adenosine receptors by their metabolism, the administered oligos have a low content of or are essentially free of adenosine. A pharmaceutical composition and formulations comprise the oligo anti-sense to an adenosine receptor, genes and mRNAs encoding them, genomic and mRNA flanking regions, intron and exon borders and all regulatory and functionally related segments of the genes and mRNAs encoding the polypeptides, their salts and mixtures. Various formulations contain a requisite carrier, and optionally other additives and biologically active agents. The low adenosine or adenosine free (des-A) agent for practicing the method of the invention may be prepared by selecting a target gene(s), genomic flanking region(s), RNA(s) and/or polypeptide(s) associated with a disease(s) or condition(s) afflicting lung airways, obtaining the sequence of the mRNA(s) corresponding to the target gene(s) and/or genomic flanking region(s), and/or RNAs encoding the target polypeptide(s), selecting at least one segment of the mRNA which may be up to 60% free of thymidine (T) and synthesizing one or more anti-sense oligonucleotide(s) to the mRNA segments which are free of adenosine (A) by substituting a universal base for A when present in the oligonucleotide. The agent may be prepared by selection of target nucleic acid sequences with GC running stretches, which have low T content, and by optionally replacing A in the anti-sense oligonucleotides with a "Universal or alternative base". The agent, composition and formulations are used for prophylactic, preventive and therapeutic treatment of ailments associated with impaired respiration, lung allergy(ies) and/or inflammation and depletion lung surfactant or surfactant hypoproduction, such as pulmonary vasoconstriction, inflammation, allergies, allergic rhinitis, asthma, impeded respiration, lung pain, cystic fibrosis, bronchoconstriction. The present treatment is suitable for administration in combination with other treatments, e.g. before, during and after other treatments, including radiation, chemotherapy, antibody therapy and surgery, among others. Alternatively, the present agent is effectively administered prophylactically or therapeutically by itself for conditions without known therapies or as a substitute for therapies exhibiting undesirable side effects. The treatment of this invention may be administered directly into the respiratory system of a subject so that the agent has direct access to the lungs, or by other effective routes of administration, e. g. topically, transdermally, by implantation, etc., in an amount effective to reduce or inhibit the symptoms of the ailment.